

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 15:40:17 : Search time 371.501 Seconds
(without alignments)
11372.097 Million cell updates/sec

Title: US-09-944-896-49

Perfect score: 1876

Sequence: 1 cctctttgtccaccagccca.....tcagctgaaaaaaaaaaaaa 1876

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

1: /SID22/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SID22/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SID22/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SID22/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SID22/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
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14: /SID22/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
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20: /SID22/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1876	100.0	1876	20	AA87260		CDNA clone encoding
2	1876	100.0	1876	20	AA80053		Human PRO347 nucle
3	1876	100.0	1876	21	AAA46918		CDNA encoding nove
4	1876	100.0	1876	21	AAA49561		Human PRO347 cDNA.
5	1776.2	94.7	1923	22	AA24152		Human secreted pro
6	1751	93.3	1856	20	AA23299		Human T139 protein
7	1751	93.3	1856	24	AD33531		Human T139 (TANGO-
8	1729.8	92.2	1786	22	AAK94246		Human full-length
9	1721	91.7	1775	22	AAAD12570		Human protein havi

10	1636	87.2	1934	23	AA591790	DNA encoding novel
11	1293	68.9	1338	20	AA223300	Human T139 protein
12	889.4	47.4	1519	23	AA576344	DNA encoding novel
13	766.6	40.9	906	23	AA576343	DNA encoding novel
14	672.8	35.9	690	21	AAA70010	Human ovarian carc
15	672.8	35.9	690	24	ABN72904	Ovarian carcinoma
16	617	32.9	855	21	AA250926	Human Protease and
17	518	27.6	602	23	AA581209	DNA encoding novel
18	451	24.0	517	22	AAH98469	Human EST-derived
19	432.6	23.1	512	22	AAK91830	Human CDNA 5'-end
20	432.6	23.1	512	22	AAK93233	Human CDNA clone r
21	234.8	12.5	792	23	AA576345	DNA encoding novel
22	191.2	10.2	3660	23	AA588505	DNA encoding novel
23	191.2	10.2	3660	23	AA589242	DNA encoding novel
24	144.8	7.7	3660	23	AA588505	DNA encoding novel
25	144.8	7.7	3660	23	AA589242	DNA encoding novel
26	137.4	7.3	480	23	AA581207	DNA encoding novel
27	133.2	7.1	1482	23	AA581210	DNA encoding novel
28	129.4	6.9	168	23	AA591789	DNA encoding novel
29	95.8	5.1	915	23	AA581206	DNA encoding novel
30	94.6	5.0	1239	23	AA573137	DNA encoding novel
31	56.8	3.0	1759	24	ABL57727	Human sbg1002620TI
32	56.8	3.0	1494	24	ABL57728	Human sbg1002620TI
33	56.8	3.0	3483	24	AAAD38692	Human LP095 secret
34	55.2	2.9	939	22	AAH98687	Rat EST-derived co
35	55.2	2.9	1491	22	AAH77686	Human protease-inh
36	55.2	2.9	1669	22	AAAD17765	Human novel trypsi
37	55.2	2.9	1690	22	AAH15690	Human cDNA sequenc
38	55.2	2.9	1824	24	ABK33563	CDNA encoding huma
39	55.2	2.9	2272	22	AAH77687	Human protease-inh
40	55.2	2.9	3836	24	AAAL39682	Human secreted pro
41	55.2	2.9	4877	22	AA560871	Human cancer agent
42	55.2	2.9	4877	22	AA560872	Human cancer agent
43	55.2	2.9	4877	22	AA560883	Human novel trypsi
44	55	2.9	2403	22	AAAD17766	Human CDNA clone (
45	54.6	2.9	840	22	AAH05058	

ALIGNMENTS

RESULT 1

AA87260

ID AA87260 standard; cDNA; 1876 BP.

XX AA87260;

AC AA87260;

XX 27-SEP-1999 (first entry)

XX CDNA clone encoding human PRO347, amplified in tumour cells.

XX PRO347; UNQ305; cancer; tumour; diagnosis; therapy; human; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 123..1490

XX sig_peptide /*tag= a

XX mat_peptide /*tag= b

XX /*tag= c

XX WO9935170-A2.

XX 15-JUL-1999.

XX 05-JAN-1999; 99WO-US00106.

XX 20-NOV-1998; 98US-0109304.

XX 05-JAN-1998; 98US-0070440.

XX 29-APR-1998; 98US-0083500.

XX 22-MAY-1998; 98US-0086414.

PR 10-JUN-1998; 98US-0088742.
XX 10-NOV-1998; 98US-0107783.
PA (GETH) GENENTECH INC.
XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
PI Roy MA, Wood WI;
XX WPI; 1999-430385/36.
DR P-PSDB; AAY06483.
XX
PT Antibody against proteins expressed in neoplastic cells, useful for
PT tumor diagnosis and treatment
XX
PS Example 1; Fig 13; 162pp; English.
XX
CC This is the nucleotide sequence of cDNA clone DNA44176 (ATCC 209532)
CC coding for human PRO347 (UNQ306) (see AAY06482). The clone was
CC isolated from a foetal kidney library. Amplification of DNA44176
CC occurs in various tumours, suggesting an association with tumour
CC formation or growth. Antagonists (e.g. antibodies) directed against
CC PRO347 may have use in cancer therapy. The invention identifies 14
CC genes (see AAX87234-67) that are amplified in the genome of tumour
CC cells. Such amplification is expected to be associated with
CC overexpression of the gene product and to contribute to
CC tumorigenesis. The encoded proteins (see AAY06477-90) may be useful
CC targets for the diagnosis and/or treatment (including prevention)
CC of certain cancers, and may act as predictors of the prognosis of
CC tumour treatment.
XX
SQ Sequence 1876 BP; 387 A; 568 C; 574 G; 347 T; 0 other;

Query Match 100.0%; Score 1876; DB 20; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTTTGTCCACAGCCAGCCCTGACTCTCTGGAGATTGTGAATAGCTCCATCCAGCCCG 60
DB 1 CTCCTTTGTCCACAGCCAGCCCTGACTCTCTGGAGATTGTGAATAGCTCCATCCAGCCCG 60
QY 61 AGAAACAAGCCGGGTGCTGAGCCAGGCTGTGCAGGGAGCACCCTGACGGGCCCAACAGAC 120
DB 61 AGAAACAAGCCGGGTGCTGAGCCAGGCTGTGCAGGGAGCACCCTGACGGGCCCAACAGAC 120
QY 121 CCATGCTGCATCAGAGACCTCCCTGCGCGGGGCGCATCTCTGCTGTGCTCTGCTGGCCCC 180
DB 121 CCATGCTGCATCAGAGACCTCCCTGCGCGGGGCGCATCTCTGCTGTGCTCTGCTGGCCCC 180
QY 181 TCCTTGGCACACCTGGGCGAGAGGTGTGGCCACCCAGCTGCAGAGCAGGCTCCGATGG 240
DB 181 TCCTTGGCACACCTGGGCGAGAGGTGTGGCCACCCAGCTGCAGAGCAGGCTCCGATGG 240
QY 241 CCGGAGCCCTGAACAGAGGAGATTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB 241 CCGGAGCCCTGAACAGAGGAGATTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 301 GCTGGGTCCAGCCCTGCGGCTGACATGCGGAGGCTGAGCTGGAGTGACAGCCTGGCCCC 360
DB 301 GCTGGGTCCAGCCCTGCGGCTGACATGCGGAGGCTGAGCTGGAGTGACAGCCTGGCCCC 360
QY 361 AACTGGCTCAAGCCAGGCGCCCTCTGTGGAATCCCAACCCAGCCTGGCATCCGGCC 420
DB 361 AACTGGCTCAAGCCAGGCGCCCTCTGTGGAATCCCAACCCAGCCTGGCATCCGGCC 420
QY 421 TGTGGCCACCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCCGGGGCTTGGGCTCCT 480
DB 421 TGTGGCCACCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCCGGGGCTTGGGCTCCT 480
QY 481 TTGTTGAAGTGGTCAAGCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACCGCGCAGGAG 540
DB 481 TTGTTGAAGTGGTCAAGCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACCGCGCAGGAG 540
QY 541 AGTGTGCTCGCAAGCCACCTGCAACCCACTACAGCAGCTCGTGTGGGCCCACTCAAGCC 600

DB 541 AGTGTGCTCGCAAGCCACCTGCAACCCACTACAGCAGCTCGTGTGGGCCACCTCAAGCC 600
QY 601 AGCTGGGCTGTGGCGGCACCTGTGCTCTGCAAGGCAGACAGCATAGAGCCCTTTGTCT 660
DB 601 AGCTGGGCTGTGGCGGCACCTGTGCTCTGCAAGGCAGACAGCATAGAGCCCTTTGTCT 660
QY 661 GTGCTTACTCCCGGGAGGCAACTGGAGGTCAACGGGAAGACAATCATCCCTATAGA 720
DB 661 GTGCTTACTCCCGGGAGGCAACTGGAGGTCAACGGGAAGACAATCATCCCTATAGA 720
QY 721 AGGTGCTGTGTTGGTCTGTCACAGCAGTGTCTCAGGCTGCTTCAAGACCTGGGACC 780
DB 721 AGGTGCTGTGTTGGTCTGTCACAGCAGTGTCTCAGGCTGCTTCAAGACCTGGGACC 780
QY 781 ATGCAGGGGGCTCTGTGAGGTCCCGAGGAATCTTGTGCTGATGCTGCCAGAACATG 840
DB 781 ATGCAGGGGGCTCTGTGAGGTCCCGAGGAATCTTGTGCTGATGCTGCCAGAACATG 840
QY 841 GACGTCTCAACATCAGCACCTGCCACTGCTGCTCCCTGCTGCTACACGGGAGAGTACT 900
DB 841 GACGTCTCAACATCAGCACCTGCCACTGCTGCTCCCTGCTGCTACACGGGAGAGTACT 900
QY 901 GCCAAGTGAAGTGCAGCTGAGTGTGTCAGCGCGGCTTCCGGGAGGAGTGTCTCGT 960
DB 901 GCCAAGTGAAGTGCAGCTGAGTGTGTCAGCGCGGCTTCCGGGAGGAGTGTCTCGT 960
QY 961 GCGTCTGTGACATCGGCTACGGGGAGGCCAGTGTGCCACCAAGGTGCTATTTCCCTTCC 1020
DB 961 GCGTCTGTGACATCGGCTACGGGGAGGCCAGTGTGCCACCAAGGTGCTATTTCCCTTCC 1020
QY 1021 ACACCTGTGACCTGAGGATCGACGGAGACTGCTTCTATGTTGCTTTCAGAGGAGACACT 1080
DB 1021 ACACCTGTGACCTGAGGATCGACGGAGACTGCTTCTATGTTGCTTTCAGAGGAGACACT 1080
QY 1081 ATTACAGAGCCAGGATGAATGTGAGAGAAAGGGGGGTGCTGCGCCACATCAAGAGCC 1140
DB 1081 ATTACAGAGCCAGGATGAATGTGAGAGAAAGGGGGGTGCTGCGCCACATCAAGAGCC 1140
QY 1141 AGAAGTGCAGGACATCCTCGCTTCTATCTGCGCGCCCTGGAGACCAACAGAGGTGA 1200
DB 1141 AGAAGTGCAGGACATCCTCGCTTCTATCTGCGCGCCCTGGAGACCAACAGAGGTGA 1200
QY 1201 CTGACAGTGAATTCAGAGACCAAGAACTTCTGATCGGGTCACTTCAAGACGCCCAAG 1260
DB 1201 CTGACAGTGAATTCAGAGACCAAGAACTTCTGATCGGGTCACTTCAAGACGCCCAAG 1260
QY 1261 ACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCTTCCAGCTTTTGGCTTTGGGCAGC 1320
DB 1261 ACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCTTCCAGCTTTTGGCTTTGGGCAGC 1320
QY 1321 CTGACAACACCGGCTGTGTGCTGAGTGTGCTGCTGAGTGTGGCACTGCTGCTGGAGC 1380
DB 1321 CTGACAACACCGGCTGTGTGCTGAGTGTGCTGCTGAGTGTGGCACTGCTGCTGGAGC 1380
QY 1381 TGCAGGCTTCAAGTCCCTTCAACTGGAACGACCCAGGCTGCAAAACCCGAAACCGTTACA 1440
DB 1381 TGCAGGCTTCAAGTCCCTTCAACTGGAACGACCCAGGCTGCAAAACCCGAAACCGTTACA 1440
QY 1441 TCTGCCAGTTTGGCCACAGGACATCTCCGGTGGGGGCCAGGGTCTCTGAGGCTTGACCA 1500
DB 1441 TCTGCCAGTTTGGCCACAGGACATCTCCGGTGGGGGCCAGGGTCTCTGAGGCTTGACCA 1500
QY 1501 CATGGCTCCCTGCTGCTGCTGGAGCAGCGGCTGTGCTTACCTGTCTGCTGCCACCTGTCT 1560
DB 1501 CATGGCTCCCTGCTGCTGCTGGAGCAGCGGCTGTGCTTACCTGTCTGCTGCCACCTGTCT 1560
QY 1561 GGAACAAGGGCCAGGTTAAGACACATGCTCATGTCCAAAGAGGTCTCAGACCTTGAC 1620
DB 1561 GGAACAAGGGCCAGGTTAAGACACATGCTCATGTCCAAAGAGGTCTCAGACCTTGAC 1620
QY 1621 AATGCCACAAGTTGGCAGAGAGCAGGGAGGCCAGTGTGAGGCCAGGAGTGTGAGTGT 1680

Db 1621 AATGCCAGAAATTGGCAGAGAGAGCAGGAGGCCAGTCCAGTCCAGGCGGAGTGGT 1680
 Qy 1681 AGAAGAAGCTGGGGCCCTTCGCTGCTTTGATGGGAAGATGGCTTCAATTAGATGGC 1740
 Db 1681 AGAAGAAGCTGGGGCCCTTCGCTGCTTTGATGGGAAGATGGCTTCAATTAGATGGC 1740
 Qy 1741 GAAGGAGAGACACCGCCAGTGGTCCAAAAGGCTGCTCTTCCACCTGGCCAGACCC 1800
 Db 1741 GAAGGAGAGACACCGCCAGTGGTCCAAAAGGCTGCTCTTCCACCTGGCCAGACCC 1800
 Qy 1801 TGTGGGCGACGGAGCTTCCTCTGGCATGAACCCACGGGGTATTAAATTATGAATCAG 1860
 Db 1801 TGTGGGCGACGGAGCTTCCTCTGGCATGAACCCACGGGGTATTAAATTATGAATCAG 1860
 Qy 1861 CTGAAAAA 1876
 Db 1861 CTGAAAAA 1876

RESULT 2

AAX80053

ID AAX80053 standard; cDNA; 1876 BP.

XX AC

XX AC

XX AC

DT 12-AUG-1999 (first entry)

XX DE

XX DE

XX DE

KW Human PRO347 nucleotide sequence.
 KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
 KW secreted protein; transmembrane protein; inflammation disorder; ss.

XX OS

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CC and primers. They can be used in a range of diseases related to proteins
 CC that they have homology with, e.g. a PRO protein having homology to
 CC complement proteins may be used in inflammatory responses.

XX

SQ

Sequence

1876 BP;

387 A;

568 C;

574 G;

347 T;

0 other;

Query Match

Best Local Similarity

100.0%;

Score 1876;

DB 20;

Length 1876;

Matches 1876;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Qy

Db

Qy

Db

Qy

Db

Qy

Db

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Db

Nucleic acids encoding PRO secreted and transmembrane proteins

Claim 2; Fig 22; 123pp; English.

The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes

Db	181	TCCTTGSCACCACTGGCGAGAGGTGTGGCCACCCCAAGCTGCAGGACGACGCTCCGATGG	240
Qy	241	CCGAGGCCCTGAACAGAGAAAGAGATTTCCTTGCTCTCCCTGCACAACCGCTCGGCA	300
Db	241	CCGAGGCCCTGAACAGAGAAAGAGATTTCCTTGCTCTCCCTGCACAACCGCTCGGCA	300
Qy	301	GCTGGGTTCAGCCCCCTGCGGCTGCATATGCGGAGGCTGGACTGGAGTGACAGCTCGGCC	360
Db	301	GCTGGGTTCAGCCCCCTGCGGCTGCATATGCGGAGGCTGGACTGGAGTGACAGCTCGGCC	360
Qy	361	AACGTGCTCAAGCCAGCGCAGCCCTCTGTGGAATCCCAACCCCGAGGCTGSCATCCGGCC	420
Db	361	AACGTGCTCAAGCCAGCGCAGCCCTCTGTGGAATCCCAACCCCGAGGCTGSCATCCGGCC	420
Qy	421	TGTGGCGCAOCCCTGCAAGTGGGCTGGAACTATGCACTGCTGCCCCGGGGCTTGGCGTCT	480
Db	421	TGTGGCGCAOCCCTGCAAGTGGGCTGGAACTATGCACTGCTGCCCCGGGGCTTGGCGTCT	480
Qy	481	TTGTTGAAGTGGTCAGCCTATGTGTTTCAGAGGGCAGCGGTACAGCCACGCGCAGGAG	540
Db	481	TTGTTGAAGTGGTCAGCCTATGTGTTTCAGAGGGCAGCGGTACAGCCACGCGCAGGAG	540
Qy	541	AGTGTGCTCGCAACGCCCACTGCACCCACTACACGCACTCGTGTGGGCCACCTCAAGCC	600
Db	541	AGTGTGCTCGCAACGCCCACTGCACCCACTACACGCACTCGTGTGGGCCACCTCAAGCC	600
Qy	601	AGCTGGGCTGTGGGGCGCACCTGTGCTCTCAGAGCCACAGCAGCATAGAACCTTTGTCT	660
Db	601	AGCTGGGCTGTGGGGCGCACCTGTGCTCTCAGAGCCACAGCAGCATAGAACCTTTGTCT	660
Qy	661	GTGCTACTCTCCCGGAGGCAACTGGGAGGTCAACGGGAAGACATATCCCTATAAGA	720
Db	661	GTGCTACTCTCCCGGAGGCAACTGGGAGGTCAACGGGAAGACATATCCCTATAAGA	720
Qy	721	AGGTTGCCTGGTGTGCTCTGCACAGCCAGTGTCTCAGGCTGCTCAAAGCTGGGACC	780
Db	721	AGGTTGCCTGGTGTGCTCTGCACAGCCAGTGTCTCAGGCTGCTCAAAGCTGGGACC	780
Qy	781	ATGCAGGGGGGCTCTGTGAGGTCCCCAGGAATCCCTGTGCGATGAGCTGCCAAGCCATG	840
Db	781	ATGCAGGGGGGCTCTGTGAGGTCCCCAGGAATCCCTGTGCGATGAGCTGCCAAGCCATG	840
Qy	841	GACGTCTCAACATCAGCACTGCCACTGGCACTGTCCCTCGGCTACAGGGCAGATACT	900
Db	841	GACGTCTCAACATCAGCACTGCCACTGGCACTGTCCCTCGGCTACAGGGCAGATACT	900
Qy	901	GCCAAAGTAGGTCAGCCTGCACTGTGTGTCAGCGCCGCTTCGGGAGGAGTGTCTGT	960
Db	901	GCCAAAGTAGGTCAGCCTGCACTGTGTGTCAGCGCCGCTTCGGGAGGAGTGTCTGT	960
Qy	961	GCGTCTGTGCATCAGCTGCTACGGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCC	1020
Db	961	GCGTCTGTGCATCAGCTGCTACGGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCC	1020
Qy	1021	ACACCTGTACCTGAGGATCGACGGAGCTGCTTCATGTGTCTTCAGAGGACAGACCT	1080
Db	1021	ACACCTGTACCTGAGGATCGACGGAGCTGCTTCATGTGTCTTCAGAGGACAGACCT	1080
Qy	1081	ATTACAGAGCCAGGATGAATGTACAGGAAAGCGGGGTGCTGGCCCCAGATCAAGAGCC	1140
Db	1081	ATTACAGAGCCAGGATGAATGTACAGGAAAGCGGGGTGCTGGCCCCAGATCAAGAGCC	1140
Qy	1141	AGAAAGTAGGACATCTTCGCGCTTATCTGGGCCGCTTGGAGACCAACCAAGAGTGA	1200
Db	1141	AGAAAGTAGGACATCTTCGCGCTTATCTGGGCCGCTTGGAGACCAACCAAGAGTGA	1200
Qy	1201	CTCAGAGTGACTTCGAGACCAAGAACTTCTGGAATCGGGCTCACTACAAGACCGCCAAAG	1260
Db	1201	CTCAGAGTGACTTCGAGACCAAGAACTTCTGGAATCGGGCTCACTACAAGACCGCCAAAG	1260
Qy	1261	ACTCTCTCGCTGGGCGCACAGGGGAGCACAGGCCCTTCAACAGTTTGGCGGACG	1320
Db	1261	ACTCTCTCGCTGGGCGCACAGGGGAGCACAGGCCCTTCAACAGTTTGGCGGACG	1320

Qy	1321	CTGACAAACCACGGGCTGGTGTGGCTGAGTGTGCTGCCATGGGGTTTGGCAACTGCCGTGGAGC	1380
Db	1321	CTGACAAACCACGGGCTGGTGTGGCTGAGTGTGCTGCCATGGGGTTTGGCAACTGCCGTGGAGC	1380
Qy	1381	TGCAGGCTTCAGCTGCGCTTCAACTGGAACGACGACGCTGCAAAACCCGAAACCGTTACA	1440
Db	1381	TGCAGGCTTCAGCTGCGCTTCAACTGGAACGACGACGCTGCAAAACCCGAAACCGTTACA	1440
Qy	1441	TCTGCCAGTTTGGCCAGGAGCACATCTCCCGGTGGGGCCCCAGGGTCTGTGAGGCCTTGACCA	1500
Db	1441	TCTGCCAGTTTGGCCAGGAGCACATCTCCCGGTGGGGCCCCAGGGTCTGTGAGGCCTTGACCA	1500
Qy	1501	CATGGCTCCCTCGCCTGCCCTGGGAGACCGGCTCTGCTTACCTGTCTGCCACCTGTCT	1560
Db	1501	CATGGCTCCCTCGCCTGCCCTGGGAGACCGGCTCTGCTTACCTGTCTGCCACCTGTCT	1560
Qy	1561	GGAACAAGGGCCAGGTTAAGACCAATGCCTCATGTCTCCAAAGAGGTCTCAGACCTTGCAC	1620
Db	1561	GGAACAAGGGCCAGGTTAAGACCAATGCCTCATGTCTCCAAAGAGGTCTCAGACCTTGCAC	1620
Qy	1621	AATGCCAGAAGTTGGGCAGAGAGAGGACGGAGGCCAGTTCAGGGCCAGGAGTGAGTGT	1680
Db	1621	AATGCCAGAAGTTGGGCAGAGAGAGGACGGAGGCCAGTTCAGGGCCAGGAGTGAGTGT	1680
Qy	1681	AGAAAGCTGGGGCCCTTCGCCTTCGCTTTGATTTGGAAGATGGGCTTCAATTAGATGGC	1740
Db	1681	AGAAAGCTGGGGCCCTTCGCCTTCGCTTTGATTTGGAAGATGGGCTTCAATTAGATGGC	1740
Qy	1741	GAAGGAGAGGACACCGCCAGTGGTCTCCAAAAGAGCTCTCTTCCACCTGGCCCCAGACCC	1800
Db	1741	GAAGGAGAGGACACCGCCAGTGGTCTCCAAAAGAGCTCTCTTCCACCTGGCCCCAGACCC	1800
Qy	1801	TGTGGGCGACGGAGCTTCCTGTGTCATGAACCCACGGGGTATTAAATTATCAATCAG	1860
Db	1801	TGTGGGCGACGGAGCTTCCTGTGTCATGAACCCACGGGGTATTAAATTATCAATCAG	1860
Qy	1861	CTCAAAAAAAAAAAAAA	1876
Db	1861	CTCAAAAAAAAAAAAAA	1876
RESULT 4			
AAA49561			
ID	AAA49561 standard; cDNA; 1876 BP.		
XX			
AC	AAA49561;		
XX			
DT	25-SEP-2000 (first entry)		
XX			
DE	Human PRO347 cDNA.		
XX			
KW	PRO; membrane bound protein; secreted protein; PRO357; PRO327;		
KW	PRO243; PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347;		
KW	PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;		
KW	antibody; screening; detection; inhibition; probe; primer; human;		
XX	ss.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	123..1490	
FT		/*tag= a	
FT		/product= PRO347 polypeptide	
XX	WO200032776-A2.		
PN			
XX	08-JUN-2000.		
XX			
PF	01-DEC-1999;	99WO-US28301.	
XX			
PF	01-DEC-1998;	98WO-US25108.	
PR			
PR	16-DEC-1998;	98US-0112850.	

PR 22-DEC-1998; 98US-0113296.
XX (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
XX WPI; 2000-412324/35.
DR P-PSDB; AAB01319.
XX
PT New human nucleic acids encoding secreted and transmembrane
PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
PT and diagnostic agents
XX
PS Claim 2; Fig 19; 187pp; English.
XX
CC New human nucleic acids encoding secreted and transmembrane
CC polypeptides which are designated as PRO polypeptides are described
CC The membrane-bound proteins have various industrial applications,
CC including as pharmaceutical and diagnostic agents. The membrane-bound
CC proteins can also be employed for screening of potential peptide or
CC small molecule inhibitors of the relevant receptor/ligand interaction.
CC Anti-PRO antibodies are useful for the affinity purification of PRO
CC from recombinant cell culture or natural sources.
XX
SQ Sequence 1876 BP; 387 A; 568 C; 574 G; 347 T; 0 other;

Query Match 100.0%; Score 1876; DB 21; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCTTTGTCCACAGCCAGCCGCTGCTCTCTGGAGATTGTAAGTCCATCCAGCCCTG 60
DB 1 CTCTTTGTCCACAGCCAGCCGCTGCTCTCTGGAGATTGTAAGTCCATCCAGCCCTG 60

QY 61 AGAAACAAGCCGGGTGCTGAGCCAGGCTGTGTCACGAGCAGCTGACGGGCCAACAGAC 120
DB 61 AGAAACAAGCCGGGTGCTGAGCCAGGCTGTGTCACGAGCAGCTGACGGGCCAACAGAC 120

QY 121 CCATGTCGATCCAGAGACCTCCCTGGCCGGGGGATCTCTCTGGCTGTGCTCTGGGCC 180
DB 121 CCATGTCGATCCAGAGACCTCCCTGGCCGGGGGATCTCTCTGGCTGTGCTCTGGGCC 180

QY 181 TCCTTGGCACCACCTGGGAGAGGTTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 TCCTTGGCACCACCTGGGAGAGGTTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 240

QY 241 CCGAGCCCTGAACAGGAAGGAGTTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB 241 CCGAGCCCTGAACAGGAAGGAGTTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300

QY 301 GCTGGTCCAGCCCTGGGCTGACATCGGAGGCTGGACTGGAGTGCAGCCTGSCCC 360
DB 301 GCTGGTCCAGCCCTGGGCTGACATCGGAGGCTGGACTGGAGTGCAGCCTGSCCC 360

QY 361 AACTGGCTCAAGCCAGGCGAGCCCTCTGTGGAACTCCACCCAGCCCTGGATCCGGCC 420
DB 361 AACTGGCTCAAGCCAGGCGAGCCCTCTGTGGAACTCCACCCAGCCCTGGATCCGGCC 420

QY 421 TGTGGCGACCTGCAAGTGGGCTGGAACATGCAGCTGTGCTGGCCGGGCTTGGCGTCT 480
DB 421 TGTGGCGACCTGCAAGTGGGCTGGAACATGCAGCTGTGCTGGCCGGGCTTGGCGTCT 480

QY 481 TTGTTGAAGTGTGAGCTATGTTTGCAGAGGGGAGCGGTACACCCAGCGGAGAG 540
DB 481 TTGTTGAAGTGTGAGCTATGTTTGCAGAGGGGAGCGGTACACCCAGCGGAGAG 540

QY 541 AGTGTGCTCGCAACGCCACCTGCACCCACTACACGAGCTGTGTGGGCCACCTCAAGC 600
DB 541 AGTGTGCTCGCAACGCCACCTGCACCCACTACACGAGCTGTGTGGGCCACCTCAAGC 600

QY 601 AGCTGGGCTGTGGGGGCGACCTGCTCTGTCAGGCCAGACAGCATAGAGCTTTGTCT 660

DB 601 AGCTGGGCTGTGGGGCGACCTGTGCTCTGCGAGCCAGACGCGATAGAACCTTTGTCT 660
QY 661 GTGCTACTCCCCCGAGGCAACTGGGAGGTCAACGGGAAGACATATCCCTATAAGA 720
DB 661 GTGCTACTCCCCCGAGGCAACTGGGAGGTCAACGGGAAGACATATCCCTATAAGA 720
QY 721 AGGTGCTGCTGTGCTCTGTCACAGCCAGTGTCTCAGGCTGTCTCAAGGCTGGGACC 780
DB 721 AGGTGCTGCTGTGCTCTGTCACAGCCAGTGTCTCAGGCTGTCTCAAGGCTGGGACC 780
QY 781 ATCAGGGGGGCTGTGAGTCCCGGAGGATCTTGTGCGATGAGCTGCCAGAACATG 840
DB 781 ATCAGGGGGGCTGTGAGTCCCGGAGGATCTTGTGCGATGAGCTGCCAGAACATG 840
QY 841 GAGCTCTCAACATCAGCACCTGCCACTGCCACTGTCCCTCTGCTACACGGGCGATACT 900
DB 841 GAGCTCTCAACATCAGCACCTGCCACTGCCACTGTCCCTCTGCTACACGGGCGATACT 900
QY 901 GCCAAGTGTGCTGAGTGTGTCACAGCCGCTGTCACGGCCGGTTCGGGAGGAGGAGTCT 960
DB 901 GCCAAGTGTGCTGAGTGTGTCACAGCCGCTGTCACGGCCGGTTCGGGAGGAGGAGTCT 960
QY 961 GGTCTGTGACATCGCTACGGGGGAGCCAGTGTGTCACCAAGTGCATTTTCCCTTCC 1020
DB 961 GGTCTGTGACATCGCTACGGGGGAGCCAGTGTGTCACCAAGTGCATTTTCCCTTCC 1020
QY 1021 ACACCTGTGCTGAGTGTGTCACGGAGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTG 1080
DB 1021 ACACCTGTGCTGAGTGTGTCACGGAGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 ATTACAGAGCCAGGATGAATGTGTCAGAGGAAAGCGGGGTGCTGGGCCAGATCAAGAG 1140
DB 1081 ATTACAGAGCCAGGATGAATGTGTCAGAGGAAAGCGGGGTGCTGGGCCAGATCAAGAG 1140
QY 1141 AGAAAGTGCAGGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
DB 1141 AGAAAGTGCAGGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1201 CTGACAGTGTGCTGAGACCCAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB 1201 CTGACAGTGTGCTGAGACCCAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY 1261 ACTCTTCCGCTGGGCGCCAGGGGAGCAGCAGGCTTCAACAGCTTTGCTTTGGGCGAG 1320
DB 1261 ACTCTTCCGCTGGGCGCCAGGGGAGCAGCAGGCTTCAACAGCTTTGCTTTGGGCGAG 1320
QY 1321 CTGACACCCAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
DB 1321 CTGACACCCAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
QY 1381 TGCAGGCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
DB 1381 TGCAGGCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
QY 1441 TCTGCCAGTTTCCAGGAGCAGATCTCCCGTGGGGCCAGGGTCTGAGGCTGACCA 1500
DB 1441 TCTGCCAGTTTCCAGGAGCAGATCTCCCGTGGGGCCAGGGTCTGAGGCTGACCA 1500
QY 1501 CATGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1501 CATGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 1561 GGAACAAGGGCCAGGTTAAGACCATGCTTCAAGAGGCTTCAAGAGGCTTCAAGAGGCT 1620
DB 1561 GGAACAAGGGCCAGGTTAAGACCATGCTTCAAGAGGCTTCAAGAGGCTTCAAGAGGCT 1620
QY 1621 AATGCCAGAGTTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
DB 1621 AATGCCAGAGTTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1680
QY 1681 AGAGAAGGCTGGGGCCCTTCCCTGCTTTGATGGGAGATGGCTTCAATTAGATGGC 1740
DB 1681 AGAGAAGGCTGGGGCCCTTCCCTGCTTTGATGGGAGATGGCTTCAATTAGATGGC 1740

[illegible]

PR 23-APR-1998; 98US-0065363.
 PR 23-APR-1998; 98US-0065661.
 PR 22-JUN-1998; 98US-0102705.
 PR 29-JUL-1998; 98US-0124538.
 PR 23-APR-1999; 99US-0298531.
 PR 22-JUN-1999; 99US-0337930.
 PR 29-JUL-1999; 99US-0363630.
 XX
 PA (HOLT/) HOLTZMAN D A.
 PA (GOOD/) GOODEARL A D J.
 PA (MCCA/) MCCARTHY S A.
 XX
 PI Holtzman DA, Goodearl ADJ, McCarthy SA;
 XX
 DR WPI; 2002-303420/34.
 DR P-PSDB; AAE21077.
 XX
 PT Novel TANGO polypeptides and nucleic acid molecules useful as
 PT modulating agents in regulating cellular processes and for diagnosing
 PT and treating heart, liver, lung, kidney, inflammatory and cellular
 PT proliferative disorders
 XX
 PS Claim 26: Fig 1; 138pp; English.
 XX
 CC The invention relates to nucleic acids encoding a variety of proteins
 CC human T139 (TANGO-139), T125 (TANGO-125), T110 (TANGO-110), murine T175
 CC (TANGO-175), human T175 or murine WDNM-2, having diagnostic, preventive,
 CC therapeutic and other uses. Polypeptide of the invention has the ability
 CC to inhibit a proteinase activity, to modulate cell-cell interactions,
 CC haemopoiesis and the ability to modulate clotting. Polypeptide and
 CC polynucleotide of the invention are useful for diagnosing and treating
 CC disorder characterised by their aberrant expression or activity. The
 CC antibodies are useful as modulating agents in regulating a variety of
 CC cellular processes e.g. cell proliferation and/or cell differentiation.
 CC TANGO-139 is useful for treating kidney defects such as kidney failure.
 CC TANGO-125 is useful in wound healing and for treating cancer. TANGO-110
 CC is useful for treating neoplasia, TANGO-177 or WDNM-2 is useful for
 CC treating cancer, are useful to treat pancreatic disorders, such as
 CC pancreatitis, cerebrovascular disease, and tumours, and injury or trauma
 CC to the brain. TANGO-125, 110, 175 molecules treat heart disorders, e.g.,
 CC ischaemic heart disease, cardiovascular disorders, such as ischaemic
 CC heart disease. TANGO-139, 125, 110 and 175 molecules are useful to treat
 CC renal (kidney) disorders, such as glomerular disease (e.g. acute and
 CC chronic glomerulonephritis). TANGO-175 is useful to treat uterine
 CC disorders, hyperplasia of the endometrium. TANGO-110 is useful to treat
 CC spleen, e.g., the fetal spleen, associated diseases and disorder. TANGO-
 CC 125 treats prostate disorders, such as inflammatory diseases, Crohn's
 CC disease and tumours. TANGO-139, 125, 110, 175 or WDNM-2 are useful for
 CC treating proliferative disorders, inflammatory disorders. TANGO-175, or
 CC WDNM-2 activity also include apoptotic disorders, rheumatoid arthritis,
 CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,
 CC immune-related disorders, e.g., immunodeficiency disorders, viral
 CC disorders, cell growth disorders, e.g., cancers and inflammatory
 CC disorders and apoptotic disorders. The nucleic acids of the invention
 CC are used in gene therapy. The present sequence is human T139 cDNA.
 XX
 SQ Sequence 1856 BP; 402 A; 560 C; 564 G; 330 T; 0 other;

Query Match 93.3%; Score 1751; DB 24; Length 1856;
 Best Local Similarity 98.0%; Pred. No. 0;
 Matches 1794; Conservative 0; Mismatches 10; Indels 27; Gaps 1;

QY	46	GCTCCATCCAGCGCTGAGAAACAGCGGGTGGCTGAGCCAGGCTGTGCACGGAGCCACTG	105
Db	18	GCTCCATCCAGCGCTGAGAAACAGCGGGTGGCTGAGCCAGGCTGTGCACGGAGTGCCTG	77
QY	106	ACGGGGCCCAACAGACCCATGCTGATCCAGAGACCTCCCTGCCCGGGGCACTCTCCTGG	165
Db	78	ACGGGGCCCAACAGACCCATGCTGATCCAGAGACCTCCCTGCCCGGGGCACTCTCCTGG	137
QY	166	CTGTGCTCTGCGCCCTCTTGGCACCACCTGGGCGAGAGTGTGGCCACCCAGCTGAGG	225
Db	138	CTGTGCTCTGCGCCCTCTTGGCACCACCTGGGCGAGAGTGTGGCCACCCAGCTGAGG	197
QY	226	ACAGAGGCTCCATGCCCGGAGGCCCTTGAAACAGAGAGAGTTTCTTGCTCTCCTCCCTGC	285
Db	198	ACAGAGGCTCCATGCCCGGAGGCCCTTGAAACAGAGAGAGTTTCTTGCTCTCCTCCCTGC	257
QY	286	ACAACCGCTCGCAGCTGGCTCCAGCCGCTCGCGCTGACATGCGGAGCTGGAGTGA	345
Db	258	ACAACCGCTCGCAGCTGGCTCCAGCCGCTCGCGCTGACATGCGGAGCTGGAGTGA	317
QY	346	GTGACAGCTTGGCCCAACTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCCGA	405
Db	318	GTGACAGCTTGGCCCAACTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCCGA	377
QY	406	GCTTGGCATCGGCGCTGTGGCGCACCTGCAAGTGGGCTGGAACATGACAGTGTCCCG	465
Db	378	GCTTGGCATCGGCGCTGTGGCGCACCTGCAAGTGGGCTGGAACATGACAGTGTCCCG	437
QY	466	CGGCTTGGCGTCCCTTTGTTGAAGTGTGACGCTATGCTTTCAGAGGGGAGCGGTACA	525
Db	438	CGGCTTGGCGTCCCTTTGTTGAAGTGTGACGCTATGCTTTCAGAGGGGAGCGGTACA	497
QY	526	GCCACGGGCGAGAGTGTCTCGCAACGCCACCTTGCACCCACTACAGCAGCTCGTGT	585
Db	498	GCCACGGGCGAGAGTGTCTCGCAACGCCACCTTGCACCCACTACAGCAGCTCGTGT	557
QY	586	GGGCCACCTCAAGCCAGCTGGCTGTGGCGGACCTGTGCTTCGAGGCGCAGACGGA	645
Db	558	GGGCCACCTCAAGCCAGCTGGCTGTGGCGGACCTGTGCTTCGAGGCGCAGACGGA	617
QY	646	TAGAAGCCTTTGCTGTGCTTACTTCCCGGAGGCAACTGGGAGTCAACGGGAGACAA	705
Db	618	TAGAAGCCTTTGCTGTGCTTACTTCCCGGAGGCAACTGGGAGTCAACGGGAGACAA	677
QY	706	TCATCCCTTATAGAGGGTGCCTGTGTTGCTTTCGACAGCAGTGTCTCAGGCTGCT	765
Db	678	TCATCCCTTATAGAGGGTGCCTGTGTTGCTTTCGACAGCAGTGTCTCAGGCTGCT	737
QY	766	TCAAAGCCTTGGGACCATGAGGGGGCTGTGAGGTCCCGAGGAATCTTGTGCGCATGA	825
Db	738	TCAAAGCCTTGGGACCATGAGGGGGCTGTGAGGTCCCGAGGAATCTTGTGCGCATGA	797
QY	826	GCTGCCAAGAACCATGACGCTTCAACATCAGCACCTGCCACTGCCCTCCCTCCCTGCT	885
Db	798	GCTGCCAAGAACCATGACGCTTCAACATCAGCACCTGCCACTGCCCTCCCTCCCTGCT	857
QY	886	ACACGGGCGAGTACTGCCAAGTGAAGTGCAGCTGCAGCTGCAGCTGCCACTGGCTGG	945
Db	858	ACACGGGCGAGTACTGCCAAGTGAAGTGCAGCTGCAGCTGCAGCTGCCACTGGCTGG	917
QY	946	AGGAGAGTGTCTCGTGGCTGTGACATCGGCTACCGGGGAGCCAGTGTGCCACCAAGG	1005
Db	918	AGGAGAGTGTCTCGTGGCTGTGACATCGGCTACCGGGGAGCCAGTGTGCCACCAAGG	977
QY	1006	TGCAATTTTCCTTCCACACCTGTGACCTGAGGATGACGAGAGTGTCTTATCGTGTCTT	1065
Db	978	TGCAATTTTCCTTCCACACCTGTGACCTGAGGATGACGAGAGTGTCTTATCGTGTCTT	1037
QY	1066	CAGAGCGAGACACCTATTACAGAGCCAGATGAAATGTTCAGAGGAAGCGGGGTGCTGG	1125
Db	1038	CAGAGCGAGACACCTATTACAGAGCCAGATGAAATGTTCAGAGGAAGCGGGGTGCTGG	1097
QY	1126	CCAGATCAAGAGCCAGAAAGTGCAGGACATCTCGCTTCTATCTGGGCGGCTGGAGA	1185
Db	1098	CCAGATCAAGAGCCAGAAAGTGCAGGACATCTCGCTTCTATCTGGGCGGCTGGAGA	1157
QY	1186	CCACCAAGAGTGTGACTGACAGTGTGAGACACAGGAACTTCGGAATCGGCTCACCT	1245
Db	1158	CCACCAAGAGTGTGACTGACAGTGTGAGACACAGGAACTTCGGAATCGGCTCACCT	1217
QY	1246	ACAAGACGCCAAGAGTCTCTTCCGCTGGGCCACAGGGGAGCACACAGGCTTCCACAGTT	1305
Db	1218	ACAAGACGCCAAGAGTCTCTTCCGCTGGGCCACAGGGGAGCACACAGGCTTCCACAGTT	1277

830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation -

Claim 8; SEQ ID NO 2850; 1380pp + sequence listing; English.

The invention relates to primers for synthesizing full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3'-ends of the cDNA molecules have been determined. Primers for synthesizing the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.

Sequence 1786 BP; 361 A; 548 C; 553 G; 324 T; 0 other;

Query Match 92.2%; Score 1729.8; DB 22; Length 1786;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 12; Indels 27; Gaps 1;

51 ATCCAGCCTGAGAAACAGCGGGTGGCTGAGCCAGAGCTGTGACGAGACACCTGACGGG 110
1 ATCCAGCCTGAGAAACAGCGGGTGGCTGAGCCAGAGCTGTGACGAGACACCTGACGGG 60
111 CCCAACAGACCCATGCTGATCCAGAGACCTCCCTGGCGGGGGCATCTCTGGCTGTG 170
61 CCCAACAGACCCATGCTGATCCAGAGACCTCCCTGGCGGGGGCATCTCTGGCTGTG 120
171 CTCCTGCGCCCTGCTGGCACCACCTGGCAGAGAGTGTGGCCACCCAGCTCAGAGAGCAG 230
121 CTCCTGCGCCCTGCTGGCACCACCTGGCAGAGAGTGTGGCCACCCAGCTCAGAGAGCAG 180
231 GCTCCGATGGCGGAGCCCTGAACAGAGAGAGATTTCTTGTCTCTCTCCCTGCACAC 290
181 GCTCCGATGGCGGAGCCCTGAACAGAGAGAGATTTCTTGTCTCTCTCCCTGCACAC 240
291 CGCCTGGCAGCTGGTCCAGCCCTCGCTGACATCGCAGAGCTGAGCTGAGTGCAC 350
241 CGCCTGGCAGCTGGTCCAGCCCTCGCTGACATCGCAGAGCTGAGCTGAGTGCAC 300
351 AGCCTGGCCCAACTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCGAGCCTG 410
301 AGCCTGGCCCAACTGGCTCAAGCCAGGCGAGCCCTCTGTGGAACCCCAACCCGAGCCTG 360
411 GCATCCGCGCTGTGGCGACCCCTGCAAGTGGCTGGAACATGACATGCTGCTGCCCGGGC 470
361 GCGTCCGCGCTGTGGCGACCCCTGCAAGTGGCTGGAACATGACATGCTGCTGCCCGGGC 420
471 TTGGCGTCTTTTGAAGTGGTCAAGCTATGTTTGGAGAGGGGAGGGGTACAGCCAC 530
421 TTGGCGTCTTTTGAAGTGGTCAAGCTATGTTTGGAGAGGGGAGGGGTACAGCCAC 480
531 GCGGAGGAGAGTGTGCTGCAAGCCAGCTGCACCCACTACAGCAGCTCTGTGTGGGC 590
481 GCGGAGGAGAGTGTGCTGCAAGCCAGCTGCACCCACTACAGCAGCTCTGTGTGGGC 540
591 ACCTCAAGCCAGCTGGGCTGTGGGCGCACCTGTGCTGTGAGGGCCAGACAGCATAGAA 650
541 ACCTCAAGCCAGCTGGGCTGTGGGCGCACCTGTGCTGTGAGGGCCAGACAGCATAGAA 600
651 GCCTTTGTCTGTGCTTACTCCCGGAGGCACTGGGAGGTCAACGGGAGAGACATC 710
601 GCCTTTGTCTGTGCTTACTCCCGGAGGCACTGGGAGGTCAACGGGAGAGACATC 660
711 CCCTATAAGAGGTCCTGGTGTCTGCTGACAGCCAGTGTCTCAGGCTGCTTCAAA 770
661 CCCTATAAGAGGTCCTGGTGTCTGCTGACAGCCAGTGTCTCAGGCTGCTTCAAA 720
771 GCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCGGAGGAATCTTGTGCGATGAGCTGC 830

1306 TTGCTTTGGGAGCCTGACAAACACGGCTGGTGGCTGAGTGTGCTGCCATGGGTTTG 1365
1278 TTGCTTTGGGAGCCTGACAAACAC-----GGGTTTG 1310
1366 GCAACTGGCTGGAGTGGAGGCTTCAAGTGGCTTCAACTGGAAACACAGCCTGCARAA 1425
1311 GCAACTGGCTGGAGTGGAGGCTTCAAGTGGCTTCAACTGGAAACACAGCCTGCARAA 1370
1426 CCCGAACCGTTACATCTGCCAGTTTGGCCAGGAGCACATCTCCGGTGGGCGCCAGGCT 1485
1371 CCCGAACCGTTACATCTGCCAGTTTGGCCAGGAGCACATCTCCGGTGGGCGCCAGGCT 1430
1486 CCGTGGGCTGACCATGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1545
1431 CCGTGGGCTGACCATGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1490
1546 TCTGCCACCTGCTGGAACAGGCGCAGGTTAAGACACATGCTCATGTCCAAAGAGG 1605
1491 TCGGCCACCTGCTGGAACAGGCGCAGGTTAAGACACATGCTCATGTCCAAAGAGG 1550
1606 TCTCAGACCTTGCACATGCGAAGTGTGGCAGAGAGAGGAGGAGGAGGAGGAGGAGG 1665
1551 TCTCAGACCTTGCACATGCGAAGTGTGGCAGAGAGAGGAGGAGGAGGAGGAGGAGG 1610
1666 CAGGAGTGTGTAGAGAGCTGGGCGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1725
1611 CAGGAGTGTGTAGAGAGCTGGGCGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1670
1726 CTTCAATTAGATGGGAGAGGAGGACACCGCCAGTGTGTCACAAAGAGGCTCTCTTCC 1785
1671 CTTCAATTAGATGGGAGAGGAGGACACCGCCAGTGTGTCACAAAGAGGCTCTCTTCC 1730
1786 ACCTGGCCAGACCTGTGGGAGGAGGAGCTTCCCTGCTGCTGCTGCTGCTGCTGCTG 1845
1731 ACCTGGCCAGACCTGTGGGAGGAGGAGCTTCCCTGCTGCTGCTGCTGCTGCTGCTG 1790
1846 TAAATTATGATCAGCTGAAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1876
1791 TAAATTATGATCAGCTGAAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1821

RESULT 8
AAK94246
ID AAK94246 standard; cDNA; 1786 BP.
AC AAK94246;
XX AAK94246;
XX AAK94246;
DT 06-NOV-2001 (first entry)
XX Human full-length cDNA, SEQ ID NO: 2850.
DE Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX Homo sapiens.
XX EP1130094-A2.
XX 05-SEP-2001.
XX 07-JUL-2000; 2000EP-0114089.
XX 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
XX (HELI-) HELIX RES INST.
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2001-524255/58.
DR P-PSDB; AAM93326.
XX

CC microbial infections and autoimmune disorders such as multiple sclerosis,
 CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
 CC haematopoiesis, to modulate tissue growth activity (e.g. for the
 CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
 CC disease), to modulate cell division and inhibit activity (e.g. for controlling
 CC fertility), to modulate chemotactic and chemokinetic activity, to
 CC modulate haemostatic and thrombolytic activity, to modulate receptor
 CC ligand activity, to modulate inflammation and to inhibit tumour growth.
 XX
 XX

Sequence 1775 BP; 360 A; 541 C; 549 G; 325 T; 0 other;

Query Match 91.7%; Score 1721; DB 22; Length 1775;

Best Local Similarity 97.9%; Pred. No. 0;

Matches 1764; Conservative 0; Mismatches 10; Indels 27; Gaps 1;

QY	63	AAACAAAGCCGGTGGCTGAGCCAGGCTGACAGGAGACCTGACGGGCCACACAGCC	122
Db	2	AAACAAAGCCGGTGGCTGAGCCAGGCTGACAGGAGTGCCTGACGGGCCACACAGCC	61
QY	123	ATGCTGCATCCAGAGACCTCCCTGGCCGGGGGCATCTCTTGCTGTGCTCTGGCCCTC	182
Db	62	ATGCTGCATCCAGAGACCTCCCTGGCCGGGGGCATCTCTTGCTGTGCTCTGGCCCTC	121
QY	183	CTTGGCAGCAGCTGGGAGAGGTGTGGCCACCCAGCTGCAGGAGGCTCCGATGGCC	242
Db	122	CTTGGCAGCAGCTGGGAGAGGTGTGGCCACCCAGCTGCAGGAGGCTCCGATGGCC	181
QY	243	GGAGCCCTGAACAGGAGAGAGTTCTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	302
Db	182	GGAGCCCTGAACAGGAGAGAGTTCTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	241
QY	303	TGGGTTCAGCCCTGGCGGTGACATCCGAGGCTGACCTGGAGTGACAGCTGGGCCAA	362
Db	242	TGGGTTCAGCCCTGGCGGTGACATCCGAGGCTGACCTGGAGTGACAGCTGGGCCAA	301
QY	363	CTGGCTCAAGCAGGAGGAGCCCTCTGTGAAATCCCAACCCGAGCCCTGGCATCCGGCTG	422
Db	302	CTGGCTCAAGCAGGAGGAGCCCTCTGTGAAATCCCAACCCGAGCCCTGGCATCCGGCTG	361
QY	423	TGGCGCACCTTGAAGTGGGTGAAATGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG	482
Db	362	TGGCGCACCTTGAAGTGGGTGAAATGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG	421
QY	483	GTTGAAGTGGTCAAGCTATGTTTGCAGAGGCGAGCGGTACAGCCAGCGCGGAGAG	542
Db	422	GTTGAAGTGGTCAAGCTATGTTTGCAGAGGCGAGCGGTACAGCCAGCGCGGAGAG	481
QY	543	TGTGCTCGCAACGGCACCCTGCACCCACTACAGCAGCTCGTGTGGGCCACCTCAAGCCAG	602
Db	482	TGTGCTCGCAACGGCACCCTGCACCCACTACAGCAGCTCGTGTGGGCCACCTCAAGCCAG	541
QY	603	CTGGCTGTGGCGGCACCTGTGCTCTGAGGCCAGAGCGATAGAGCCCTTTCTGCTGT	662
Db	542	CTGGCTGTGGCGGCACCTGTGCTCTGAGGCCAGAGCGATAGAGCCCTTTCTGCTGT	601
QY	663	GCTACTCTCCCGAGGCAACTGGAGGTCAACGGGAGAGCAATCATCCCTATAGAAG	722
Db	602	GCTACTCTCCCGAGGCAACTGGAGGTCAACGGGAGAGCAATCATCCCTATAGAAG	661
QY	723	GCTGCTGTGGTGTGCTGTGACAGCAGTGTCTGAGGCTGCTTCAAGCCCTGGGACCAT	782
Db	662	GCTGCTGTGGTGTGCTGTGACAGCAGTGTCTGAGGCTGCTTCAAGCCCTGGGACCAT	721
QY	783	GCAGGGGGCTCTGTGAGTGTCCCGAGGAATCTTGTGCGATGAGCTGCCAGAACCATGGA	842
Db	722	GCAGGGGGGGCTCTGTGAGTGTCCCGAGGAATCTTGTGCGATGAGCTGCCAGAACCATGGA	781
QY	843	CGTCTCAACATCAGACACCTGCCACTGTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTG	902
Db	782	CGTCTCAACATCAGACACCTGCCACTGTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTG	841
QY	903	CAAGTGAAGTGCAGCCCTGCAGTGTGTGCAGGCGCGGTTCGGGAGGAGGAGTCTGCTGC	962

Db	842	CAAGTGAAGTGCAGCCTGCAGTGTGTGCAGCGCGGTTCCGGGAGGAGGAGTCTCGTGC	901
QY	963	GTCTGTGACATCGGTACGGGGAGGCCAGTGTGCCACCAAGTGCATTTCCCTTCCAC	1022
Db	902	GTCTGTGACATCGGTACGGGGAGGCCAGTGTGCCACCAAGTGCATTTCCCTTCCAC	961
QY	1023	ACCTGTGACCTGAGGATGACGAGAGTGTCTCATGCTGTCTTCAGAGGAGACACCTAT	1082
Db	962	ACCTGTGACCTGAGGATGACGAGAGTGTCTCATGCTGTCTTCAGAGGAGACACCTAT	1021
QY	1083	TACAGAGCCAGGATGAAATGTTCAGAGAAAGCGGGGTGCTGCCCCAGATCAAGAGCCAG	1142
Db	1022	TACAGAGCCAGGATGAAATGTTCAGAGAAAGCGGGGTGCTGCCCCAGATCAAGAGCCAG	1081
QY	1143	AAAGTCAGGACATCTCGCTTCTATCTGGGCCCTGAGACCAACCAAGAGGTGACT	1202
Db	1082	AAAGTCAGGACATCTCGCTTCTATCTGGGCCCTGAGACCAACCAAGAGGTGACT	1141
QY	1203	GACAGTGACTTTCAGAGACAGGAATCTTGTGATCGGGCTCACTTACAAAGCCGCCAAGGAC	1262
Db	1142	GACAGTGACTTTCAGAGACAGGAATCTTGTGATCGGGCTCACTTACAAAGCCGCCAAGGAC	1201
QY	1263	TCCTTCGGCTGGGCCACAGGGAGCAGCCTTCCAGTGTTCCTTGGGAGCCT	1322
Db	1202	TCCTTCGGCTGGGCCACAGGGAGCAGCCTTCCAGTGTTCCTTGGGAGCCT	1261
QY	1323	GACAAACACCGGCTGGTGTGGCTGAGTGTGCCATGGGGTTTGCAACTGGGAGGCTG	1382
Db	1262	GACAAACACCGGCTGGTGTGGCTGAGTGTGCCATGGGGTTTGCAACTGGGAGGCTG	1294
QY	1383	CAGGCTTTCAGTGTGCTTCAACTGGAACAGCAGCGCTGCAAAACCCGAAACCGTTACATC	1442
Db	1295	CAGGCTTTCAGTGTGCTTCAACTGGAACAGCAGCGCTGCAAAACCCGAAACCGTTACATC	1354
QY	1443	TGCCAGTTTGGCCAGGAGCAGTCTCCCGGTGGGGCCCGAGGCTCTGAGGCTGACACCA	1502
Db	1355	TGCCAGTTTGGCCAGGAGCAGTCTCCCGGTGGGGCCCGAGGCTCTGAGGCTGACACCA	1414
QY	1503	TGGCTCCCTCGCTGCGCTGGGAGACCGGCTCTGCTTACCTGTCTGCCACCTCTCTGG	1562
Db	1415	TGGCTCCCTCGCTGCGCTGGGAGACCGGCTCTGCTTACCTGTCTGCCACCTCTCTGG	1474
QY	1563	AACAAGGCCAGGTAAAGACACACATGCTCATGTCCAAAGAGTCTCAGACCTTGACACA	1622
Db	1475	AACAAGGCCAGGTAAAGACACACATGCTCATGTCCAAAGAGTCTCAGACCTTGACACA	1534
QY	1623	TGCCAAGAGTTGGGCAGAGAGAGGAGGAGGCCAGTGTAGGGCCAGGAGTGTGTAG	1682
Db	1535	TGCCAAGAGTTGGGCAGAGAGAGGAGGAGGCCAGTGTAGGGCCAGGAGTGTGTAG	1594
QY	1683	AAGAAGCTGGGGCCCTTGGCCCTGCTTTGATTTGGGAAGATGGCTTCAATTAGATGGCGA	1742
Db	1595	AAGAAGCTGGGGCCCTTGGCCCTGCTTTGATTTGGGAAGATGGCTTCAATTAGATGGCGA	1654
QY	1743	AGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTCTCCACTGCCCCAGACCCCTG	1802
Db	1655	AGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTCTCCACTGCCCCAGACCCCTG	1714
QY	1803	TGGGCGAGCGGAGCTTCCCTGTGGCATGAACCCACGGGTTTAAATTAATGAATCAGCT	1862
Db	1715	TGGGCGAGCGGAGCTTCCCTGTGGCATGAACCCACGGGTTTAAATTAATGAATCAGCT	1774
QY	1863	G 1863	
Db	1775	G 1775	

RESULT 10
 AAS91790
 ID AAS91790 standard; cDNA; 1934 BP.
 XX
 AAS91790;
 XX

DT XX 13-FEB-2002 (first entry)
DE XX DNA encoding novel human diagnostic protein #27594.
KW XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX DR P-PSDB; ABG27603.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PS biodiversity -
XX PS Claim 1; SEQ ID No 27594; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC imaging of sites expressing (II). (I) and (II) are useful in medical
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. AAS64197-AAS94564 represent novel human
XX CC diagnostic coding sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 1934 BP; 409 A; 577 C; 576 G; 372 T; 0 other;

Query Match 87.2%; Score 1636; DB 23; Length 1934;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 1803; Conservative 0; Mismatches 45; Indels 50; Gaps 9;

QY 2 TCTTTTGTCCACAGCCGACCTGACCTCTGGAGATGTGAATAGCTCCATCCAGCCCTGA 61
DB 60 TCTTTTGTCCACAGCCGACCTGACCTCTGGAGATGTGAATAGCTCCATCCAGCCCTGA 119

QY 62 GAAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGACC 121
DB 120 GAAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCCCTGACGGGCCCAACAGACC 179

QY 122 CATGCTGCATCAGAGACCTCCCTGGCGGGGGGACATCTCTGGCTGTGCTCTGGCCCT 181
DB 180 CATGCTGCATCAGAGACCTCCCTGGCGGGGGGACATCTCTGGCTGTGCTCTGGCCCT 239

QY 182 CCTTGGCACCACTGGGAGAGTGTGGGCCACCCGACGCTGCAGGAGCGCTCCGATGGC 241

DB 240 CCTTGGCACCACTGGGAGAGTGTGGGCCACCCGACGCTGCAGGAGCGCTCCGATGGC 299
QY 242 CGGAGCCCTGAACAGGAAGGAGAGTTCCTGCTCTCTCCCTGCACAAACCCGCTGGCGAG 301
DB 300 CGGAGCCCTGAACAGGAAGGAGAGTTCCTGCTCTCTCCCTGCACAAACCCGCTGGCGAG 359
QY 302 CTGGGTCCAGCCCTCTGGGCTGACATCGGAGGCTGGAGTGCAGAGCTTGGCCCA 361
DB 360 CTGGGTCCAGCCCTCTGGGCTGACATCGGAGGCTGGAGTGCAGAGCTTGGCCCA 419
QY 362 ACTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCAAACCCGAGCCTGGCGCT 421
DB 420 GCTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCAAACCCGAGCCTGGCGCT 479
QY 422 GTGGCGCACCTTGCAGTGGGCTGGAAACATGCAGCTGCTGCCCGGGCTTGGCTTCCTT 481
DB 480 GTGGCGCACCTTGCAGTGGGCTGGAAACATGCAGCTGCTGCCCGGGCTTGGCTTCCTT 539
QY 482 TGTGTAAGTGGTCAAGCTATGTTTGCAGAGGGGAGCGGTACAGCCACGCGGAGGAGA 541
DB 540 TGTGTAAGTGGTCAAGCTATGTTTGCAGAGGGGAGCGGTACAGCCACGCGGAGGAGA 599
QY 542 GTGTGCTCGCAACGCCACCTGCACCCACTACACGAGCTCGTGTGGGCGACCTCAAGCCA 601
DB 600 GTGTGCTCGCAACGCCACCTGCACCCACTACACGAGCTCGTGTGGGCGACCTCAAGCCA 659
QY 602 GCTGGGCTGTGGGCGGACCTGTGCTGTGAGCCAGACAGCGATAGAGCTTTTGTCTG 661
DB 660 GCTGGGCTGTGGGCGGACCTGTGCTGTGAGCCAGGCGATAGAGCTTTTGTCTG 719
QY 662 TGCTTACTCTCCCGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAA 721
DB 720 TGCTTACTCTCCCGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAA 779
QY 722 GGTGTGCTGGTGTCTGCTGACAGCCAGTGTCTCAGGCTGTCTTCAAGGCTCTGGAGCA 781
DB 780 GGTGTGCTGGTGTCTGCTGACAGCCAGTGTCTCAGGCTGTCTTCAAGGCTCTGGAGCA 839
QY 782 TGCAGGGGGCTCTGTGAGGTCTCCAGGATCTCTTGTGCGATGAGCTGCCAAGACCATG 841
DB 840 TGCAGGGGGCTCTGTGAGGTCTCCAGGATCTCTTGTGCGATGAGCTGCCAAGACCATG 899
QY 842 ACCTCTCAACATCAGCACCTGCCACTGCCACTGTCCCTCTGGCTTACACGGGACAGATCTG 901
DB 900 ACCTCTCAACATCAGCACCTGCCACTGCCACTGTCCCTCTGGCTTACACGGGACAGATCTG 959
QY 902 CCAAGTGAGGTGAGCTGAGTGTGTCAGCGCCGGTTCGGGAGGAGTGTCTGCTG 961
DB 960 CCAAGTGAGGTGAGCTGAGTGTGTCAGCGCCGGTTCGGGAGGAGTGTCTGCTG 1019
QY 962 CGTCTGTGACATCGGCTACGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCA 1021
DB 1020 CGTCTGTGACATCGGCTACGGGGAGCCAGTGTGCCACCAAGTGTGCATTTTCCCTTCCA 1079
QY 1022 CACCTGTGACCTGAGATGTCAGCGAGACTGCTTCATGTTGTTTC-AGAGGAGACACCT 1080
DB 1080 CACCTGTGACCTGAGATGTCAGCGAGACTGCTTCATGTTGTTTC-AGAGGAGACACCT 1139
QY 1081 ATTACAGAGCCAGGATGAATGT-----CAGAGGAAAGCGGGGTGCTGGCC 1127
DB 1140 ATTACAGAGCCAGGATGAATGTGAGGGTGGGTTTACAGAGGAAAGCGGGGTGCTGGCC 1199
QY 1128 CAGATCAAGAGCCAGAAAGTGCAGGACATCTCGCTTCTATCTGGCGCCCTGGAGACC 1187
DB 1200 CAGATCAAGAGCCAGAAAGTGCAGGACATCTCTCGCTTCTATCTGGGCTCGCTGGAGACC 1259
QY 1188 ACCAAGAGGTGACTGACAGTGTGTCAGACCCAGAACTTCTGGATCGGGCTCACCTAC 1247
DB 1260 ACCAAGAGGTGATTTGACAGTGTGTCAGACCCAGAACTTCTGGATCGGGCTCACCTAC 1319
QY 1248 AAGACCGCCAAAGGACTCTCTCGCTGGGCCACAGGGGAGCAGCGCTTTCACAGCTTTT 1307

Db	1320	AAGACGGCAAGGACTCTTCGCTGGCCACAGGGAGCAACGAGGCTTCACCAAGTTT	1379
Qy	1308	GCGTTTGGCAGCCTGACAAACAGGGCTGGTGCTGAGTCTGCCATGGGGTTGGC	1367
Db	1380	GCGTTTGGCAGCCTTGAAACAC-----GGGTTGGC	1412
Qy	1368	AACCTGGTGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACACCAAGCGCTGC AAAAC	1427
Db	1413	AACCTGGTGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACACCAAGCGCTGC AAAAC	1472
Qy	1428	CGAAACCGTTACATCTGCCAGTTTGGCCAGGAGACACA-TCCTCCGGTGGGGCCCA--GGG	1484
Db	1473	CGAAACCGTTACATCTGCCAGTTTGGCCAGGAGACACA-TCCTCCGGTGGGGCCCAAGGT	1532
Qy	1485	TCCTGAGGCGCTGACCACATGGCTCCCTCGCTGCCTGGGAGCACCGGCTCTGCTTACCT	1544
Db	1533	CTGTATGGCGCTGACCACATGGCTCCCTCGCTGCCTGGGAGCACCGGCTCTGCTTACCT	1592
Qy	1545	GTCTGCCCCACCTGTCTGGAACAAAGGCC--AGTTTAAGACACATGCTCATGTCCAAAG-	1602
Db	1593	GTCTGCCCCACCTGTCTGGAACAAAGGCCAAGGTTTAAGATCATGCTCATGTCCAAAGA	1652
Qy	1603	AGGCTCTCAGACCTTGACACAATGCCAGAAGTTGGGCAGAGAGCGAGGAGCGCAGTGAG	1662
Db	1653	AGGTCTCAGACTTTGCACAATGCCAGAAGTTGGGCAGAAAAGCAGGAGGCCAGTTAG	1712
Qy	1663	GGCCAGGGAGTGAGTGTAGAAAGAGCTGGGGCCCTTCGCTGCTTTTGATTTGGGAAGAT	1722
Db	1713	GGCCAGGGAGTGAGTGTAAAAAAGAGCTGGGGCCCTTCGCTGCTTTTGATTTGGGAAGAT	1772
Qy	1723	GGGCTTCAATTAGATGGCGAAGAGAGGACCGCCAGTGTGTC AAAAAGGCTCTCTCT	1782
Db	1773	GGGCTTCAATTAGATGGCGAAGAGAGGACCGCCAGTGTGTC AAAAAGGCTCTCTCT	1832
Qy	1783	TCCACCTGGCCAGACCCCTGTGGGGCAGCGGAGCTTCCC---TGTGGCATGAACCCCAAG	1839
Db	1833	TCCACCTGGCCAGACCCCTGTGGGGCAACGAGCTTCCCCTTTGGCATTAACCCCAAG	1892
Qy	1840	GGGTATTAAA--TTATGAATCAGCTGA AAAA AAAA 1876	
Db	1893	GGTATTAAAATTTATGAATCAGCTGA AAAA AAAA AAAA 1930	

RESULT 11
2273300

AAZ23300
ID AAZ23300 standard: cDNA: 1338 BP.

XX
AC

XX
DT 31-JAN-2000 (first entry)

XX Human T139 protein coding sequence.

Human; T139 polypeptide; immune system disorder; spermatogenesis; ss;
 testicular cancer; gene mapping;
 testicular fusion; testicular disorder;
 testicular cancer; gene mapping;

AA Homo sapiens.

XX
PN
W09954343-A2.XX
28-OCT-1999
PD

XX 23-APR-1999. 99W0-0508896.

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PP 23-APR-1998. 98US-0065661

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1000-633050/EA

DR P-PSDB; AAY41266.

PT Human T139 nucleic acids and polypeptides, useful for treating
PT proliferative disorders associated with aberrant T139 expression or
PT activity - PT

XX This represents the coding sequence of the human Tl39 polypeptide. The
CC Tl39 polypeptide can be expressed by standard recombinant methodology.
CC The Tl39 cDNA insert is deposited with ATCC under accession number
CC 98694. The Tl39 polypeptides and polynucleotides can be administered
CC therapeutically or prophylactically to treat/prevent disorders associated
CC with aberrant Tl39 expression or activity, especially proliferative or
CC differentiative disorders, e.g. of the immune system. They can be used to
CC modulate spermatogenesis, e.g. as a contraceptive to decrease
CC spermatogenesis or to treat disorders related to defects in sperm-egg
CC fusion. They may also be useful to treat testicular disorders e.g.
CC testicular cancer. The polypeptides may be used to identify selectively
CC binding compounds which may be useful for detecting the polypeptides in
CC samples; and identifying compounds modulating polypeptide activity. The
CC polynucleotides are useful for producing probes or primers that
CC selectively hybridize to the polynucleotides which may be useful for
CC detecting the polynucleotides in a sample, gene mapping; identifying
CC cells or tissues expressing aberrant Tl39 levels; determining if a gene
CC has been mutated or deleted to identify subjects at risk for or having a
CC disorder associated with Tl39 expression or activity and to monitor
CC therapeutic interventions; and for producing antisense sequences for
CC therapeutic administration to modulate/prevent Tl39 expression.

Sequence 1338 BP: 259 A: 420 C: 413 G: 246 T: 0 other; XX SO

Query Match 68.98; Score 1293; DB 20; Length 1338;

Query Match	Score	Pred.
Best Local Similarity	97.78	pred. No. 5.2e-301;
Query Match	88.98	score 1235, ES 20

Best Local Similarity 97.7%, Freq: NO: 5.28 501)
Matches 1333: Conservative 0; Mismatches 5; Indels 27;

123 ATGCTGCATCCAGAGAGACCTCCCCCTGGCCCGGGGCATCTCCTGGCTGTGCTCCTGGCCCTC 182

1 ATCTCTCCACACACCTCCCTGGCCGGGGCATCTCTGGCTGTGCTCCTGGCCCTC 60

183 CTTCCGACGACCTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCC 242

61 CTTCCGACCGCCCTGGCCACCCACGCTGCAGGACAGGCTCCGATGGCC 120

CGCCGCTGGCACAACGGCTGGGCAGC 302

180

362

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

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DD
301 G1IGAS19GTCHCOCCTH1001ATGCHS1836272890

[illegible]

DB 421 TGIGCTGGCAACGCCCACCCTGCACCCCGATACGCCCGCAGTGTTCCTTTCT

QY
603 C TGGGCTGTGGCGGCACCTGTGGCTCAGCCAGGCCCAATTAAGGCTTCTTTT
|||||

D6
481 CTGGGCCTGTGGCGGACCTGTGCTCTGCAAGGCCAGGCGATAGAAACCATTGCTCTT

Qy 663 GCCTACTCCCGGAGGCAACTGGGAGGTCAACGGGAAAGACAATCAACCCCTATTCAGT

Db 547 CTGGCTGTGGGGCGGACCTGCTCTGTCAGGCGCCAGGACGATAGAGCCCTTGTCTGT 606
QY 663 GCCTACTCCCGGAGGCAACTGGGAGTCAACGGGAAGACAATCATCCCTTATAAGAAG 722
Db 607 GCCTACTCCCGGAGGCAACTGGGAGTCAACGGGAAGACAATCGTCCCTTATAAGAAG 666
QY 723 GGTGCTGTGTGCTCTGTCACAGCCAGTCTCAGGCTGCTCAAGGCTGGGACCAT 782
Db 667 GGTGCTGTGTGCTCTGTCACAGCCAGTCTCAGGCTGCTCAAGGCTGGGACCAT 726
QY 783 GCAGGGGGGCTGTGAGGTCCCGAGGAATCCCTTGTGCGATGAGCTGCCAGAACCATGGA 842
Db 727 GCAGGGGGGCTGTGAGGTCCCGAGGAATCCCTTGTGCGATGAGCTGCCAGAACCATGGA 786
QY 843 CGTCTCAACATACAGACCTCCCACTGCGCACTGTCCCTCCCTGGCTACAGGGCAGATAGTC 902
Db 787 CGTCTCAACATACAGACCTCCCACTGCGCACTGTCCCTCCCTGGCTACAGGGCAGATAGTC 846
QY 903 CAAGTAGGTGCGAGCTGCACTGTGTGCACGGCGGTTCCGGGAGGAGTGTCTGCTGTC 962
Db 847 CAAGTAGGTGCGAGCTGCACTGTGTGCACGGCGGTTCCGGGAGGAGTGTCTGCTGTC 906
QY 963 GTCTGTGACATCGGCTACGGGGGAGCCAGTGTGCCACCAAGTGTCAATTTCCCTTCCAC 1022
Db 907 GTCTGTGACATCGGCTACGGGGGAGCCAGTGTGCCACCAAGTGTCAATTTCCCTTCCAC 966
QY 1023 ACCTGTGACCTGAGGATCGAGGAGACTGCTCATGTGTCTTCAGAGGCGAGACCATAT 1082
Db 967 ACCTGTGACCTGAGGATCGAGGAGACTGCTCATGTGTCTTCAGAGGCGAGACCATAT 1026
QY 1083 TACAGAGCCAGGATGAATGTACAGAGAAAGCGGGGTGCTGGCCCAAGATCAAGAGCCAG 1142
Db 1027 TACAGAGCCAGGATGAATGTACAGAGAAAGCGGGGTGCTGGCCCAAGATCAAGAGCCAG 1086
QY 1143 AAAGTCAGAGACAPCTCGGCTTCTATCTGGGGCCCTTGGAGACCAACCAAGAGGTGACT 1202
Db 1087 AAAGTCAGAGACATCTCTCGCTTCTATCTGGGGCCCTTGGAGACCAACCAAGAGGTGATT 1146
QY 1203 GACAGTGACTCGAGACAGGAACTTCTGGATCGG 1237
Db 1147 GACAGTGACTCGAGACAGGAACTTCTGGATCGG 1181

RESULT 13

AAS76343
ID AAS76343 standard; cdna; 906 BP.

XX AAS76343;

AC XX
DT 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #12147.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR P-PSDB; ABG12156.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

XX Claim 1: SEQ ID No 12147; 103pp; English.

PS

XX The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes.
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations in
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 906 BP; 175 A; 294 C; 286 G; 151 T; 0 other;

Query Match 40.9%; Score 766.6; DB 23; Length 906;

Best Local Similarity 95.2%; Pred. No. 1.7e-174;

Matches 801; Conservative 0; Mismatches 39; Indels 1; Gaps 1;

QY 4 TTTTTCACACAGCCACGCTGACTCTCTGGAGATTGTGAATAGCTCCAGCTGAGA 53

Db 8 TTTCTCTGTCAGCCACGCTGACTCTCTGGAGATTGTGAATAGCTCCAGCTGAGA 67

QY 64 AACAGCCGGTGTGCTGAGCCAGGCTGTGACGGAGCACCTGACGGGCCCAACACACCA 123

Db 68 AACAGCCGGTGTGCTGAGCCAGGCTGTGACGGAGCGCTGACGGGCCCAACACACCA 127

QY 124 TGCTGCATCCAGAGACCTCCCTGCGCGGGGCATCTCTTGCTGTCTTGGCCCTCC 183

Db 128 TGCTGCATCCAGAGACCTCCCTGCGCGGGGCATCTCTTGCTGTCTTGGCCCTCC 187

QY 184 TTGGCACCACCTGGCGCAGAGTGTGGCCACCCAGCTGCAGAGCAGGCTCCGATGGCCG 243

Db 188 TTGGCACCACCTGGCGCAGAGTGTGGCCACCCAGCTGCAGAGCAGGCTCCGATGGCCG 247

QY 244 GAGCCCTGAACAGGAGAGAGTCTTCTCTCTCTCCCTGCACACACCCCTGCGCAGCT 303

Db 248 GAGCCCTGAACAGGAGAGAGTCTTCTCTCTCTCCCTGCACACACCCCTGCGCAGCT 307

QY 304 GGGTCCAGCCCTCGGGCTGACATCGGAGGCTGGAGTGGAGTGACAGCCCTGGCCCAAC 363

Db 308 GGGTCCAGCCCTCGGGCTGACATCGGAGGCTGGAGTGGAGTGACAGCCCTGGCCCAAC 367

QY 364 TGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCTGT 423

Db 368 TGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCGGTCTGGGCTGT 427

QY 424 GCGCACCTCTGCAAGTGGGCTGGAACATGACGTGCTGCGCGGGCTTGGCTCTCTTTG 483

Db 428 GCGCACCTCTGCAAGTGGGCTGGAACATGACGTGCTTACCCGGGGCTTGGCTCTCTTTG 487

QY 484 TTGAAGTGGTACGCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACGCGGAGAGAGT 543

Db 488 TCGAAGTGGTACGCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACGCGGAGAGAGT 547

QY 544 GTGCTCGCAACGCCACCTGCACCCACTACAGCAGCTCTGTGTGGGCCACCTCAAGCCAGC 603

Db 548 GAGCTCGCAACGCCACCTGCACCCACTACATGAGCTCGTGTGGGCCACCTCAAGCCAGC 607
Qy 604 TGGGCTGTGGGGGCGCACCTGTCTGTGCAGGCCAGACGATAGAGCCCTTTGCTCTGTG 663
Db 608 TGGGCTGTGGGGGCGCACCTGTCTGTGCAGGCCAGGCGATAGAGCCCTTTGCTCTGTG 667
Qy 664 CTTACTTCCCGGAGGCAACTGGGAGGTCAACGGGAGAGCAATCATCCCTATAAAGAGG 723
Db 668 CTTACTTCCCGGAGGCAACTGGGAGGTCAACGGGAGAGCAATCATCCCTATAAAGAGG 727
Qy 724 GTGCTGTGTGTGCTGTGCAGACGAGTGTCTCAGGCTGCTTCAAGGCTTGGACCATG 783
Db 728 GGGCCCTGGGGCTGTGCTGCACAGCCAGTGTCTCAAGCCCTGCTTAAAGCCCTGGACCATG 787
Qy 784 CAGGGGGGCT-CTGTGAGGTCCCGAGGAATCTTGTGCGATGAGTCCGAGAACCATGGA 842
Db 788 CCAGGGGGCTACTGGGGGGCCCCCGGAAACCTTGGGGAAGGAGCGACAGAACCCCTTGA 847
Qy 843 C 843
Db 848 C 848
RESULT 14
AA70010
ID AAA70010 standard; cdNA; 690 BP.
AC AAA70010;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human ovarian carcinoma antigen polynucleotide SEQ ID NO:321.
XX
KW Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
KW tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200036107-A2.
XX
PD 22-JUN-2000.
XX
PF 17-DEC-1999; 99WO-US30270.
XX
PR 17-DEC-1998; 98US-0215681.
PR 17-DEC-1998; 98US-0216003.
PR 23-JUN-1999; 99US-0338933.
PR 24-SEP-1999; 99US-0404879.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Frudakis TN;
XX
DR WPI; 2000-431589/37.
XX
PT Immunogenic portion of an ovarian carcinoma protein and the nucleic
PT acid encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer -
XX
XX
XX Claim 1; Page 177; 299pp; English.
XX
PS The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants).
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytostatic activity and can be used in gene therapy and vaccines.
CC Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines
CC are useful for the prevention, diagnosis and treatment of cancer.
CC preferably ovarian cancer. AA69691 to AA70077 and AAB12552 to AAB12557
CC represent human ovarian carcinoma polynucleotides and proteins used in
CC the exemplification of the present invention.
XX
SQ Sequence 690 BP; 148 A; 197 C; 212 G; 131 T; 2 other;

Query Match 35.9%; Score 672.8; DB 21; Length 690;
Best Local Similarity 99.3%; Pred No. 5.5e-152;
Matches 685; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
Qy 604 TGGGCTGTGGGGGCGCACCTGTCTGTGCAGGCCAGACGATAGAGCCCTTTGCTCTGTG 663
Db 1 TGGGCTGTGGGGGCGCACCTGTCTGTGCAGGCCAGACGATAGAGCCCTTTGCTCTGTG 60
Qy 664 CTTACTTCCCGGAGGCAACTGGGAGGTCAACGGGAGAGCAATCATCCCTATAAAGAGG 723
Db 61 CTTACTTCCCGGAGGCAACTGGGAGGTCAACGGGAGAGCAATCATCCCTATAAAGAGG 120
Qy 724 GTGCTGTGTGTGCTGTGCAGACGAGTGTCTCAGGCTGCTTCAAGGCTTGGACCATG 783
Db 121 GTGCTGTGTGCTGTGCAGACGAGTGTCTCAGGCTGCTTCAAGGCTTGGACCATG 180
Qy 784 CAGGGGGGCTCTGTGAGGTCCCGAGGAATCTTGTGCGATGAGTCCGAGAACCATGGA 843
Db 181 CAGGGGGGCTCTGTGAGGTCCCGAGGAATCTTGTGCGATGAGTCCGAGAACCATGGA 240
Qy 844 GTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACAGGGCAGATAGTGC 903
Db 241 GTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACAGGGCAGATAGTGC 300
Qy 904 AAGTGAGGTGAGCCTGCAGTGTGTGCACGGCCGGTTCGGGGAGGAGGTGCTCGTGGC 963
Db 301 AAGTGAGGTGAGCCTGCAGTGTGTGCACGGCCGGTTCGGGGAGGAGGTGCTCGTGGC 360
Qy 964 TCTGTGACATCGGCTACGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCACA 1023
Db 361 TCTGTGACATCGGCTACGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCACA 420
Qy 1024 CTTGTGACCTGAGGATCGACGGAGACTGCTTTCATGGTGTCTTCAGAGGAGACACCTATT 1083
Db 421 CTTGTGACCTGAGGATCGACGGAGACTGCTTTCATGGTGTCTTCAGAGGAGACACCTATT 480
Qy 1084 ACAG-AGCCAGGATGAAATGTACAGGAAAGCGGGGTGCTGCCCCAGATCAAGAGCCAG 1142
Db 481 ACAGAGCCAGGATGAAATGTACAGGAAATGCGGGGTGCTGCCCCAGATCAAGAGCCAG 540
Qy 1143 AAAGTGAGGACATCTCGCCTTCTATCTGGGCCCGCTGGAGACACCAACGAGGTGACT 1202
Db 541 AAAGTGAGGACATCTCGCCTTCTATCTGGGCCCGCTGGAGACACCAACGAGGTGACT 600
Qy 1203 GACAGTGACTTCGAGACCAAGGAATCTTCGGATCGGGCTCACCTACAAGACCGCAAGGAC 1262
Db 601 GACAGTGACTTCGAGACCAAGGAATCTTCGGATCGGGCTCACCTACAAGACCGCAAGGAC 660
Qy 1263 TCCTTCCGCTGGGCCACAGGGGAGCACCAG 1292
Db 661 TCCTTNGGCTGGGCCACAGGGGAGCACCAG 690

RESULT 15

ABN72904
ID ABN72904 standard; DNA; 690 BP.

XX
AC ABN72904;
XX

DT 02-JUL-2002 (first entry)
XX

DE Ovarian carcinoma antigen polynucleotide #9.
XX

KW Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; ds.
XX

OS Homo sapiens.
XX

PN WO200206317-A2.
XX

PD 24-JAN-2002.
XX

PF 17-JUL-2001; 2001WO-US22635.
XX

XX 17-JUL-2000; 2000US-0617747.
PR 10-AUG-2000; 2000US-0636801.
PR 20-SEP-2000; 2000US-0667857.
PR 04-APR-2001; 2001US-0827271.
PR 18-JUN-2001; 2001US-0884441.
XX (CORI-) CORIXA CORP.
PA Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
XX Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX WPI; 2002-164781/21.
XX Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer -
XX Example 2; Page 296; 408pp; English.
XX This invention relates to polypeptides comprising an immunogenic
CC portion of an ovarian carcinoma protein which acts as an
CC immunostimulant and is cytostatic. The polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells that express the polypeptides are useful for stimulating an
CC immune response in a patient and treating ovarian cancer. This
CC sequence represents DNA related to the invention.
XX
XX Sequence 690 BP; 148 A; 197 C; 212 G; 131 T; 2 other;
SQ
Query Match 35.9%; Score 672.8; DB 24; Length 690;
Best Local Similarity 99.3%; Pred. No. 5.5e-152;
Matches 685; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 604 TGGGCTGTGGCGGCACCTGTGCTCTCAGGCCACAGCAGCATAGAACCTTTGTCTGTG 663
DB 1 TGGGCTGTGGCGGCACCTGTGCTCTCAGGCCACAGCAGCATAGAACCTTTGTCTGTG 60
QY 664 CCTACTCCCCGGGAGGCACTGGGAGGTCAACGGGAAGACATCATCCCTATAGAAGG 723
DB 61 CCTACTCCCCGGGAGGCACTGGGAGGTCAACGGGAAGACATCATCCCTATAGAAGG 120
QY 724 GTGCTGTGTCTGCTGTGCACAGCCAGTGTCTCAGGCTGTCTCAAAGCTGGGACCATG 783
DB 121 GTGCTGTGTCTGCTGTGCACAGCCAGTGTCTCAGGCTGTCTCAAAGCTGGGACCATG 180
QY 784 CAGGGGGGCTGTGTAGGTGCCCCAGGAATCCTTGTGCGATGAGTGTCCAGAACCATGGAC 843
DB 181 CAGGGGGGCTGTGTAGGTGCCCCAGGAATCCTTGTGCGATGAGTGTCCAGAACCATGGAC 240
QY 844 GTCTCAACATCAGCACCTGCCACTGCCACTGTCCCTGCTACACGGGCAGATACTGCC 903
DB 241 GTCTCAACATCAGCACCTGCCACTGCCACTGTCCCTGCTACACGGGCAGATACTGCC 300
QY 904 AAGTGAGTGCAGCTGTGCTGTGCACGGCGGTTCGGGAGGAGGAGTGTCTGTGG 963
DB 301 AAGTGAGTGCAGCTGTGCTGTGCACGGCGGTTCGGGAGGAGGAGTGTCTGTGG 360
QY 964 TCTGTACATGGGTACGGGGAGCCCAAGTGTGCCACCAAGTGCATTTTCCCTTCCACA 1023
DB 361 TCTGTACATGGGTACGGGGAGCCCAAGTGTGCCACCAAGTGCATTTTCCCTTCCACA 420
QY 1024 CCTGTGACCTGAGGATCGACGAGACTGCTTCATGTTCTTCAGAGGCAGACACTATT 1083
DB 421 CCTGTGACCTGAGGATCGACGAGACTGCTTCATGTTCTTCAGAGGCAGACACTATT 480
QY 1084 ACAG-AGCCAGGATGAATGTTCAGAGGAAGAGCGGGGTGCTGGCCCGAGATCAAGAGCCAG 1142
DB 481 ACAGAGCCAGGATGAATGTTCAGAGGAATGCGGGGGTGTGCGCCAGATCAAGAGCCAG 540
QY 1143 AAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCTGGAGACCAACCAAGGTGACT 1202
DB 541 AAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCTGGAGACCAACCAAGGTGACT 600

QY 1203 GACAGTGAATTCGAGACCAAGGAACTTCTGATCGGCTCACTACAAGACGCCCAAGGAC 1262
DB 601 GACAGTGAATTCGAGACCAAGGAACTTCTGATNGGCTCACTACAAGACGCCCAAGGAC 660
QY 1263 TCCTTCCGCTGGGCCACAGGGGAGCACCAG 1292
DB 661 TCCTTNCGCTGGGCCACAGGGGAGCACCAG 690

Search completed: December 28, 2002, 17:01:35
Job time : 380.501 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: December 28, 2002, 15:41:47 ; Search time 630.14 Seconds
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Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	245.4	99.4	1341	6	AX191493	Sequence
2	245.4	99.4	1775	6	AX191503	Sequence
3	240.6	97.4	3293	9	HSM804852	Sequence
4	231	93.5	2900	9	AB060195	Homo sapi
5	108.8	44.0	163427	9	AC009053	AB060195 Homo sapi
6	108.8	44.0	174779	9	AC009153	AC009153 Homo sapi
7	108.8	44.0	180596	9	AC009060	AC009060 Homo sapi
8	108.8	44.0	197460	2	AC126771	AC126771 Homo sapi
9	108.8	44.0	205044	2	AC009125	AC009125 Homo sapi
10	107.4	43.5	200409	2	AC097331	AC097331 Pan trogl
11	107.2	43.4	79023	2	AC021951	AC021951 Homo sapi
12	107.2	43.4	204182	2	AC097271	AC097271 Pan trogl
13	105.6	42.8	179675	9	AC026468	AC026468 Homo sapi
14	105.6	42.8	190595	9	AC009022	AC009022 Homo sapi
15	104	42.1	191108	2	AC097265	AC097265 Pan trogl
16	95.8	38.8	2340	9	AK096051	AK096051 Homo sapi
17	95.8	38.8	200409	2	AC097331	AC097331 Pan trogl
18	69	27.9	200755	2	AC093451	AC093451 Mus muscu
19	62.2	25.2	179237	2	AC111287	AC111287 Rattus no
20	62.2	25.2	179236	2	AC098076	AC098076 Rattus no
21	46.6	18.9	857	9	BC007689	BC007689 Homo sapi
22	46.6	18.9	1491	6	AX101173	AX101173 Sequence
23	46.6	18.9	1669	6	AX235371	AX235371 Sequence
24	46.6	18.9	1690	9	AK027395	AK027395 Homo sapi
25	46.6	18.9	1824	6	AX358802	AX358802 Sequence
26	46.6	18.9	1824	6	AX362295	AX362295 Sequence
27	46.6	18.9	2272	6	AX101175	AX101175 Sequence
28	46.6	18.9	2400	6	AX235369	AX235369 Sequence
29	46.6	18.9	2403	6	AX235373	AX235373 Sequence
30	46.6	18.9	2412	6	AX235375	AX235375 Sequence
31	46.6	18.9	4574	6	AX086850	AX086850 Sequence
32	46.6	18.9	4574	9	HSM801829	AX136861 Homo sapi
33	46.6	18.9	4877	6	AX285067	AX285067 Sequence
34	46.6	18.9	4877	6	AX285068	AX285068 Sequence
35	46.6	18.9	4877	6	AX285079	AX285079 Sequence
36	46	18.6	205044	2	AC009125	AC009125 Homo sapi
37	45.6	18.5	2305	6	AX235367	AX235367 Sequence
38	42.8	17.3	2849	1	STMAMPEP	L23172 Streptomyce
39	42.8	17.3	33084	1	SC8E4A	AL138562 Streptomy
40	39.2	15.9	39525	1	SCF91	AL132973 Streptomy
41	38.2	15.5	2139	9	AK091893	AK091893 Homo sapi
42	38.2	15.5	10746	1	AE004671	AE004671 Pseudomon
43	38.2	15.5	113193	1	AF357202	AF357202 Streptomy
44	38.2	15.5	133004	2	AC068965	AC068965 Homo sapi
45	38.2	15.5	151828	9	AL354740	AL354740 Human DNA

ALIGNMENTS

RESULT 1
AX191493
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

AX191493
Sequence 15 from Patent WO0149728.
AX191493
AX191493.1 GI:15209675
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1341)
Kato,S. and Kimura,T.
Human proteins having hydrophobic domains and dnas encoding these proteins

linear DNA 1341 bp PAT 15-AUG-2001

JOURNAL Patent: WO 0149728-A 15 12-JUL-2001;
Protegene Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)
FEATURES
source
Location/Qualifiers
1. .1341
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 260 a 420 c 414 g 247 t
ORIGIN
Query Match 99.4%; Score 245.4; DB 6; Length 1341;
Best Local Similarity 99.6%; Pred. No. 1.9e-46;
Matches 246; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGAGCCCTGAACAGGAAG 60
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Db 79 GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGAGCCCTGAACAGGAAG 138
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QY 61 GAGAGTTTCTTGTCTCTCTCCCTGTCACAAACCGCTGGCGAGCTGGTCCAGCCCTGCG 120
|||||
Db 139 GAGAGTTTCTTGTCTCTCTCCCTGTCACAAACCGCTGGCGAGCTGGTCCAGCCCTGCG 198
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QY 121 GCTGACATGGGAGGCTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGGCA 180
|||||
Db 199 GCTGACATGGGAGGCTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGGCA 258
|||||
QY 181 GCCTCTGTGGAAATCCAAACCCGAGCCTGGCATCCGGCCCTGTGGCGCACCCCTGCAAGTG 240
|||||
Db 259 GCCTCTGTGGAAATCCAAACCCGAGCCTGGCGTCCGGCTGTGGCGCACCCCTGCAAGTG 318
|||||
QY 241 GGCTGGA 247
|||||
Db 319 GGCTGGA 325
RESULT 2
AX191503
LOCUS AX191503 1775 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 25 from Patent WO0149728.
ACCESSION AX191503
VERSION AX191503.1 GI:15209689
KEYWORDS
SOURCE human.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Kato, S. and Kimura, T.
TITLE Human proteins having hydrophobic domains and dnas encoding these proteins
JOURNAL Patent: WO 0149728-A 25 12-JUL-2001;
Protegene Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)
FEATURES
source
Location/Qualifiers
1. .1775
/organism="Homo sapiens"
/db_xref="taxon:9606"
62. .1402
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC51149.1"
/db_xref="GI:15209690"
/translation="MLHPETSPGRGHLLAVLLALLGTAWAEVWPQLOEQAPWAGNALN
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TLQVWNQMLLPAGLASFEVYVLSWFAEGORYSHAAGECARNATCTHYTOLVWATSSQ
LGCGHLICAGAAAEAVFCAYSPGNWEVNGKTIIPYKGAWSLICLTASVSGCPKAW
DHAGLCEVPNRCNQNCHRLNISTCHCHCPGYTGRCQVRCSLQCVHGRPRE
ECSVCVDIGGAQCATVHPFFHPCDLRIDGDFWSEADTYRARKCKORKGVL
AQIKSQKVDILAFVLGRLETTNVIDSDFTNFWIGLTKYTKADSPWATGEHQAF
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BASE COUNT 360 a 541 c 549 g 325 t
ORIGIN
Query Match 99.4%; Score 245.4; DB 6; Length 1775;
Best Local Similarity 99.6%; Pred. No. 1.8e-46;

Matches 246; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGAGCCCTGAACAGGAAG 60
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Db 140 GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGAGCCCTGAACAGGAAG 199
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QY 61 GAGAGTTTCTTGTCTCTCTCCCTGTCACAAACCGCTGGCGAGCTGGTCCAGCCCTGCG 120
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Db 200 GAGAGTTTCTTGTCTCTCTCCCTGTCACAAACCGCTGGCGAGCTGGTCCAGCCCTGCG 259
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QY 121 GCTGACATGGGAGGCTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGGCA 180
|||||
Db 260 GCTGACATGGGAGGCTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGGCA 319
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QY 181 GCCTCTGTGGAAATCCAAACCCGAGCCTGGCATCCGGCCCTGTGGCGCACCCCTGCAAGTG 240
|||||
Db 320 GCCTCTGTGGAAATCCAAACCCGAGCCTGGCGTCCGGCTGTGGCGCACCCCTGCAAGTG 379
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QY 241 GGCTGGA 247
|||||
Db 380 GGCTGGA 386
RESULT 3
HSM804652 3293 bp mRNA linear PRI 10-JUL-2002
LOCUS HSM804652
DEFINITION Homo sapiens mRNA; cDNA DKFP686E1934 (from clone DKFP686E1934).
ACCESSION AL833339
VERSION AL833339.1 GI:21733974
KEYWORDS
SOURCE human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Ottenwaelder, B., Obermaier, B., Mewes, H.W., Weil, B., Amid, C. and Wiemann, S.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
COMMENT Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the CDNA sequencing consortium of the German Genome Project. This clone (DKFP686E1934) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
FEATURES
source
Location/Qualifiers
1. .3293
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFP686E1934"
/tissue_type="cDNA-collection"
/clone_lib="686 (synonym: hlccc3). Vector pSport1_sfi; host DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
polyA_signal 3171..3176
polyA_site 3190..597 t
BASE COUNT 783 a 946 c 967 g 597 t
ORIGIN
Query Match 97.4%; Score 240.6; DB 9; Length 3293;
Best Local Similarity 98.4%; Pred. No. 2e-45;
Matches 243; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGAGCCCTGAACAGGAAG 60
|||||
Db 272 GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGAGCCCTGAACAGGAAG 331
|||||
QY 61 GAGAGTTTCTTGTCTCTCTCCCTGTCACAAACCGCTGGCGAGCTGGTCCAGCCCTGCG 120
|||||
Db 332 GAGAGTTTCTTGTCTCTCTCCCTGTCACAAACCGCTGGCGAGCTGGTCCAGCCCTGCG 391
|||||

Db 125634 CAGGACTGAGTGCAGAGCTGGCCCAACTGGCTCAGCCAGGCGACCCCTCTGTGGAATC 125693

QY 196 CCAACCCCGAGCTGCATCCGCGCTGTGGCGACACCTCGAAGTGGCTGGA 247

Db 125694 CCAACCCCGAGCTGGCGTCCGCGCTGTGGCGACACCTCGAAGTGGCTGGA 125745

RESULT 9

AC009125/2
LOCUS Homo sapiens chromosome 16 clone RP11-492H8, WORKING DRAFT
DEFINITION SEQUENCE, 60 unordered pieces.
AC009125
VERSION AC009125.5 GI:8575963
KEYWORDS HTG; HIGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE DOE Joint Genome Institute.
JOURNAL Sequencing of Human Chromosome 16
REFERENCE
AUTHORS 1 (bases 1 to 205044)
TITLE DOE Joint Genome Institute.
JOURNAL Direct Submission
AUTHORS 2 (bases 1 to 205044)
TITLE Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Jun 21, 2000 this sequence version replaced gi:7689944.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 595469
Center clone name: RPCI-11_492H8

Summary Statistics
Consensus quality: 156671 bases at least Q40
Consensus quality: 183548 bases at least Q30
Consensus quality: 188961 bases at least Q20
Estimated insert size: 189500; agarose-gel estimation
Quality coverage: 3.4 in Q20 bases; sum-of-contigs estimation
Quality coverage: 3.23 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 60 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1059: contig of 1059 bp in length
* 1060 1159: gap of unknown length
* 1160 2165: contig of 1006 bp in length
* 2166 2265: gap of unknown length
* 2266 3328: contig of 1063 bp in length
* 3329 3429: gap of unknown length
* 3430 4435: contig of 1007 bp in length
* 4436 5539: gap of unknown length
* 5540 5640: contig of 1004 bp in length
* 5641 6729: gap of unknown length
* 6730 6829: contig of 1090 bp in length
* 6830 8057: gap of unknown length
* 8058 8157: contig of 1228 bp in length
* 8158 9287: gap of unknown length
* 9288 9387: contig of 1129 bp in length
* 9388 10701: gap of unknown length
* 10702 11829: contig of 1314 bp in length
* 11830 11829: contig of 1029 bp in length

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE DOE Joint Genome Institute.
JOURNAL Sequencing of Human Chromosome 16
REFERENCE
AUTHORS 1 (bases 1 to 197460)
TITLE DOE Joint Genome Institute.
JOURNAL Direct Submission
AUTHORS 2 (bases 1 to 197460)
TITLE Submitted (09-JUL-2002) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 558525
Center clone name: RPCI-11_396D24

Summary Statistics
Consensus quality: 191546 bases at least Q40
Consensus quality: 193703 bases at least Q30
Consensus quality: 194840 bases at least Q20
Estimated insert size: 0; null estimation
Quality coverage: 2.1474836E7 in Q20 bases; null estimation
Quality coverage: 8.2 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1600: contig of 1600 bp in length
* 1601 1700: gap of unknown length
* 1701 3466: contig of 1766 bp in length
* 3467 3567: gap of unknown length
* 3568 5710: contig of 2143 bp in length
* 5711 5809: gap of unknown length
* 5810 7800: contig of 1991 bp in length
* 7801 7900: gap of unknown length
* 7901 14727: contig of 6827 bp in length
* 14728 14827: gap of unknown length
* 14828 26876: contig of 12049 bp in length
* 26877 26977: gap of unknown length
* 26978 46712: contig of 19736 bp in length
* 46713 46812: gap of unknown length
* 46813 70129: contig of 23317 bp in length
* 70130 70229: gap of unknown length
* 70230 93613: contig of 23383 bp in length
* 93614 93712: gap of unknown length
* 93713 197460: contig of 103748 bp in length.

Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-396D24"
/clone_lib="RPCI human BAC library 11"
BASE COUNT 50025 a 47482 c 47491 g 51562 t 900 others
ORIGIN

Query Match
Best Local Similarity 44.0%; Score 108.8; DB 2; Length 197460;
Matches 110; Conservative 98.2%; Pred. No. 1.9e-15;
0; Mismatches 2; Indels 0; Gaps 0;

QY 136 CTGGACTGAGTGCAGAGCTGGCCCAACTGGCTCAGCCAGGCGACCCCTCTGTGGAATC 195

Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Hawley, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hoques, M., Holloway, C., Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, H., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsegad, H., Lozano, R., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Massey, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pul, L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I., Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczky, R., Woodson, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 200409)
Worley, K.C.

Direct Submission
Submitted (14-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 200409)
Worley, K.C.

Direct Submission
Submitted (22-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 21, 2002 this sequence version replaced gi:21450389.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: ZUAQ
Center clone name: RP43-53A2
----- Summary Statistics
Sequencing vector: Plasmid; M77789
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 187810 bases at least Q40
Consensus quality: 190821 bases at least Q30
Consensus quality: 193098 bases at least Q20
Estimated insert size: 212811; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 9.3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

* be preserved.
* 39411: contig of 39411 bp in length
* 39511: gap of unknown length
* 61229: contig of 22418 bp in length
* 61230: gap of unknown length
* 61231: contig of 25417 bp in length
* 61232: gap of unknown length
* 61233: contig of 26077 bp in length
* 61234: gap of unknown length
* 61235: contig of 17025 bp in length
* 61236: gap of unknown length
* 61237: contig of 11552 bp in length
* 61238: gap of unknown length
* 61239: contig of 14250 bp in length
* 61240: gap of unknown length
* 61241: contig of 12707 bp in length
* 61242: gap of unknown length
* 61243: contig of 10083 bp in length
* 61244: gap of unknown length
* 61245: contig of 11898 bp in length
* 61246: gap of unknown length
* 61247: contig of 2153 bp in length
* 61248: gap of unknown length
* 61249: contig of 2047 bp in length
* 61250: gap of unknown length
* 61251: contig of 2043 bp in length
* 61252: gap of unknown length
* 61253: contig of 2028 bp in length.
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* 198383: 200409: contig of 2028 bp in length.
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* 198393: 200409: contig of 2028 bp in length.
* 198394: 200409: contig of 2028 bp in length.
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Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
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McPheeters, R., Meldrum, J., Meneus, L., Morrow, J., Naylor, J.,
Norman, C. H., O'Connor, T., O'Donnell, P., Olivari, T. M., Peterson, K.,
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Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
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Zimmer, A. and Zody, M.
Direct Submission
Submitted (22-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6730807.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L5885
Center clone name: 396_D_24

TITLE
JOURNAL
COMMENT

* NOTE: This record contains 79 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 909: contig of 909 bp in length
* 910 1009: gap of 100 bp
* 1010 1922: contig of 913 bp in length
* 1923 2022: gap of 100 bp
* 2023 2941: contig of 919 bp in length
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Query Match	Best Local Similarity	Matches	Score	DB 1	DB 2	Length	79023	Indels	Gaps	0
55015	55924	contig of 910 bp	in length							
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57903	58002	gap of 100 bp	in length							
58003	58884	contig of 882 bp	in length							
58885	58984	gap of 100 bp	in length							
58985	58995	contig of 911 bp	in length							
58996	59995	gap of 100 bp	in length							
59996	60882	contig of 887 bp	in length							
60883	60982	gap of 100 bp	in length							
60983	61906	contig of 924 bp	in length							
61907	62006	gap of 100 bp	in length							
62007	62901	contig of 895 bp	in length							
62902	63001	gap of 100 bp	in length							
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63893	63992	gap of 100 bp	in length							
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69972	70884	contig of 913 bp	in length							
70885	70984	gap of 100 bp	in length							
43.4%	Score 107.2	DB 2	Length 79023							
97.3%	Pred. No. 5.1e-15									
Conservative	0	Mismatches	3	Indels	0	Gaps	0			
109										
136	CTGACTGGAGTGACAGCTGGCCCACTGGCTCAACGACGAGGACGACCCCTCTGTGGAATC	195								
53278	CAGGACTGGAGTGACAGCTGGCCCACTGGCTCAACGACGAGGACGACCCCTCTGTGGAATC	53219								
196	CCAAACCCGAGCTGGCATCGGCTGGCGGACCCCTGCAAGTGGGCTGGA	247								
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AC097271	204182 bp	DNA	linear	HTG 20-OCT-2001						
Pan troglodytes clone RP43-35B16, WORKING DRAFT SEQUENCE, 8										
AC097271	204182 bp	DNA	linear	HTG 20-OCT-2001						
Pan troglodytes clone RP43-35B16, WORKING DRAFT SEQUENCE, 8										
AC097271	GI:16117534									
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.										
Pan troglodytes										
Pan troglodytes										
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.										
1 (bases 1 to 204182)										
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C., Alsdorfs,S.L., Amarantune,H.C., Are,J.R., Banks,T., Barbara,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowles,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., G										

source
location/qualifiers
1. .179675

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misc_feature      91050. .91410
/clone="RP11-106J23"
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Direct Submission
Submitted (13-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 23, 2001 this sequence version replaced gi:16258969.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: ZUAR
Center clone name: RP43-119N13
----- Summary Statistics
Sequencing vector: Plasmid: M77789
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 191814 bases at least Q40
Consensus quality: 193054 bases at least Q30
Consensus quality: 194113 bases at least Q20
Estimated insert size: 193275; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 9.3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 121806: contig of 121806 bp in length
* 121807 121906: gap of unknown length
* 121907 172531: contig of 50625 bp in length
* 172532 172631: gap of unknown length
* 172632 180970: contig of 8339 bp in length
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Search completed: December 28, 2002, 20:22:08
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TITLE
JOURNAL
AUTHORS
REFERENCE
2 (bases 1 to 191108)
Worley,K.C.
Direct Submission
Unpublished
2 (bases 1 to 191108)
Worley,K.C.
TITLE
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AUTHORS
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ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Mon 'Dec 30 09:16:11 2002

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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405	19	1.0	287	13	BI805681	BI805681	S043B12.S	477	19	1.0	323	14	BQ287518
406	19	1.0	288	9	AV076905	AV076905		478	19	1.0	323	14	BQ287518
407	19	1.0	289	9	AV053935	AV053935		479	19	1.0	324	14	BQ287518
408	19	1.0	289	9	AV057223	AV057223		480	19	1.0	324	14	BQ287518
409	19	1.0	289	12	BG203382	BG203382		481	19	1.0	324	14	BQ287518
410	19	1.0	290	9	AV052577	AV052577		482	19	1.0	325	9	AV072524
411	19	1.0	290	9	AV059370	AV059370		483	19	1.0	325	10	BE242203
412	19	1.0	290	12	BG209151	BG209151		484	19	1.0	327	13	BI437899
413	19	1.0	291	9	AV078174	AV078174		485	19	1.0	328	9	AV051815
414	19	1.0	292	9	AV053054	AV053054		486	19	1.0	329	9	AV090298
415	19	1.0	292	9	AV076532	AV076532		487	19	1.0	332	9	AA560291
416	19	1.0	292	13	BM218960	BM218960		488	19	1.0	332	12	BE947347
417	19	1.0	293	9	AI357527	AI357527	QY14A06.x	489	19	1.0	332	13	BI439417
418	19	1.0	293	9	AV051894	AV051894		490	19	1.0	332	13	BI439417
419	19	1.0	293	9	AV072293	AV072293		491	19	1.0	333	13	BM669019
420	19	1.0	293	9	AV072398	AV072398		492	19	1.0	333	13	BI715725
421	19	1.0	293	9	AV076866	AV076866		493	19	1.0	334	13	BI789797
422	19	1.0	293	12	BG271032	BG271032		494	19	1.0	334	13	BI789797
423	19	1.0	294	9	AV053808	AV053808		495	19	1.0	336	10	AW436875
424	19	1.0	294	9	AV072258	AV072258		496	19	1.0	337	12	BC881099
425	19	1.0	294	13	BI494649	BI494649		497	19	1.0	339	10	AW517193
426	19	1.0	295	9	AV051937	AV051937		498	19	1.0	339	13	BI792184
427	19	1.0	295	9	AV052449	AV052449		499	19	1.0	339	13	BI902376
428	19	1.0	295	12	BF248631	BF248631		500	19	1.0	340	12	BF712816
429	19	1.0	296	9	AV056758	AV056758		501	19	1.0	341	9	AUI70786
430	19	1.0	296	9	AV050537	AV050537		502	19	1.0	341	9	AV072532
431	19	1.0	297	9	AV050614	AV050614		503	19	1.0	341	10	AW238759
432	19	1.0	297	9	AV052570	AV052570		504	19	1.0	342	9	AA955073
433	19	1.0	297	9	AV076885	AV076885		505	19	1.0	343	12	BG881227
434	19	1.0	298	9	AV049740	AV049740		506	19	1.0	343	14	RI2591
435	19	1.0	298	9	AV049741	AV049741		507	19	1.0	344	9	AA413648
436	19	1.0	298	9	AV051129	AV051129		508	19	1.0	344	10	AW468895
437	19	1.0	298	9	AV076417	AV076417		509	19	1.0	348	14	BQ447491
438	19	1.0	298	12	BF475983	BF475983	naa15e12.	510	19	1.0	349	12	BF365848
439	19	1.0	299	9	AV051899	AV051899		511	19	1.0	350	9	AI215997
440	19	1.0	299	9	AV072922	AV072922		512	19	1.0	350	10	AW215730
441	19	1.0	299	14	R02404	R02404		513	19	1.0	351	12	BG928078
442	19	1.0	300	9	AV054361	AV054361		514	19	1.0	352	13	EG312024
443	19	1.0	300	13	BI715064	BI715064		515	19	1.0	353	14	H48344
444	19	1.0	300	13	BI790017	BI790017		516	19	1.0	354	13	BI282306
							517	19	1.0	355	10	AW047883	

664	19	1.0	472	13	BM570138	BM570138	737	19	1.0	527	10	AV914813	AV914813
665	19	1.0	474	9	AA684165	AA684165	738	19	1.0	527	10	AW514103	AW514103
666	19	1.0	474	9	AA895820	AA895820	739	19	1.0	527	14	BM681386	BM681386
667	19	1.0	474	9	AI391235	AI391235	740	19	1.0	528	14	BM681386	BM681386
668	19	1.0	474	9	AI391235	AI391235	741	19	1.0	530	12	BM681386	BM681386
669	19	1.0	474	14	BM688317	BM688317	742	19	1.0	530	12	BM681386	BM681386
670	19	1.0	474	17	AO598417	AO598417	743	19	1.0	532	9	AI666121	AI666121
671	19	1.0	475	9	AI957446	AI957446	744	19	1.0	532	10	AW632196	AW632196
672	19	1.0	476	12	BM247500	BM247500	745	19	1.0	533	9	AA804284	AA804284
673	19	1.0	477	13	BM011271	BM011271	746	19	1.0	534	9	AI834523	AI834523
674	19	1.0	478	10	BE357414	BE357414	747	19	1.0	534	13	BM270182	BM270182
675	19	1.0	479	9	AL701993	AL701993	748	19	1.0	534	13	BM270182	BM270182
676	19	1.0	479	12	BF568002	BF568002	749	19	1.0	535	17	TA258A01Q	TA258A01Q
677	19	1.0	479	12	BF568002	BF568002	750	19	1.0	535	14	BQ101462	BQ101462
678	19	1.0	480	12	BG049889	BG049889	751	19	1.0	536	12	BF395363	BF395363
679	19	1.0	480	12	BG049889	BG049889	752	19	1.0	537	12	BG879598	BG879598
680	19	1.0	481	13	BG925901	BG925901	753	19	1.0	537	12	BG881121	BG881121
681	19	1.0	481	14	BQ100472	BQ100472	754	19	1.0	540	12	BG878641	BG878641
682	19	1.0	482	14	BQ130107	BQ130107	755	19	1.0	540	12	BG924675	BG924675
683	19	1.0	484	9	AI314943	AI314943	756	19	1.0	540	14	BQ159611	BQ159611
684	19	1.0	484	12	BF508129	BF508129	757	19	1.0	542	14	BQ169608	BQ169608
685	19	1.0	484	14	BQ885536	BQ885536	758	19	1.0	542	17	AO352027	AO352027
686	19	1.0	486	9	AA390864	AA390864	759	19	1.0	543	9	AA706375	AA706375
687	19	1.0	486	14	BM688076	BM688076	760	19	1.0	543	12	BG879037	BG879037
688	19	1.0	487	9	AA846256	AA846256	761	19	1.0	544	12	BG879037	BG879037
689	19	1.0	487	10	BE118824	BE118824	762	19	1.0	544	17	TA299D08P	TA299D08P
690	19	1.0	489	12	BG312033	BG312033	763	19	1.0	545	12	BG312000	BG312000
691	19	1.0	490	17	TA41D02Q	TA41D02Q	764	19	1.0	545	10	AW207680	AW207680
692	19	1.0	491	9	AA939243	AA939243	765	19	1.0	546	12	BG878819	BG878819
693	19	1.0	493	12	BG085100	BG085100	766	19	1.0	546	12	BG878819	BG878819
694	19	1.0	495	12	BG376666	BG376666	767	19	1.0	547	13	BH032117	BH032117
695	19	1.0	495	12	BG408255	BG408255	768	19	1.0	547	13	BH032117	BH032117
696	19	1.0	497	12	BG311963	BG311963	769	19	1.0	547	13	BH032117	BH032117
697	19	1.0	497	13	BM565326	BM565326	770	19	1.0	547	13	BH032117	BH032117
698	19	1.0	498	12	BF708396	BF708396	771	19	1.0	548	13	BH032117	BH032117
699	19	1.0	498	13	BF348696	BF348696	772	19	1.0	548	13	BH032117	BH032117
700	19	1.0	499	17	BH881267	BH881267	773	19	1.0	551	12	BG879873	BG879873
701	19	1.0	499	9	AI694641	AI694641	774	19	1.0	551	12	BG879873	BG879873
702	19	1.0	502	12	BG798887	BG798887	775	19	1.0	552	13	BM570698	BM570698
703	19	1.0	503	9	AA018789	AA018789	776	19	1.0	552	14	BM570698	BM570698
704	19	1.0	503	12	BG671024	BG671024	777	19	1.0	553	13	BM141985	BM141985
705	19	1.0	503	12	BG878726	BG878726	778	19	1.0	553	13	BM141985	BM141985
706	19	1.0	504	13	BM052234	BM052234	779	19	1.0	554	12	BF897862	BF897862
707	19	1.0	506	12	BG312164	BG312164	780	19	1.0	554	12	BF897862	BF897862
708	19	1.0	508	10	AV916833	AV916833	781	19	1.0	555	13	BI493117	BI493117
709	19	1.0	509	9	AI809894	AI809894	782	19	1.0	555	10	AV920741	AV920741
710	19	1.0	510	9	AI647708	AI647708	783	19	1.0	555	10	AV920741	AV920741
711	19	1.0	510	12	BG397917	BG397917	784	19	1.0	555	10	AV920741	AV920741
712	19	1.0	510	12	BG879077	BG879077	785	19	1.0	555	12	BG183461	BG183461
713	19	1.0	511	12	BF365814	BF365814	786	19	1.0	555	12	BG183461	BG183461
714	19	1.0	513	9	AA602691	AA602691	787	19	1.0	555	14	BQ128997	BQ128997
715	19	1.0	513	17	AF262536	AF262536	788	19	1.0	556	9	AA854202	AA854202
716	19	1.0	514	13	BE672066	BE672066	789	19	1.0	557	14	BQ125916	BQ125916
717	19	1.0	516	12	BG311928	BG311928	790	19	1.0	558	13	BQ125916	BQ125916
718	19	1.0	516	12	BG655196	BG655196	791	19	1.0	558	13	BQ125916	BQ125916
719	19	1.0	516	13	BI900617	BI900617	792	19	1.0	558	13	BQ125916	BQ125916
720	19	1.0	517	9	AI408428	AI408428	793	19	1.0	558	13	BQ125916	BQ125916
721	19	1.0	518	9	AA438004	AA438004	794	19	1.0	558	13	BQ125916	BQ125916
722	19	1.0	519	9	AI689626	AI689626	795	19	1.0	558	13	BQ125916	BQ125916
723	19	1.0	520	10	BH284644	BH284644	796	19	1.0	558	13	BQ125916	BQ125916
724	19	1.0	523	12	BEA139409	BEA139409	797	19	1.0	558	13	BQ125916	BQ125916
725	19	1.0	523	12	BEA139409	BEA139409	798	19	1.0	558	13	BQ125916	BQ125916
726	19	1.0	523	12	BF080032	BF080032	799	19	1.0	558	13	BQ125916	BQ125916
727	19	1.0	523	12	BF334736	BF334736	800	19	1.0	558	13	BQ125916	BQ125916
728	19	1.0	523	17	TA51C10Q	TA51C10Q	801	19	1.0	558	13	BQ125916	BQ125916
729	19	1.0	524	9	AA836348	AA836348	802	19	1.0	558	13	BQ125916	BQ125916
730	19	1.0	524	9	AA836348	AA836348	803	19	1.0	558	13	BQ125916	BQ125916
731	19	1.0	524	12	BG312045	BG312045	804	19	1.0	558	13	BQ125916	BQ125916
732	19	1.0	524	12	BF007284	BF007284	805	19	1.0	558	13	BQ125916	BQ125916
733	19	1.0	524	14	H36787	H36787	806	19	1.0	558	13	BQ125916	BQ125916
734	19	1.0	526	12	BG311980	BG311980	807	19	1.0	558	13	BQ125916	BQ125916
735	19	1.0	526	13	BI349051	BI349051	808	19	1.0	558	13	BQ125916	BQ125916
736	19	1.0	526	17	AQ719059	AQ719059	809	19	1.0	558	13	BQ125916	BQ125916

810	19	1.0	573	12	BF181796	BF418796	UI-R-BJ2-	883	19	1.0	614	14	BM729610	ih83f07.x	BM729610	ih83f07.x
811	19	1.0	573	13	BM069944	BM069944	id78f03.x	884	19	1.0	614	14	BM876731	ih70g05.x	BM876731	ih70g05.x
812	19	1.0	574	13	BI439659	BI439659	id91a08.x	885	19	1.0	615	9	AI587560	tr52d05.x	AI587560	tr52d05.x
813	19	1.0	574	13	BM069970	BM069970	id79a09.x	886	19	1.0	615	14	BM730997	ih65h04.x	BM730997	ih65h04.x
814	19	1.0	574	14	BM877991	BM877991	id45g10.x	887	19	1.0	615	17	AZ023692	RPCI-23-3	AZ023692	RPCI-23-3
815	19	1.0	576	13	BI902344	BI902344	id86b04.x	888	19	1.0	616	13	BM569514	kt62g03.y	BM569514	kt62g03.y
816	19	1.0	577	13	BI900573	BI900573	ib81h06.x	889	19	1.0	618	9	AI009785	EST204236	AI009785	EST204236
817	19	1.0	577	13	BJ463501	BJ463501	BJ463501	890	19	1.0	618	10	AW123180	UI-M-BH2-	AW123180	UI-M-BH2-
818	19	1.0	577	14	BQ129589	BQ129589	ib31h08.x	891	19	1.0	618	14	BM729571	ih83a09.x	BM729571	ih83a09.x
819	19	1.0	579	13	BM565282	BM565282	ib36e05.x	892	19	1.0	618	17	AZ564781	201PVD09	AZ564781	201PVD09
820	19	1.0	579	17	AZ119330	AZ119330	RPCI-23-4	893	19	1.0	619	13	BM544417	AGENCOURT	BM544417	AGENCOURT
821	19	1.0	580	12	BF400659	BF400659	UI-R-CA0-	894	19	1.0	621	13	BI468249	ih86e08.x	BI468249	ih86e08.x
822	19	1.0	580	13	BI440667	BI440667	ib93b04.x	895	19	1.0	621	13	BM505792	ih35g12.x	BM505792	ih35g12.x
823	19	1.0	580	13	BI900665	BI900665	ib83e04.x	896	19	1.0	621	17	AZ746896	RPCI-24-6	AZ746896	RPCI-24-6
824	19	1.0	581	12	BE957256	BE957256	UI-M-BG2-	897	19	1.0	622	12	BG301168	HVSMED001	BG301168	HVSMED001
825	19	1.0	581	13	BM508270	BM508270	ib37a03.x	898	19	1.0	622	13	BM507102	ih28a02.x	BM507102	ih28a02.x
826	19	1.0	582	17	AZ960085	AZ960085	2M0228E02	899	19	1.0	623	10	AV913396	AV913396	AV913396	AV913396
827	19	1.0	582	10	AV915747	AV915747	AV915747	900	19	1.0	623	10	BG659663	BG659663	BG659663	BG659663
828	19	1.0	583	13	BI790864	BI790864	id02b10.x	901	19	1.0	623	14	BM786690	K-EST0065	BM786690	K-EST0065
829	19	1.0	583	14	BQ031130	BQ031130	UI-1-CF0-	902	19	1.0	625	14	BM731090	ih67d07.x	BM731090	ih67d07.x
830	19	1.0	584	13	BI288790	BI288790	UI-R-DK0-	903	19	1.0	625	14	BQ602199	MI-P-H0-A	BQ602199	MI-P-H0-A
831	19	1.0	584	13	BM570812	BM570812	ib03g09.x	904	19	1.0	626	10	AV921174	AV921174	AV921174	AV921174
832	19	1.0	585	9	A1781708	A1781708	EST262587	905	19	1.0	627	10	BE262911	BE262911	BE262911	BE262911
833	19	1.0	586	9	AI709001	AI709001	DKFZP686J	906	19	1.0	627	12	BG216941	RST36626	BG216941	RST36626
834	19	1.0	586	9	AI107309	AI107309	mp06d09.r	907	19	1.0	627	13	BI348617	ib89g11.x	BI348617	ib89g11.x
835	19	1.0	587													

956	19	1.0	671	12	BG321803	BG321803	lb33b06.y
957	19	1.0	673	9	A1013913	A1013913	EST208588
958	19	1.0	675	14	B0180952	B0180952	UI-H-EU0-
959	19	1.0	676	14	B0018201	B0018201	UI-H-D71-
960	19	1.0	677	14	B0773110	B0773110	UI-H-FE0-
961	19	1.0	677	13	B1197752	B1197752	602757692
962	19	1.0	678	12	BF281312	BF281312	EST445903
963	19	1.0	678	13	BM541116	BM541116	qj68e11.b
965	19	1.0	679	10	B8552596	B8552596	BB52596
966	19	1.0	680	12	BG719693	BG719693	602690408
967	19	1.0	686	12	BG141674	BG141674	ia92f02.x
968	19	1.0	686	17	AQ341023	AQ341023	RPC111-12
969	19	1.0	689	14	BM677386	BM677386	UI-E-E01-
970	19	1.0	689	17	AQ325182	AQ325182	mgxb0021A
971	19	1.0	693	10	AV918387	AV918387	AV918387
972	19	1.0	693	12	BF723810	BF723810	EST00623
973	19	1.0	696	12	BF723840	BF723840	EST00653
974	19	1.0	697	9	AJ441573	AJ441573	AJ441573
975	19	1.0	698	10	AW300908	AW300908	xk08a12.x
976	19	1.0	698	14	BM682559	BM682559	UI-E-EU0-
977	19	1.0	700	9	AL036834	AL036834	DKFZp564N
978	19	1.0	701	14	BO767081	BO767081	EBR008.SQ
979	19	1.0	702	14	BQ181354	BQ181354	UI-H-EU0-
980	19	1.0	703	13	BM074145	BM074145	MEST80-H1
981	19	1.0	704	14	BQ183750	BQ183750	UI-H-EU0-
982	19	1.0	708	14	BQ191129	BQ191129	UI-R-DZ0-
983	19	1.0	708	17	AG148049	AG148049	Pan.trog1
984	19	1.0	711	14	BM975548	BM975548	UI-CF-EN1
985	19	1.0	712	10	AW190051	AW190051	x111d01.x
986	19	1.0	713	14	BM969132	BM969132	UI-CF-EN0
987	19	1.0	714	13	BI761470	BI761470	603046503
988	19	1.0	716	10	AV920868	AV920868	AV920868
989	19	1.0	719	14	BM999342	BM999342	UI-H-DP0-
990	19	1.0	719	14	BQ573784	BQ573784	UI-H-EZ0-
991	19	1.0	721	10	AW266507	AW266507	L0-1362T3
992	19	1.0	721	14	BQ910199	BQ910199	QHA13H23
993	19	1.0	724	14	BQ176255	BQ176255	UI-M-D72-
994	19	1.0	727	13	BG929307	BG929307	HNC60-1-G
995	19	1.0	729	9	A1956170	A1956170	wt35h04.x
996	19	1.0	729	14	BQ183051	BQ183051	UI-H-EU0-
997	19	1.0	731	13	BI181264	BI181264	UNL-P-FN-
998	19	1.0	735	17	AQ324203	AQ324203	mgxb0017E
999	19	1.0	742	9	AA310764	AA310764	EST181686
1000	19	1.0	742	10	BM6539195	BM6539195	BB639195
	19	1.0	744	13	BI459797	BI459797	603200849

ALIGNMENTS

RESULT 1	
BM695392	
LOCUS	
DEFINITION	645 bp mRNA linear EST 28-FEB-2002
	UI-E-CQ1-aev-n-19-0-UI.r1 UI-E-CQ1 Homo sapiens CDNA clone
	UI-E-CQ1-aev-n-19-0-UI 5' mRNA sequence.
ACCESSION	BM695392
VERSION	BM695392.1
KEYWORDS	GI:19008650
SOURCE	EST
ORGANISM	human.
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1 (bases 1 to 645)
	Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene
	discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	9704477
COMMENT	Contact: Soares, MB
	Program for Rat Gene Discovery and Mapping
	University of Iowa
	451 Eckstein Medical Research Building Iowa City, IA 52242, USA
	Tel: 319 335 8250

Fax: 319 335 9562
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
1. 645
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-CQ1-aer-n-19-0-UI"
/clone_lib="UI-E-CQ1"
/tissue_type="optic nerve"
/dev_stage="adult"
/lab_host="PH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site.1: EcoR I; Site.2: Not I;
UI-E-CQ1 is a normalized cDNA library containing the
following tissue(s): optic nerve. The library was
constructed according to Bonaïdo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA,
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CCATTAAGTG. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye

Fax: 319 335 9565
Email: mscaores@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Dr. M. Bento Soares, University of Iowa
Genetics (www.resgen.com). Researchers may obtain clones from Research
Seq primer: M13 Reverse.

[illegible]

RESULT 3	BM547887	1076 bp	mRNA	linear	EST 20-FEB-2002
LOCUS	BM547887	1076 bp	mRNA	linear	EST 20-FEB-2002
DEFINITION	ACENSCOURT_6531767 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5732633 5', mRNA sequence.				
ACCESSION	BM547887				
VERSION	BM547887.1	GI:18782034			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 1076)	NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Invitrogen cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			
	Plate: LLAM12735	row: a	column: 18	
	High quality sequence start: 9			
	High quality sequence stop: 677.			

FEATURES	source
location/Qualifiers	
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/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone=IMAGE:5732633"	
/clone_lib="NIH_MGC_124"	
/tissue_type="hippocampus"	
/lab_host="DH10B"	
/note="Organ: brain; Vector: pCMV-SPORT6; site_1: EcorV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcorV site is destroyed upon cloning). Average	

[illegible]


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BASE COUNT      114 a      177 c      174 g      147 t
ORIGIN

Query Match      22.8%; Score 427; DB 14; Length 612;
Best Local Similarity 99.8%; Pred. No. 4.8e-133;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1359 GGGTTTGGCAACTGCGTGGAGCTGCAAGGCTTCAGCTGCGCTTCAACTGGAACGACGAGCGC 1418
DB 524 GGGTTTGGCAACTGCGTGGAGCTGCAAGGCTTCAGCTGCGCTTCAACTGGAACGACGAGCGC 465
QY 1419 TCGAAACCCGAAACCGTTACATCTGCCAGTGTGGCCAGGACACATCTCCCGGTGGGCG 1478
DB 464 TCGAAACCCGAAACCGTTACATCTGCCAGTGTGGCCAGGACACATCTCCCGGTGGGCG 405
QY 1479 CCAGGCTCTGAGGCTGACCATGCTCCCTGCGCTTCCCGGTGGGAGGAGCGGCTCTGC 1538
DB 404 CCAGGCTCTGAGGCTGACCATGCTCCCTGCGCTTCCCGGTGGGAGGAGCGGCTCTGC 345
QY 1539 TTACCTGTCTGCCACCTGTCTGGAACAGGCGGCGAGTGAAGACACATGCTCATGTCC 1598
DB 344 TTACCTGTCTGCCACCTGTCTGGAACAGGCGGCGAGTGAAGACACATGCTCATGTCC 285
QY 1599 AAAGAGTCTCAGACCTTGCACATGCGCAAGTGTGGCCAGGAGGAGGAGGAGGCGCAG 1658
DB 284 AAAGAGTCTCAGACCTTGCACATGCGCAAGTGTGGCCAGGAGGAGGAGGAGGCGCAG 225
QY 1659 TGAGGGCCAGGAGTGTAGTGTAGGAAGCTGGGGCGCTTCCGCTGCTTTTGTATTGGGA 1718
DB 224 TGAGGGCCAGGAGTGTAGTGTAGGAAGCTGGGGCGCTTCCGCTGCTTTTGTATTGGGA 165
QY 1719 AGATGGCTTCAATTAGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1778
DB 164 AGATGGCTTCAATTAGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 105
QY 1779 CTCTTCCACCTGGCCAGACCCCTGTGGGCGAGCGGAGCTTCCCTGTGGCATGAACCCC 1836
DB 104 CTCTTCCACCTGGCCAGACCCCTGTGGGCGAGCGGAGCTTCCCTGTGGCATGAACCCC 47

RESULT 7
B006636/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

B006636
UI-H-EII-aza-p-20-0-UI.s1 NCI_CGAP_EII Homo sapiens cDNA clone
IMAGE:5846275 3', mRNA sequence.
B006636
B006636.1 GI:19731536
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 744)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1. .744
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5846275"
/clone_lib="NCI_CGAP_EII"

BASE COUNT      130 a      225 c      214 g      175 t
ORIGIN

TAG_L1B=UI-H-EII
TAG_TISSUE=chondrosarcoma
TAG_SEQ=ACACTTGCAC"

Query Match      22.8%; Score 427; DB 14; Length 744;
Best Local Similarity 99.8%; Pred. No. 4.2e-133;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1359 GGGTTTGGCAACTGCGTGGAGCTGCAAGGCTTCAGCTGCGCTTCAACTGGAACGACGAGCGC 1418
DB 524 GGGTTTGGCAACTGCGTGGAGCTGCAAGGCTTCAGCTGCGCTTCAACTGGAACGACGAGCGC 465
QY 1419 TCGAAACCCGAAACCGTTACATCTGCCAGTGTGGCCAGGAGGAGGAGGAGGAGGAGG 1478
DB 464 TCGAAACCCGAAACCGTTACATCTGCCAGTGTGGCCAGGAGGAGGAGGAGGAGGAGG 405
QY 1479 CCAGGCTCTGAGGCTGACCATGCTCCCTGCGCTTCCCGGTGGGAGGAGGAGGAGGAGG 1538
DB 404 CCAGGCTCTGAGGCTGACCATGCTCCCTGCGCTTCCCGGTGGGAGGAGGAGGAGGAGG 345
QY 1539 TTACCTGTCTGCCACCTGTCTGGAACAGGCGGCGAGTGAAGACACATGCTCATGTCC 1598
DB 344 TTACCTGTCTGCCACCTGTCTGGAACAGGCGGCGAGTGAAGACACATGCTCATGTCC 285
QY 1599 AAAGAGTCTCAGACCTTGCACATGCGCAAGTGTGGCCAGGAGGAGGAGGAGGAGGAGG 1658
DB 284 AAAGAGTCTCAGACCTTGCACATGCGCAAGTGTGGCCAGGAGGAGGAGGAGGAGGAGG 225
QY 1659 TGAGGGCCAGGAGTGTAGTGTAGGAAGCTGGGGCGCTTCCGCTGCTTTTGTATTGGGA 1718
DB 224 TGAGGGCCAGGAGTGTAGTGTAGGAAGCTGGGGCGCTTCCGCTGCTTTTGTATTGGGA 165
QY 1719 AGATGGCTTCAATTAGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1778
DB 164 AGATGGCTTCAATTAGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 105
QY 1779 CTCTTCCACCTGGCCAGACCCCTGTGGGCGAGCGGAGCTTCCCTGTGGCATGAACCCC 1836
DB 104 CTCTTCCACCTGGCCAGACCCCTGTGGGCGAGCGGAGCTTCCCTGTGGCATGAACCCC 47

RESULT 8
AW299257/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AW299257
xS48f01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
similar to SW:MANR_HUMAN P22857 MACROPHAGE MANNOS RECEPTOR
PRECURSOR. ; mRNA sequence.
AW299257
AW299257.1 GI:6708934
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
611 bp
mrna
linear
EST 18-JAN-2000
IMAGE:2772889 3'

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Db 200 CAGGAGTGTAGTGTAGGAAGCTGGGCGCTTCGCTGCTTTGATTGGGAAGATGG 141
QY 1726 CTTCAATTAGATGGCAGAGAGACACCGCAGTGGTCCAAAAGAGCTGCTCTTCC 1785
Db 140 CTTCAATTAGATGGCAGAGAGAGACACCGCAGTGGTCCAAAAGAGCTGCTCTTCC 81
QY 1786 ACCTGGCCAGACCTGTGGGGCAGCGAGCTTCCCTGTGGCATGAACCCAC 1838
Db 80 ACCTGGCCAGACCTGTGGGGCAGCGAGCTTCCCTGTGGCATGAACCCAC 28

RESULT 10
AW001740/c
LOCUS
DEFINITION
  ws04c06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496202 3',
  mRNA sequence.
ACCESSION
  AW001740
VERSION
  AW001740.1 GI:5848656
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
  Emmert-Buck, M.D., Ph.D.
  CDNA Library Preparation: M. Bento Soares, Ph.D.
  DNA Sequencing by: Greg Lennon, Ph.D.
  Cloning by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html
  Insert Length: 846 Std Error: 0.00
  Seq primer: -40UP from Gibco
  High quality sequence stop: 477.
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    /db_xref="taxon:9606"
    /clone="IMAGE:2496202"
    /clone_lib="NCI_CGAP_Kid11"
    /lab_host="DH102"
    /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
    a modified polylinker; Site_1: Not I; Site_2: Eco RI;
    Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
    prepared, and ss circles were made in vitro. Following HAP
    purification, this DNA was used as tracer in a subtractive
    hybridization reaction. The driver was PCR-amplified cDNAs
    from a pool of 5,000 clones made from the same library
    (cloneIDs 1322376-1323911, 1456007-1456775, and
    1500352-1502855). Subtraction by Bento Soares and M.
    Fatima Bonaldo."
  BASE COUNT 94 a 148 c 137 g 110 t 1 others
  ORIGIN
    Query Match 20.7%; Score 388; DB 10; Length 490;
    Best Local Similarity 99.6%; Pred. No. 6.le-120;
    Matches 488; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
    QY 1376 GGAGCTGCAGGCTTACGCTTCACTTGAACACCGCTGCAAAACCGGAACCG 1435
    Db 490 GGAGCTGCAGGCTTACGCTTCACTTGAACACCGCTGCAAAACCGGAACCG 431
    QY 1436 TTACATCTGCCAGTTGCCAGGACACATCTCCCGTGGGGCCCGAGGCTCTGAGGCT 1495
    Db 430 TTACATCTGCCAGTTGCCAGGACACATCTCCCGTGGGGCCCGAGGCTCTGAGGCT 371

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QY 1496 GACCACATGGCTCCCTCGCCTGGCCTGGGAGCACCGGCTTGTCTTACCTGTGCCCCACC 1555
Db 370 GACCACATGGCTCCCTCGCCTGGCCTGGGAGCACCGGCTTGTCTTACCTGTGCCCCACC 311
QY 1556 TGCTGTGAACAAGGGCCAGGTTAAGACACATGCTCTATGCTCCAAAGAGGTCTCAGACCT 1615
Db 310 TGCTGTGAACAAGGGCCAGGTTAAGATCATCATGCTCTATGCTCCAAAGAGGTCTCAGACCT 251
QY 1616 TGCACATATGCCAGAGTTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1675
Db 250 TGCACATATGCCAGAGTTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191
QY 1676 GTGTTAAGAAAGCTGGGCGCTTTCGCTCTTTGATTGGGAAGATGGGCTTCAATTAG 1735
Db 190 GTGTTAAGAAAGCTGGGCGCTTTCGCTCTTTGATTGGGAAGATGGGCTTCAATTAG 131
QY 1736 ATGGCGAAGGAGAGACACCGCCAGTGGTCCAAAAGAGGTCTCTTCCACCTGGGCCA 1795
Db 130 ATGGCGAAGGAGAGACACCGCCAGTGGTCCAAAAGAGGTCTCTTCCACCTGGGCCA 71
QY 1796 GACCTGTGGGCGAGCGAGCTTCCCTGTGGCATGAACCCACCGGCTATTAATTATGA 1855
Db 70 GACCTGTGGGCGAGCGAGCTTCCCTGTGGCATGAACCCACCGGCTATTAATTATGA 11
QY 1856 ATCAGCTGAA 1865
Db 10 ATCAGCTGAA 1

RESULT 11
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LOCUS
DEFINITION
  UI-H-BI3-alt-d-07-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone
  IMAGE:3068581 3', mRNA sequence.
ACCESSION
  AW451907
VERSION
  AW451907.1 GI:6992683
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  The sequence contained an oligo-dT track that was present in the
  oligonucleotide that was used to prime the synthesis of first
  strand cDNA and therefore this may represent a bonafide poly A
  tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
  NCI-CGAP clone distribution information can be found through the
  I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html
  Seq primer: M13 Forward
  POLYA=Yes.
FEATURES
  Location/Qualifiers
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    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:3068581"
    /clone_lib="NCI_CGAP_Sub5"
    /lab_host="DH10B (Life Technologies)"
    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
    polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub5
    is a subtracted library derived from NCI_CGAP_Sub4. The
    NCI_CGAP_Sub5 library had 3 million recombinants. A
    single-stranded DNA preparation of NCI_CGAP_Sub4 was used
    as a tracer in a subtractive hybridization with a driver
    comprising: the IMAGE pool (NCI_CGAP_Kid3 pool 1 LLAM
    3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs
    1322376-1323911, 1456008-1456775, 1500352-1502855));

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QY 1789 TGGCCAGACCCCTGTGGGGAGCGGAGCTTCCCTGTGGCATGAACCCAC 1838
 Db 75 TGGCCAGACCCCTGTGGGGAGCGGAGCTTCCCTGTGGCATGAACCCAC 26

RESULT 13
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 LOCUS
 DEFINITION ty80a06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285362 3', mRNA linear EST 07-MAR-2000
 AI627475
 mRNA sequence.
 AI627475
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 509)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/ohrp/image/image.html
 Insert Length: 655 Std Error: 0.00
 Seq primer: -400P from Gibco
 High quality sequence stop: 464
 POLYA=No.

FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2285362"
 /clone_lib="NCI_CGAP_Kid11"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo." Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 98 a 152 c 143 g 116 t
 ORIGIN

Query Match 19.3%; Score 363; DB 9; Length 509;
 Best Local Similarity 99.6%; Pred. No. 1.4e-111;
 Matches 463; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1374 GTGGAGCTGCAGGCTTCAGCTCCCTTCACTGGAAGCAGGCTGCAAAACCGAAAC 1433
 Db 492 GTGGAGCTGCAGGCTTCAGCTCCCTTCACTGGAAGCAGGCTGCAAAACCGAAAC 433

QY 1434 GCTTACATCTGCCAGTTTGCCAGGAGCACATCTCCCGTGGGGCCAGGGTCTGAGGC 1493
 Db 432 GCTTACATCTGCCAGTTTGCCAGGAGCACATCTCCCGTGGGGCCAGGGTCTGAGGC 373

QY 1494 CTGACCACATGCTCCCTCGGCTGCGGAGCACCGGCTCTGCTTACCTGTCTGCCCA 1553
 Db 372 CTGACCACATGCTCCCTCGGCTGCGGAGCACCGGCTCTGCTTACCTGTCTGCCCA 313

QY 1554 CCTGTCTGGAACAAGGGCCAGGTTAAGACCACTGCTCATGTCCAAAGAGTCTCAGAC 1613
 Db 312 CCTGTCTGGAACAAGGGCCAGGTTAAGACCACTGCTCATGTCCAAAGAGTCTCAGAC 253

QY 1614 CTTGCACAATGCCAGAAGTTGGGCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1673
 Db 252 CTTGCACAATGCCAGAAGTTGGGCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGT 193

QY 1674 GAGTGTAGAAAGAGCTGGGGCCCTTCGCTCTTTTGAATTTGGGAAGATGGGCTTCAAT 1733
 Db 192 GAGTGTAGAAAGAGCTGGGGCTTCCTTCGCTCTTTTGAATTTGGGAAGATGGGCTTCAAT 133

QY 1734 AGATGGCGAAGGAGGAGACACCGCCAGTGGTCCAAAAAGGTGCTCTTCCACCTGGCC 1793
 Db 132 AGATGGCGAAGGAGGAGACACCGCCAGTGGTCCAAAAAGGTGCTCTTCCACCTGGCC 73

QY 1794 CAGACCCCTGTGGGCGAGGAGCTTCCCTGTGGCATGAACCCAC 1838
 Db 72 CAGACCCCTGTGGGCGAGGAGCTTCCCTGTGGCATGAACCCAC 28

RESULT 14
 AI792411
 LOCUS
 DEFINITION an34b09.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700537 5', similar to TR:043692 043692 25 KDA TRYPSIN INHIBITOR. ; mRNA sequence.

ACCESSION AI792411
 VERSION AI792411.1 GI:5340127
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 463)
 NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute / National Institute of Dental Research,
 Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 This read is a RESEQUENCE of a previously sequenced human clone.
 Original clone citation: see original entry for original citation information
 This 5' resequenced clone has no previous 5' data to verify this new read against
 Seq primer: -40RP from Gibco
 High quality sequence stop: 429.
 Location/Qualifiers
 1..463
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1700537"
 /clone_lib="Gessler Wilms tumor"
 /sex="pooled (6)"
 /lab_host="DH10B"
 /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; RNA was prepared from a pool of 6 anonymous Wilms' tumor RNAs. RNA was prepared by acid-phenol, followed by one round of oligo dr selection. cDNA library preparation was with the BRL/Life Tech. Superscript Plasmid system. An oligo-dr NotI primer for first strand synthesis generated gcggcgcgc(t)n at the 3' end of the clones. A 5' SalI adaptor was used with sequence 5'-gtcagccacgcgcgcg-3'. Resulting cDNAs were size selected (average size 2 kb), NotI digested, and ligated into NotI/SalI-cut pSPORT1. Library was constructed by Dr. Manfred Gessler."

BASE COUNT 80 a 163 c 143 g 77 t
 ORIGIN

Query Match 18.6%; Score 348; DB 9; Length 463;

Mon Dec 30 09:16:11 2002

purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1322376-132311, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 94 a 147 c 142 g 111 t
ORIGIN

Query Match 17.4%; Score 326; DB 9; Length 494;
Best Local Similarity 99.5%; Pred. No. 3.3e-99;
Matches 426; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 ACAGGCTGCAAAACCCGAAACCGTTACATCTGCAGATTGCCCCAGGACACATCTCCC 1470
DB 453 ACCAGGCTGCAAAACCCGAAACCGTTACATCTGCAGATTGCCCCAGGACACATCTCCC 394
QY 1471 GGTGGGCCCCAGGCTCTGAGGCTTGACCATGTTGCTCCCTGCGCTGGGAGCACC 1530
DB 393 GGTGGGCCCCAGGCTCTGAGGCTTGACCATGTTGCTCCCTGCGCTGGGAGCACC 334
QY 1531 GGCTCTGCTTACCTGTGCTCCACCTCTCTGGAACAGGCGCAGGTTAAGACACATGCCC 1590
DB 333 GGCTCTGCTTACCTGTGCTCCACCTCTCTGGAACAGGCGCAGGTTAAGACACATGCCC 274
QY 1591 TCATGTCCTCAAGAGGCTCTGAGGCTTGACCATGTTGCTCCCTGCGCTGGGAGCACC 1650
DB 273 TCATGTCCTCAAGAGGCTCTGAGGCTTGACCATGTTGCTCCCTGCGCTGGGAGCACC 214
QY 1651 GAGGCCAGTGGGCGCAGGAGTGTAGAGAGAGCTGGGCGCTTCCCTGCTGCTTTT 1710
DB 213 GAGGCCAGTGGGCGCAGGAGTGTAGAGAGAGCTGGGCGCTTCCCTGCTGCTTTT 154
QY 1711 GATTGGGAAGATGGCTTCAATTAGATGGCGAAGAGAGGACACCGCAGTGGTCCAAA 1770
DB 153 GATTGGGAAGATGGCTTCAATTAGATGGCGAAGAGAGGACACCGCAGTGGTCCAAA 94
QY 1771 AGGCTGCTCTTCCACCTGGCCAGGCTGTGGGCGCAGGAGCTTCCCTGCTGGCATG 1830
DB 93 AGGCTGCTCTTCCACCTGGCCAGGCTGTGGGCGCAGGAGCTTCCCTGCTGGCATG 34
QY 1831 AACCCAC 1838
DB 33 AACCCAC 26

RESULT 16
BM708158
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

BM708158 405 bp mRNA linear EST 28-FEB-2002
UI-E-C11-aft-b-08-0-UI.r1 UI-E-C11 Homo sapiens cDNA clone
UI-E-C11-aft-b-08-0-UI 5', mRNA sequence.
BM708158
BM708158.1 GI:19021416
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 405)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

Best Local Similarity 99.7%; Pred. No. 1.5e-106; Indels 0; Gaps 0;
Matches 398; Conservative 0; Mismatches 1;

QY 14 CAGCCAGCTGACTCTGAGAGTTGTAATAGTCTCCATCCAGCTGAGAAACAGCCGG 73
DB 18 CAGCCAGCTGACTCTGAGAGTTGTAATAGTCTCCATCCAGCTGAGAAACAGCCGG 77
QY 74 GTGGCTGAGCAGGCTGTGCACAGGAGCACCCTGACGGGCGCAACACCCATGCTCATCC 133
DB 78 GTGGCTGAGCAGGCTGTGCACAGGAGCACCCTGACGGGCGCAACACCCATGCTCATCC 137
QY 134 AGAGACTCCCTGCTGGGCGGCGATCTCTGCTGTGCTCTGCGCTCTCTTGGCACCAC 193
DB 138 AGAGACTCCCTGCTGGGCGGCGATCTCTGCTGTGCTCTGCGCTCTCTTGGCACCAC 197
QY 194 CTGGGCGAGAGTGTGCCACCCAGCTGTCAGGAGGAGGCTCGATGGGCGGAGCCCTGAA 253
DB 198 CTGGGCGAGAGTGTGCCACCCAGCTGTCAGGAGGAGGCTCGATGGGCGGAGCCCTGAA 257
QY 254 CAGGAAGGAGAGTTCTTCTCTCTCTCTGTCACACCCGCTGCGAGCTGGGTCCAGCC 313
DB 258 CAGGAAGGAGAGTTCTTCTCTCTCTCTGTCACACCCGCTGCGAGCTGGGTCCAGCC 317
QY 314 CCTCTGGGCTGACATCGGAGGCTGGAGTGGAGTGGAGCTGGGCGCAACTGCTCAAGC 373
DB 318 CCTCTGGGCTGACATCGGAGGCTGGAGTGGAGTGGAGCTGGGCGCAACTGCTCAAGC 377
QY 374 CAGGCGAGCCTCTGTGGAAATCCCAACCCCGAGCCTGGC 412
DB 378 CAGGCGAGCCTCTGTGGAAATCCCAACCCCGAGCCTGGC 416

RESULT 15
AI433291/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AI433291 494 bp mRNA linear EST 13-APR-1999
ti86501.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138857 3',
mRNA sequence.
AI433291
AI433291.1 GI:4288147
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 494)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Cloning distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 891 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 473.
Location/Qualifiers
1. .494
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2138857"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site: 1; Not 1; Site 2: Eco RI;
plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP

FEATURES
source

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 Reverse.

FEATURES

source
 1..405
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-E-C11-aft-b-08-0-UI"
 /clone_lib="UI-E-C11"
 /tissue_type="RPE and Choroid"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-E-C11 is a normalized cDNA library containing the
 following tissue(s): RPE and Choroid. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pT7T3-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is ACCGA.
 This library was created for the program, Gene Discovery
 in the Visual System, supported by National Eye Institute
 (NEI)."

BASE COUNT 92 a 111 c 127 g 75 t

Query Match 17.1%; Score 320; DB 14; Length 405;
 Best Local Similarity 99.7%; Pred. No. 3.8e-97;
 Matches 370; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1369 ACTGGTGGAGCTGACGCTTTCAGTGGCTTCAACTGGAAGACACGAGCGCTGCAAAACCC 1428
 Db 1 ACTGGTGGAGCTGACGCTTTCAGTGGCTTCAACTGGAAGACACGAGCGCTGCAAAACCC 60
 QY 1429 GAAACCGTTACATCTGCCAGTTTCCCGAGGACACATCTCCCGTGGGGCCAGGGTCT 1488
 Db 61 GAAACCGTTACATCTGCCAGTTTCCCGAGGACACATCTCCCGTGGGGCCAGGGTCT 120
 QY 1489 GAGCGCTGACACATGCTCCCTGCGCTGGGAGCAGCGCTCTGCTTACCTGTCT 1548
 Db 121 GAGCGCTGACACATGCTCCCTGCGCTGGGAGCAGCGCTCTGCTTACCTGTCT 180
 QY 1549 GCGCACCTGTCTGAACAAGGGCCAGGTTAAGACCATGCTTCCAAAGAGGCT 1608
 Db 181 GCGCACCTGTCTGAACAAGGGCCAGGTTAAGATCATGCTTCCAAAGAGGCT 240
 QY 1609 CAGACCTTGCAATGCCAAGTTGGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1668
 Db 241 CAGACCTTGCAATGCCAAGTTGGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
 QY 1669 GGAGTGAAGTTAGAGAGCTGGGGCCCTTCCCTGCTTTTATTGGGAAGATGGGCT 1728
 Db 301 GGAGTGAAGTTAGAGAGCTGGGGCCCTTCCCTGCTTTTATTGGGAAGATGGGCT 360
 QY 1729 CAATTAGATGG 1739
 Db 361 CAATTAGATGG 371

RESULT 17
 BI764403
 LOCUS 603046141F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186219 5',
 DEFINITION mRNA sequence.
 BI764403
 BI764403.1 GI:15755981

KEYWORDS

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 836)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE Unpublished (1999)
 JOURNAL Mammalian Gene Collection (MGC)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-femail.nih.gov
 Tissue procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Cloning Distribution: Incyte Genomics, Inc.
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M11465 row: b column: 12
 High quality sequence stop: 761.

FEATURES

source
 1..836
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5186219"
 /clone_lib="NIH_MGC_116"
 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH_MGC Library."
 BASE COUNT 157 a 255 c 271 g 153 t
 ORIGIN

Query Match 16.4%; Score 308; DB 13; Length 836;
 Best Local Similarity 99.2%; Pred. No. 2.5e-93;
 Matches 628; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 QY 284 GCACAACCGCTGCGCAGCTGGGTCCAGCCCTCGCGCTGACATGCGGAGGCTGGACTG 343
 Db 61 GCACAACCGCTGCGCAGCTGGGTCCAGCCCTCGCGCTGACATGCGGAGGCTGGACTG 120
 QY 344 GAGTGACAGCTTGGCCCAACTGGCTCAAGCCAGGCGAGCCCTCTGTGAATCCCAACCCC 403
 Db 121 GAGTGACAGCTTGGCCCAACTGGCTCAAGCCAGGCGAGCCCTCTGTGAATCCCAACCCC 180
 QY 404 GAGCCTGGCATCCGGCTTGGCGCACCTGCAAGTGGGCTGGAACATGCAAGTGGCTGCC 463
 Db 181 GAGCCTGGCATCCGGCTTGGCGCACCTGCAAGTGGGCTGGAACATGCAAGTGGCTGCC 240
 QY 464 CGCGGGCTTGGCGCTCTTTTGAAGTGGTCAAGTGGGCTGGAACATGCAAGTGGCTGCC 523
 Db 241 CGCGGGCTTGGCGCTCTTTTGAAGTGGTCAAGTGGGCTGGAACATGCAAGTGGCTGCC 300
 QY 524 CAGCCACGCGGAGGAGAGTGTCTCGCAACGCCACTGCAACCCACTACACGAGCTCGT 583
 Db 301 CAGCCACGCGGAGGAGAGTGTCTCGCAACGCCACTGCAACCCACTACACGAGCTCGT 360
 QY 584 GTGGGCCACTCAAGCCAGCTGGGCTGTGGGGCGACCTGTGCTGCGAGGCCAGCAGC 643
 Db 361 GTGGGCCACTCAAGCCAGCTGGGCTGTGGGGCGACCTGTGCTGCGAGGCCAGCAGC 420
 QY 644 GATAGAGCCTTGTCTGTGCTTACTTCCCGGAGGCAACTGGGAGTCAACGGGAGAC 703
 Db 421 GATAGAGCCTTGTCTGTGCTTACTTCCCGGAGGCAACTGGGAGTCAACGGGAGAC 480

QY 704 AATCATCCCTATATAAGAGGTCCTGGTTCCTGCTCTGCACAGCAGTCTCTCAGGCTG 763
 Db 481 ATCTGTCCTCTATATAAGAGGTCCTGGTTCCTGCTCTGCACAGCAGTCTCTCAGGCTG 540
 QY 764 CTTCAAGCTGGACCATCGAGGGGCTCTGTGAGTCCCGAGGAATCCTTGTGCGCAT 823
 Db 541 CTTCAAGCTGGACCATCGCA-GGGGCTCTGTGAGTCCCGAGGAATCCTTGTGCGCAT 599
 QY 824 GAGTGTCCAGAACCATGGAGCTCTCAACATCAGACCTGCCACTTGTCCCGCTGG 883
 Db 600 GAGTGTCCAGAACCATGGAGCTCTCAACATCAGACCTGCCACTTGTCCCGCTGG 659
 QY 884 CTACACGGGAGTACTGCAAGTGAAGTGCAG 916
 Db 660 CTACACGGGAGTACTGCAAGTGAAGTGCAG 692

RESULT 18
 AA903561/c 383 bp mRNA linear EST 09-JUN-1998
 LOCUS OK63a05.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1518608 3',
 DEFINITION mRNA sequence.
 ACCESSION AA903561
 VERSION AA903561.1 GI:3038684
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 383)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 846 Std Error: 0.00
 Seq primer: -40m13 fwd. Et from Amersham
 High quality sequence stop: 302.

FEATURES
 source
 1..383
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1518608"
 /clone_lib="NCI_CGAP_GC4"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from 3 pooled
 germ cell tumors, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT73
 vector. Library is normalized. Library was constructed by
 Bento Soares and M. Fatima Bonaldo."
 77 a 114 c 105 g 87 t

BASE COUNT
 ORIGIN
 Query Match 15.2%; Score 285; DB 9; Length 383;
 Best Local Similarity 99.7%; Pred. No. 2e-85;
 Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1486 CTTGAGGCTGACCATGCTCCCTGCGCTGGAGCAGCGCTCTTACCTG 1545
 Db 383 CTTGAGGCTGACCATGCTCCCTGCGCTGGAGCAGCGCTCTTACCTG 324

QY 1546 TCTGCCACCTGCTGTGAACAAGGCCAGGTTAAGACCATGCTCTATGCTCCAAAGG 1605
 Db 323 TCTGCCACCTGCTGTGAACAAGGCCAGGTTAAGACCATGCTCTATGCTCCAAAGG 264
 QY 1606 TCTCAGACCTTGCACATGCAAGTGGCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 1665
 Db 263 TCTCAGACCTTGCACATGCAAGTGGCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 204
 QY 1666 CAGGAGTGTAGTGTGTAGAAGAAGCTGGGGCCCTTCGGCTGCTTTTGTGAGATGGG 1725
 Db 203 CAGGAGTGTAGTGTGTAGAAGAAGCTGGGGCCCTTCGGCTGCTTTTGTGAGATGGG 144
 QY 1726 CTTCAATAGATGCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1785
 Db 143 CTTCAATAGATGCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 84

QY 1786 ACCTGGCCAGACCTGTGGGGCAGCGAGCTTCC 1821
 Db 83 ACCTGGCCAGACCTGTGGGGCAGCGAGCTTCC 48

RESULT 19
 AI827695/c 492 bp mRNA linear EST 18-DEC-1999
 LOCUS wfilla11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
 DEFINITION IMAGE:2350268 3', mRNA sequence.
 ACCESSION AI827695
 VERSION AI827695.1 GI:5448366
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 492)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 759 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 455.

FEATURES
 source
 1..492
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2350268"
 /clone_lib="Soares_NFL_T_GBC_S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBHL19W, testis NHT, and B-cell
 NCI_CGAP_GCB1) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."
 98 a 149 c 142 g 103 t

BASE COUNT
 ORIGIN
 Query Match 15.2%; Score 285; DB 9; Length 492;
 Best Local Similarity 99.5%; Pred. No. 1.7e-85;
 Matches 385; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1452 GCCCAGGAGCAGCATCTCCCGTGGGCCAGCGGCTCTGAGGCTGACACATGGCTCCCT 1511

FEATURES

High quality sequence stop: 480.
Location/Qualifiers
1..500
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5183898"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

BASE COUNT 84 a 180 c 151 g 85 t
ORIGIN

Query Match 13.8%; Score 259; DB 13; Length 500;
Best Local Similarity 99.4%; Pred. No. 8.3e-77;
Matches 359; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCCTTTGTCCACAGCCAGCCGCTGACTCTCTGGAGATTGTGAATAGCTCCATCCAGCCTG 60
Db 15 CTCCTTTGTCCACAGCCAGCCGCTGACTCTCTGGAGATTGTGAATAGCTCCATCCAGCCTG 74
QY 61 AGAACAAGCCGGTGGCTGAGCAGGCTGTGCACGAGCAGCTGACGGGCCCAACAGAC 120
Db 75 AGAACAAGCCGGTGGCTGAGCAGGCTGTGCACGAGCAGCTGACGGGCCCAACAGAC 134
QY 121 CCATGCTGCATCCAGAGACCTCCCTGGCCGGGGGCACTCTCTGGCTGTGCTCTGGCCC 180
Db 135 CCATGCTGCATCCAGAGACCTCCCTGGCCGGGGGCACTCTCTGGCTGTGCTCTGGCCC 194
QY 181 TCCTTGGCCACACCGCTGGGCGAGAGGTGTGGCCACCCAGCTGCAGGAGAGGCTCCGATGG 240
Db 195 TCCTTGGCCACCGCTGGGCGAGAGGTGTGGCCACCCAGCTGCAGGAGAGGCTCCGATGG 254
QY 241 CGGAGCCCTGAACAGGAGGAGAGTTCTTGTCTCCTCTCCCTGCACAAACCGCTCGCGCA 300
Db 255 CGGAGCCCTGAACAGGAGGAGAGTTCTTGTCTCCTCTCCCTGCACAAACCGCTCGCGCA 314
QY 301 GCTGGTCCAGCCCTCGGCTGACATCGGAGGCTGGACTGGAGTGACAGCCTGGCCCC 360
Db 315 GCTGGTCCAGCCCTCGGCTGACATCGGAGGCTGGACTGGAGTGACAGCCTGGCCCC 374
QY 361 A 361
Db 375 A 375

RESULT 24
BI759120
LOCUS
DEFINITION
603042530F1 NIH_MGC_116 Homo sapiens mRNA linear EST 25-SEP-2001
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
BI759120.1 GI:15750698

ORGANISM

human.
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 709)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: L1A11456 row: 1 column: 08
High quality sequence stop: 709.

FEATURES

Location/Qualifiers
1..709
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5182999"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

BASE COUNT 124 a 240 c 220 g 125 t
ORIGIN

Query Match 13.8%; Score 259; DB 13; Length 709;
Best Local Similarity 99.4%; Pred. No. 6.7e-77;
Matches 359; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCCTTTGTCCACAGCCAGCCTGACTCTCTGGAGATTGTGAATAGCTCCATCCAGCCTG 60
Db 48 CTCCTTTGTCCACAGCCAGCCTGACTCTCTGGAGATTGTGAATAGCTCCATCCAGCCTG 107
QY 61 AGAACAAGCCGGTGGCTGAGCAGGCTGTGCACGAGCAGCTGACGGGCCCAACAGAC 120
Db 108 AGAACAAGCCGGTGGCTGAGCAGGCTGTGCACGAGCAGCTGACGGGCCCAACAGAC 167
QY 121 CCATGCTGCATCCAGAGACCTCCCTGGCCGGGGCACTCTCTGGCTGTGCTCTGGCCCC 180
Db 168 CCATGCTGCATCCAGAGACCTCCCTGGCCGGGGCACTCTCTGGCTGTGCTCTGGCCCC 227
QY 181 TCCTTGGCCACACCTGGCAGAGGTGTGGCCACCCAGCTGCAGGAGAGGCTCCGATGG 240
Db 228 TCCTTGGCCACACCTGGCAGAGGTGTGGCCACCCAGCTGCAGGAGAGGCTCCGATGG 287
QY 241 CGGAGCCCTGAACAGGAGGAGAGTTCTTGTCTCTCTCTCCCTGCACAAACCGCTCGCGCA 300
Db 288 CGGAGCCCTGAACAGGAGGAGAGTTCTTGTCTCTCTCTCCCTGCACAAACCGCTCGCGCA 347
QY 301 GCTGGTCCAGCCCTGGCGCTGACATGCGGAGGCTGGAGTGGAGTGACAGCCTGGCCCC 360
Db 348 GCTGGTCCAGCCCTGGCGCTGACATGCGGAGGCTGGAGTGGAGTGACAGCCTGGCCCC 407
QY 361 A 361
Db 408 A 408

RESULT 25

BI760121

LOCUS

DEFINITION

603044615F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5184962 5',
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BI760121 710 bp mRNA linear EST 25-SEP-2001
603044615F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5184962 5',
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

human.
Homo sapiens

LOCUS BM924615 1034 bp mRNA linear EST 12-MAR-2002
 DEFINITION AGENCOURT_6767842 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5761001
 5', mRNA sequence.
 ACCESSION BM924615
 VERSION BM924615.1 GI:19374994
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1034)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12808 row: o column: 18
 High quality sequence stop: 685.

FEATURES
 source
 1..1034
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NIH_MGC_116"
 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

BASE COUNT 186 a 336 c 321 g 189 t 2 others
 ORIGIN
 Query Match 13.1%; Score 246; DB 14; Length 1034;
 Best Local Similarity 99.4%; Pred. No. 1.2e-72;
 Matches 346; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CAGCCAGCCTGACTCTGGAGATTGTGAATAGCTCCATCCAGCCTGAGAAACAGCCGG 73
 Db 11 CAGCCAGCCTGACTCTGGAGATTGTGAATAGCTCCATCCAGCCTGAGAAACAGCCGG 70
 QY 74 GTGGCTGAGCAGGCTGTGCACGAGCAGCCTGACGGGCCCAACAGACCCATGCTGCATCC 133
 Db 71 GTGGCTGAGCAGGCTGTGCACGAGCAGCCTGACGGGCCCAACAGACCCATGCTGCATCC 130
 QY 134 AGAGACCTCCCTGGCGGGGATCTCTGGCTGTGCTCTGGCCCTCTTGGCCACCAC 193
 Db 131 AGAGACCTCCCTGGCGGGGATCTCTGGCTGTGCTCTGGCCCTCTTGGCCACCAC 190
 QY 194 CTGGGAGAGGTGTGGCCACCCAGCTGACGAGCAGCCTGCGGATGCGCGGAGCCCTGAA 253
 Db 191 CTGGGAGAGGTGTGGCCACCCAGCTGACGAGCAGCCTGCGGATGCGCGGAGCCCTGAA 250
 QY 254 CAGGAGAGAGTTTCTTGTCT 313
 Db 251 CAGGAGAGAGTTTCTTGTCT 310
 QY 314 CCCTGCGGCTGACATGCGGAGGCTGGAGTGACAGCTGGGCCA 361
 Db 311 CCCTGCGGCTGACATGCGGAGGCTGGAGTGACAGCTGGGCCA 358

LOCUS BM924615 1034 bp mRNA linear EST 12-MAR-2002
 DEFINITION AGENCOURT_6767842 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5761001
 5', mRNA sequence.
 ACCESSION BM924615
 VERSION BM924615.1 GI:19374994
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1034)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: MGC Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11461 row: n column: 03
 High quality sequence stop: 704.

FEATURES
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 1..710
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NIH_MGC_116"
 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

BASE COUNT 131 a 228 c 226 g 125 t
 ORIGIN
 Query Match 13.5%; Score 254; DB 13; Length 710;
 Best Local Similarity 99.3%; Pred. No. 3.1e-75;
 Matches 404; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 486 GAAGTGTGACGCTATGGTTTGAGAGGGGCGGTACAGCCAGCGGAGGAGGTGT 545
 Db 283 GAAGTGTGACGCTATGGTTTGAGAGGGGCGGTACAGCCAGCGGAGGAGGTGT 342
 QY 546 GCTCGCAACGCCACTGCACCTACACGAGCTGTGTGGGCCACCTCAAGCCAGCTG 605
 Db 343 GCTCGCAACGCCACTGCACCTACACGAGCTGTGTGGGCCACCTCAAGCCAGCTG 402
 QY 606 GGCTGTGGGGGCGACCTGTGCTCTGCGAGCGGCGAGACGATAGAGCCTTTGTGTGCC 665
 Db 403 GGCTGTGGGGGCGACCTGTGCTCTGCGAGCGGCGAGACGATAGAGCCTTTGTGTGCC 462
 QY 666 TACTCCCCGGAGCACTGGGAGGTCAACGGGAGACAATCATCCCTATAGAAGGTT 725
 Db 463 TACTCCCCGGAGCACTGGGAGGTCAACGGGAGACAATCATCCCTATAGAAGGTT 522
 QY 726 GCCTGGTGTTCGCTCTGACACGCCAGTGTCTCAGCTGCTTCAAGCCTGGGACCATGCA 785
 Db 523 GCCTGGTGTTCGCTCTGACACGCCAGTGTCTCAGCTGCTTCAAGCCTGGGACCATGCA 582
 QY 786 GGGGGGCTCTGTGAGTCTCCAGGATCTTGTGATGAGTGTGCGCATGAGCTGCCAAGCATGGAGT 845
 Db 583 GGGGGGCTCTGTGAGTCTCCAGGATCTTGTGATGAGTGTGCGCATGAGCTGCCAAGCATGGAGT 642
 QY 846 CTCAACATCAGCAGCTGCCACTGCCACTGTCCCTTGGCTACACGG 892
 Db 643 CTCAACATCAGCAGCTGCCACTGCCACTGTCCCTTGGCTACACGG 689

RESULT 26
 BM924615

QY	1795	AGACCTGTGGGCGCGGAGCTTCCTGTGGCATGAACCCAC	1838
Db	74		
		AGACCTGTGGGCGCGGAGCTTCCTGTGGCATGAACCCAC	31
RESULT 28			
AA976491/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			

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BASE COUNT
ORIGIN
          95 a 143 c 131 g 112 t
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Best Local Similarity 99.7%; Pred. No. 8,9e-71;
Matches 291; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
/Note=Organ: kidney; Vector: Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Pooled kidney tumors. 5' adaptor sequence: 5'
GAATTCGGCACCAG 3' 3' adaptor sequence: 5'
CUCGATGGTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."

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Query Match	12.8%	Score	241;	DB	9;	Length	481;
Best Local Similarity	99.7%;	Pred. No.	8.9e-71;				
Matches	291;	Conservative	0;	Mismatches	1;	Indels	0;
Gaps							
QY	1505	GTCTCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTTACCTGTCTGCCCACCTGCTCTGGAA	1564				
Db	364						
QY	1565	CAAGGGCCAGGTTTAAGACACCATGCCCTCATGTCCAAAGAGGTTCTCAGACCTTCGCACATG	1624				
Db	304	CAAGGGCCAGGTTTAAGATCATCATGCCCTCATGTCTCCAAAGAGGTTCTCAGACCTTCGCACATG	245				
QY	1625	CCGAAAGTTTGGGCAGAGAGAGGCCAGGGAGGCCCACTGAGGCCACGAGGAGTGAGTGTAGAA	1684				
Db	244	CCGAAAGTTTGGGCAGAGAGAGGCCAGGGAGGCCCACTGAGGCCACGAGGAGTGAGTGTAGAA	185				
QY	1685	GAAGCTGGGGCCCTTCGCCCTGCTTTTGATTTGGGAAGATGGGCTTCAAATTAGATGGCGAAG	1744				
Db	184	GAAGCTGGGGCCCTTCGCCCTGCTTTTGATTTGGGAAGATGGGCTTCAAATTAGATGGCGAAG	125				

1745 GAGAGGACACCGCCAGTGGTCCAAAAAGGTGCTCTCTTCACCTGGCCCG 1796
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RESULT 29
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LOCUS
DEFINITION
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nn48f01.r1 NCI_CGAP_Kid6 Homo sapiens CDNA clone IMAGE:1087129 5',
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288 bp linear EST 26-SEP-1997
AA582202
mRNA sequence.
AA582202
AA582202.1 GI:2359562
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 288)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, ph.D.

Email: Cgaps@remail.ru
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Stratagene, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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 High quality sequence stop: 256.

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High quality sequence stop: 256.	
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/note="Organ: kidney; Vector: Bluescript SK-; Site:1: ECORI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Pooled kidney tumors. 5' adaptor sequence: 5', GAATTCGCACGAG 3', 3' adaptor sequence: 5', CTCGATGTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."	
57 a	92 c 73 g 66 t
BASE COUNT	

	Query Match	12.6%	Score 237;	DB 9;	Length 288;
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	Matches 287;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
QY	1534	TCTGTTTACCTGTCGTGCCACCTGTCCTGGACACAGGCGCAGGTTAAGACACACATGCCTCA	1593		
DB	288	TCGTGTTTACCTGTCGTGCCACCTGTCCTGGACACAGGCGCAGGTTAAGACACACATGCCTCA	229		
QY	1594	TGTCACAAAGAGTCTCAGACCTTGCACAATGCCAAGTTGGCGACAGAGGCGAGGAG	1653		
DB	228	TGTCACAAAGAGTCTCAGACCTTGCACAATGCCAAGTTGGCGACAGAGGCGAGGAG	169		
QY	1654	GCCAGTGAAGGGCCAGGGAGTGAGTGTTAGAAAGCTGGGGGCCCTTCGCGCTCTTTTGAT	1713		
DB	168	GCCAGTGAAGGGCCAGGGAGTGAGTGTTAGAAAGCTGGGGTCCCTTCGCGCTCTTTTGAT	109		
QY	1714	TGGGAAGATGGCGCTCAATTAGATGGCGAAGAGAGGACACGCCAGTGGTCCAAAAGG	1773		
DB	108	TGGGAAGATGGCGCTCAATTAGATGGCGAAGAGAGGACACGCCAGTGGTCCAAAAGG	49		
QY	1774	CTGCTCTCTTCCACCTTGGCCCGACACCTCTGGGGCGACGGAGCTTCCC	1821		


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Db 54 GCGGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAATAATTATGAATCAGCTG 1
RESULT 31
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LOCUS a31h02.sl Soares_testis_NHT Homo sapiens cDNA clone 1391955 3',
DEFINITION mRNA sequence.
ACCESSION AA812725
VERSION AA812725.1 GI:2882789
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 330)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbrrp/image/image.html
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 254.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1391955"
/clone_lib="Soares_testis_NHT"
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/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGGCCCATTTTATTTTATTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 64 a 102 c 81 g 83 t
ORIGIN
Query Match 10.7%; Score 200; DB 9; Length 330;
Best Local Similarity 99.3%; Pred. No. 5.9e-57;
Matches 300; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1537 GCTTACCTCTGCCACCTGTCTGAAACAGGCGGCTTAGACACACATGCTCATGT 1596
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QY 1597 CCAAGAGGCTCTAGACCTTGCACATGCCAGAAAGTTGGSCAGAGAGCGAGGCC 1656
Db 270 CCAAGAGGCTCTAGACCTTGCACATGCCAGAAAGTTGGSCAGAGAGCGAGGCC 211

QY 1657 AGTAGGGCCAGGAGTGAGTCTTAGAACAGCTGGGGCCCTTCGCCCTTTGATTGG 1716
Db 210 AGTAGGGCCAGGAGTGAGTCTTAGAACAGCTGGGGCCCTTCGCCCTTTGATTGG 151

QY 1717 GAAGATGGGCTTCAATTAGATGGCGAAGAGAGGACACCGCCAGTGGTCCAAAAGGCTG 1776
Db 150 GAAGATGGGCTTCAATTAGATGGCGAAGAGAGGACACCGCCAGTGGTCCAAAAGGCTG 91

QY 1777 CTCCTCTCCACCTGCCCCAGACCCCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCC 1836

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Db 90 CTCTCTTCCACCTGGCCAGACCTGTGGGCGAGGAGCTTCCCTGTGGCATGAACCCC 31
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Db 30 AC 29
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DEFINITION similar to contains TAR1.C1 TAR1 repetitive element ;, mRNA
sequence.
ACCESSION AI657201
VERSION AI657201.1 GI:4741180
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 312)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbrrp/image/image.html
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Seq primer: -40UP from Gibco
High quality sequence stop: 287.
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/db_xref="taxon:9606"
/clone="IMAGE:2244211"
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/tissue_type="pooled germ cell tumors"
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI-CGAP_GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 60 a 101 c 84 g 67 t
ORIGIN
Query Match 10.3%; Score 193; DB 9; Length 312;
Best Local Similarity 99.6%; Pred. No. 1.3e-54;
Matches 243; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1514 CCTGCCCTGGGAGCAGCGGCTCTGCTTACCTGTCTGCCACCTGTCTGAAACAGGCCA 1573
Db 244 CCTGCCCTGGGAGCAGCGGCTCTGCTTACCTGTCTGCCACCTGTCTGAAACAGGCCA 185

QY 1574 GGTTAAGACACATGCTCATGTCCAAAGAGGTCTCAGACCTTGCACATGCCAGAGTT 1633
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QY 1634 GGGCAGAGAGGAGGAGGAGGCCAGTGGAGGCCAGGAGTGTAGTGTAGAGAGCTGGG 1693

```


Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Insert length: 310 Std Error: 0.00
Seq primer: -40UP from Gibco.

FEATURES
source
1. .229
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1870704"
/clone_lib="NCI-CGAP_Kid3"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 44 a 76 c 53 g 56 t
ORIGIN

Query Match 7.7%; Score 144; DB 9; Length 229;
Best Local Similarity 99.5%; Pred. No. 4e-38;
Matches 194; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 AGAGCGAGGAGGCGAGTGGCCAGGAGTGTAGAGAGCTGGGGCCCTTCG 1701
DB 229 AGAGCGAGGAGGCGAGTGGCCAGGAGTGTAGAGAGCTGGGGCCCTTCG 170
QY 1702 CCTCTTTTGGAGATGGGCTTCAATTAGATGGCGAGAGGACACCGCCAGT 1761
DB 169 CCTCTTTTGGAGATGGGCTTCAATTAGATGGCGAGAGGACACCGCCAGT 110
QY 1762 GGTCCAAAAGGCTCTCTTCCACCTGGCCAGACCTGTGGGCGAGGAGCTTCC 1821
DB 109 GGTCCAAAAGGCTCTCTTCCACCTGGCCAGACCTGTGGGCGAGGAGCTTCC 50
QY 1822 TGTGCGATGAACCCC 1836
DB 49 TGTGCGATGAACCCC 35

RESULT 39
W79362 411 bp mRNA linear EST 17-OCT-1996
LOCUS 2d72d09.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
DEFINITION IMAGE:346193.5 similar to SW:MANR_HUMAN P22897 MACROPHAGE MANNOS
RECEPTOR PRECURSOR. [1]; mRNA sequence.

ACCESSION W79362
VERSION W79362.1 GI:1390151
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 411)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine

DKFZp434F2413 5', mRNA sequence.
AL040183
AL040183.1 GI:5409148
EST.
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 704)
AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Koehrer K
MIPS

Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
SI sequence also available.
This clone (DKFZp434F2413) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
1. .704
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp434F2413"
/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

BASE COUNT 150 a 207 c 207 g 139 t 1 others
ORIGIN

Query Match 7.7%; Score 145; DB 9; Length 704;
Best Local Similarity 100.0%; Pred. No. 8.9e-39;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 840 GGACGCTCAACATCAGACCTGCCACTGTCCTCCCTGGCTTACACGGGCGAGATAC 899
DB 184 GGACGCTCAACATCAGACCTGCCACTGTCCTCCCTGGCTTACACGGGCGAGATAC 243
QY 900 TGCCAAAGTCAGCTGACGCTGCAGTGTGTGCACGGCGCGTTCGGGAGGAGGAGTGTCTG 959
DB 244 TGCCAAAGTCAGCTGACGCTGCAGTGTGTGCACGGCGCGTTCGGGAGGAGGAGTGTCTG 303
QY 960 TCGGCTGTGACATCGGCTACGGGG 984
DB 304 TCGGCTGTGACATCGGCTACGGGG 328

RESULT 38
AI245843/c 229 bp mRNA linear EST 28-JAN-1999
LOCUS qk32g01.x1 NCI-CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1870704 3',
DEFINITION mRNA sequence.

ACCESSION AI245843
VERSION AI245843.1 GI:3841240
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 229)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 698 Std Error: 0.00
 Seq primer: mob.REGA+ET.

FEATURES

Location/Qualifiers

1..411

/organism="Homo sapiens"

/db_xref="GDB:1271568"

/db_xref="taxon:9606"

/clone="IMAGE:346193"

/clone_lib="Soares_fetal_heart_NbHH19w"

/sex="unknown"

/dev_stages="19 weeks"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: heart; Vector: p7T3D (Pharmacia) with a

modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTACCAATCTGAAGTGGGAGCGCCGCACTTTTCTTTTCTTTTCTTTT

3'] double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified p7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by

M.Patino Bonaldo. This library was constructed from the

same fetus as the fetal lung library, Soares fetal lung

NbHL19w."

BASE COUNT 88 a 130 c 108 g 82 t 3 others

ORIGIN

Query Match 6.6%; Score 123; DB 14; Length 411;

Best Local Similarity 100.0%; Pred. No. 2.9e-31;

Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1359 GGGTTTGGCAACTCGGTGGAGCTCAGGCTTCAGCTGCTTCAACTGGAACGACGCGC 1418

Db 128 GGGTTTGGCAACTCGGTGGAGCTCAGGCTTCAGCTGCTTCAACTGGAACGACGCGC 187

QY 1419 TGCAAAACCCGAAACCGTTACATCTGCGAGTTTGCACGAGGACATCTCCGGTGGGCG 1478

Db 188 TGCAAAACCCGAAACCGTTACATCTGCGAGTTTGCACGAGGACATCTCCGGTGGGCG 247

QY 1479 CCA 1481

Db 248 CCA 250

RESULT 40

BI759353

LOCUS

DEFINITION

603043013F1 NTH_MGC_116 Homo sapiens cDNA clone IMAGE:5183330 5',

mRNA sequence.

ACCESSION

BI759353

VERSION

BI759353.1 GI:15750931

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM11457 row: j column: 03

High quality sequence stop: 723.

Location/Qualifiers

1..916

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5183330"

/clone_lib="NIH_MGC_116"

/lab_host="DH10B"

/note="Organ: pooled colon, kidney, stomach; Vector:

PCMV-SPORf6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA

source anonymous pool of 3 colons, age 26 yo male, 49 yo

female, 71 yo male colon; 46 yo male kidney, and pool of 2

stomachs, 62 yo male and 70 yo female. Library is

oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.4 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

023. Note: this is a NIH_MGC Library."

BASE COUNT 153 a 306 c 278 g 178 t 1 Others

ORIGIN

Query Match 6.0%; Score 113; DB 13; Length 916;

Best Local Similarity 99.4%; Pred. No. 3.8e-28;

Matches 163; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCTTTTGTCTCCACGAGCCGCTGACTCTCTGGAGATTGTGAATAGCTCCATCCAGCCGTG 60

Db 21 CTCTTTTGTCTCCACGAGCCGCTGACTCTCTGGAGATTGTGAATAGCTCCATCCAGCCGTG 80

QY 61 AGAAACAAGCCGGTGGCTGAGCAGGCTGTGCACGAGCAGCTGTACGGGCCCAACAGAC 120

Db 81 AGAAACAAGCCGGTGGCTGAGCAGGCTGTGCACGAGCAGCTGTACGGGCCCAACAGAC 140

QY 121 CCATGCTGCATCAGAGACCTCCCTGCGCGGGGCATCTCCTG 164

Db 141 CCATGCTGCATCAGAGACCTCCCTGCGCGGGGCATCTCCTG 184

RESULT 41

BI759735

LOCUS

DEFINITION

603045609F1 NTH_MGC_116 Homo sapiens cDNA clone IMAGE:5185803 5',

mRNA sequence.

ACCESSION

BI759735

VERSION

BI759735.1 GI:15751313

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM11464 row: a column: 04

High quality sequence stop: 453.

Location/Qualifiers

1..457

/organism="Homo sapiens"

/db_xref="taxon:9606"

FEATURES

source

prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 91 a 117 c 106 g 111 t
ORIGIN

Query Match 5.2%; Score 97; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.4e-22;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1742 AAGGAGGACACCGCAGTGGTCCAAAAGGCTCTCTCCACCTGCCACGACCCCT 1801
|||||
DB 388 AAGGAGGACACCGCAGTGGTCCAAAAGGCTCTCTCTCCACCTGCCACGACCCCT 329
|||||

QY 1802 GTGGGCGAGCGAGCTTCCCTGTGGCATGAACCCAC 1838
|||||
DB 328 GTGGGCGAGCGAGCTTCCCTGTGGCATGAACCCAC 292
|||||

RESULT 43
AI150446/c
LOCUS
DEFINITION
AI150446
3', mRNA sequence.
ACCESSION
AI150446.1 GI:3678915
VERSION
KEYWORDS
SOURCE
EST.
human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 460)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 732 Std Error: 0.00
Seq primer: -40ml3 fwd. Et from Amersham
High quality sequence stop: 458.
Location/Qualifiers
1. 460
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1752556"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and treated with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGCGGCGCCCAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."

FEATURES
source
88 a 130 c 127 g 115 t
BASE COUNT
ORIGIN

/clone="IMAGE:5185803"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector: RNA
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

BASE COUNT 80 a 163 c 139 g 75 t
ORIGIN

Query Match 5.8%; Score 109; DB 13; Length 457;
Best Local Similarity 99.4%; Pred. No. 1.3e-26;
Matches 159; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCTTTTGTCCACGAGCCGCTGACTCTGGAGATTGTGAATAGCTCCATCCAGCCTG 60
|||||
DB 142 CTCTTTTGTCCACGAGCCGCTGACTCTGGAGATTGTGAATAGCTCCATCCAGCCTG 201
|||||

QY 61 AGAACAAGCCGGTGGCTGAGCAGCTGTGCACGAGCAGCTGACGGGCGCCACAGAC 120
|||||
DB 202 AGAACAAGCCGGTGGCTGAGCAGCTGTGCACGAGCAGCTGACGGGCGCCACAGAC 261
|||||

QY 121 CCATGCTGCATCCAGAGACCTCCCTGGCGGGGGCATCT 160
|||||
DB 262 CCATGCTGCATCCAGAGACCTCCCTGGCGGGGGCATCT 301
|||||

RESULT 42
AI522123/c
LOCUS
DEFINITION
AI522123
mRNA sequence.
AI522123
VERSION
AI522123.1 GI:4436258
KEYWORDS
SOURCE
EST.
human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 425)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 519 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. 425
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2138136"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was

FEATURES
source
88 a 130 c 127 g 115 t
BASE COUNT
ORIGIN

```

Query Match
Best Local Similarity 5.1%; Score 95; DB 9; Length 450;
Matches 195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1422 AAAACCGGAACGTTACATCTCCAGTTCCTCCAGGAGACACATCTCCCGTGGGGCCCA 1481
|||||
Db 460 AAAACCGGAACGTTACATCTCCAGTTCCTCCAGGAGACACATCTCCCGTGGGGCCCA 401
|||||

QY 1482 GGTCTCTGAGGCGCTGACCATGCTCCCTCGCTGCGCTGGGAGCAGCGCTCTGCTTA 1541
|||||
Db 400 GGTCTCTGAGGCGCTGACCATGCTCCCTCGCTGCGCTGGGAGCAGCGCTCTGCTTA 341
|||||

QY 1542 CTTGCTGCTCCCTCTCTGGAACAGGCGGAGGTAAGACCATGCTCTCAATGTCACAA 1601
|||||
Db 340 CTTGCTGCTCCCTCTCTGGAACAGGCGGAGGTAAGACCATGCTCTCAATGTCACAA 281
|||||

QY 1602 GAGGTCTCAGACCTTGC 1618
|||||
Db 280 GAGGTCTCAGACCTTGC 264
|||||

RESULT 44
BF527554
LOCUS
DEFINITION
602040477F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4178394
5', mRNA sequence.
ACCESSION
BF527554
VERSION
BF527554.1 GI:11614917
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 756)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LIA9486 row: i column: 19
High quality sequence stop: 721.
FEATURES
Location/Qualifiers
1..756
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4178394"
/tissue_type="anaplastic oligodendroglioma with lp/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT
164 a 213 c 248 g 131 t
ORIGIN

Query Match
Best Local Similarity 3.9%; Score 73; DB 12; Length 756;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1619 ACAATGCCAGAGTTGGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1678
|||||
Db 598 ACAATGCCAGAGTTGGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGT 657
|||||

QY 1679 TTAGAAGAAGCTG 1691
|||||

```

```

Db 658 TTAGAAGAAGCTG 670
|||||

RESULT 45
AI942280
LOCUS
DEFINITION
AI942280.1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461520 3',
mRNA sequence.
ACCESSION
AI942280
VERSION
AI942280.1 GI:5706936
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 264)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 538 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 229.
FEATURES
Location/Qualifiers
1..264
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:2461520"
/lab_host="NCI-CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 132376-132391, 1456007-1456775, and
150552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."
BASE COUNT
50 a 77 c 54 g 83 t
ORIGIN

Query Match
Best Local Similarity 3.5%; Score 66; DB 9; Length 264;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1811 CGGAGCTTCCCTGTCATGACCCACCGGGGTATTAATATGATCAGCTGAAAAA 1870
|||||
Db 73 CGGAGCTTCCCTGTCATGACCCACCGGGGTATTAATATGATCAGCTGAAAAA 14
|||||

QY 1871 AAAAAA 1876
|||||
Db 13 AAAAAA 8
|||||

RESULT 46
BG608968
LOCUS
DEFINITION
322458 MARG 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION
BG608968
VERSION
BG608968.1 GI:13658946

```


EST.
 SOURCE pig.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 REFERENCE 1 (bases 1 to 339)
 AUTHORS Fahrrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
 Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
 and Keele,J.W.
 TITLE Design and use of two pooled tissue normalized cDNA libraries for
 EST discovery in swine
 JOURNAL Unpublished (2000)
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt_trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCAGTCACGACG
 Plate: 97 row: P column: 1
 Seq primer: ATTTAGGTGACACTATAG.
 Location/Qualifiers
 1..339
 /organism="Sus scrofa"
 /db_xref="taxon:9823"
 /clone_lib="MARC lPig"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
 Library made from pooled tissue from day 11, 13, 15, 20,
 and 30 embryos."
 BASE COUNT 67 a 100 c 109 g 63 t
 ORIGIN
 Query Match 1.9%; Score 35; DB 12; Length 339;
 Best Local Similarity 100.0%; Pred. NO. 0.087;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1029 GACCTGAGGATCGAGGAGCTGCTCATGCTGTC 1063
 ||||||||||||||||||||||||||||||||||||||||
 Db 251 GACCTGAGGATCGAGGAGCTGCTCATGCTGTC 285
 ||||||||||||||||||||||||||||||||||||||||
 RESULT 47
 BF198258 248012 MARC 2Pig Sus scrofa cDNA 5', mRNA linear EST 03-NOV-2000
 LOCUS
 DEFINITION
 ACCESSION BF198258
 VERSION BF198258.1 GI:11089145
 KEYWORDS EST.
 SOURCE pig.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 REFERENCE 1 (bases 1 to 429)
 AUTHORS Fahrrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
 Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
 and Keele,J.W.
 TITLE Design and use of two pooled tissue normalized cDNA libraries for
 EST discovery in swine
 JOURNAL Unpublished (2000)
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt_trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCAGTCACGACG
 Plate: 78 row: B column: 9
 Seq primer: ATTTAGGTGACACTATAG.
 Location/Qualifiers
 1..429
 /organism="Sus scrofa"
 /db_xref="taxon:9823"
 /clone_lib="MARC 2Pig"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
 Library made from pooled tissue from testis, ovary,
 endometrium, hypothalamus, pituitary, and placenta."
 BASE COUNT 97 a 125 c 122 g 85 t
 ORIGIN
 Query Match 1.8%; Score 34; DB 12; Length 429;
 Best Local Similarity 100.0%; Pred. NO. 0.16;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1135 AGAGCCAGAAAGTCAGGACATCTCGCCTTCTA 1168
 ||||||||||||||||||||||||||||||||||||||||
 Db 176 AGAGCCAGAAAGTCAGGACATCTCGCCTTCTA 209
 ||||||||||||||||||||||||||||||||||||||||
 RESULT 48
 BM481198 53084 MARC 4BOV Bos taurus cDNA 5', mRNA linear EST 05-FEB-2002
 LOCUS
 DEFINITION
 ACCESSION BM481198
 VERSION BM481198.1 GI:18531526
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 263)
 AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
 Casas,E., Wray,J.E., White,J., Cho,J., Fahrrenkrug,S.C., Bennett,
 G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
 Perteau,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
 Keele,J.W.
 TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 JOURNAL Genome Res. 11 (4), 626-630 (2001)
 MEDLINE 21180013
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt_trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCAGTCACGACG
 Plate: 3 row: L column: 9
 Seq primer: ATTTAGGTGACACTATAG.
 Location/Qualifiers
 1..263
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="MARC 4BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;

Library made from pooled tissue from day 20 and day 40 embryos."

BASE COUNT 45 a 72 c 98 g 47 t 1 others

ORIGIN

Query Match 1.7%; Score 32; DB 13; Length 263;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1170 CTGGCGCCCTGGAGACCAACAGGTGAC 1201
|||||
Db 73 CTGGCGCCCTGGAGACCAACAGGTGAC 104

RESULT 49
AI628809/c

LOCUS ty72g03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2284660 3',
DEFINITION mRNA sequence.

ACCESSION AI628809
VERSION AI628809.1 GI:4665609
KEYWORDS EST.
SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 241)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco.

FEATURES

source

1..241
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2284660"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: pMT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid11
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."

BASE COUNT 48 a 56 c 48 g 88 t 1 others

ORIGIN

Query Match 1.7%; Score 31; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 CTGGGCGCCCTGCCTGCTTTTGTATGGAA 1719
|||||
Db 209 CTGGGCGCCCTGCCTGCTTTTGTATGGAA 179

RESULT 50
BI518200/c

LOCUS BI518200
DEFINITION 603042018T1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5182397 3',
mRNA sequence.

ACCESSION BI518200
VERSION BI518200.1 GI:15342992
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 911)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM11455 row: c column: 06

High quality sequence start: 37

High quality sequence stop: 202.

FEATURES

source

1..911
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5182397"
/lab_host="DH10B"
/note="Organ: Pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

BASE COUNT 144 a 288 c 259 g 220 t

ORIGIN

Query Match 1.7%; Score 31; DB 13; Length 911;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1757 CCAGTGGTCCAAAAGGCTGCTCTTCCAC 1787
|||||
Db 64 CCAGTGGTCCAAAAGGCTGCTCTTCCAC 34

Search completed: December 29, 2002, 01:11:31
Job time : 2479 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 15:41:47 ; Search time 4786 Seconds
(without alignments)
11407.612 Million cell updates/sec

Title: US-09-944-896-49
Perfect score: 1876
Sequence: 1 cttctttgtccaccagccca.....tcagctgaaaaaaaaaaaaa 1876

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_higo_hum.*
40: em_higo_mus.*
41: em_higo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	1721	91.7	1775	6	AX191503	AX191503 Sequence
2	1296	69.1	1341	6	AX191493	AX191493 Sequence
3	981.6	52.3	3293	9	HSM804652	AL833339 Homo sapi
4	704.4	37.5	2900	9	AB060195	AB060195 Macaca fa
5	672.8	35.9	690	6	AX366554	AX366554 Sequence
6	550	29.3	1328	9	BC008616	BC008616 Homo sapi
7	414.6	22.1	163427	9	AC009053	AC009053 Homo sapi
8	414.6	22.1	177479	9	AC009153	AC009153 Homo sapi
9	414.6	22.1	197460	9	AC126771	AC126771 Homo sapi
10	411.4	21.9	179675	2	AC026468	AC026468 Homo sapi
11	411.4	21.9	190595	9	AC009022	AC009022 Homo sapi
12	409.8	21.8	180596	9	AC009060	AC009060 Homo sapi
13	409.8	21.8	191108	2	AC097265	AC097265 Pan trogl
14	380	20.3	204182	2	AC097271	AC097271 Pan trogl
15	373.6	19.9	200409	2	AC097331	AC097331 Pan trogl
16	244.4	13.0	200409	2	AC097331	AC097331 Pan trogl
17	241.2	12.9	205044	2	AC009125	AC009125 Homo sapi
18	240.4	12.8	205044	2	AC009125	AC009125 Homo sapi
19	192.6	10.3	79023	2	AC021951	AC021951 Homo sapi
20	145.6	7.8	179237	2	AC111287	AC111287 Rattus no
21	145.6	7.8	179237	2	AC098076	AC098076 Rattus no
22	139.4	7.4	200755	2	AC093451	AC093451 Mus muscu
23	133.8	7.1	79023	2	AC021951	AC021951 Homo sapi
24	95.8	5.1	2340	9	AK096051	AK096051 Homo sapi
25	75	4.0	125020	9	AF429315	AF429315 Homo sapi
26	73.8	3.9	179237	2	AC111287	AC111287 Rattus no
27	67.2	3.6	125020	9	AF429315	AF429315 Homo sapi
28	55.2	2.9	1491	6	AX101173	AX101173 Sequence
29	55.2	2.9	1669	9	AK027395	AK027395 Homo sapi
30	55.2	2.9	1690	9	AK027395	AK027395 Homo sapi
31	55.2	2.9	1824	6	AX358802	AX358802 Sequence
32	55.2	2.9	1824	6	AX362295	AX362295 Sequence
33	55.2	2.9	2272	6	AX101175	AX101175 Sequence
34	55.2	2.9	4574	6	AX086850	AX086850 Sequence
35	55.2	2.9	4574	9	HSM801829	AX136861 Homo sapi
36	55.2	2.9	4877	6	AX285067	AX285067 Sequence
37	55.2	2.9	4877	6	AX285068	AX285068 Sequence
38	55.2	2.9	4877	6	AX285079	AX285079 Sequence
39	55	2.9	2403	6	AX235373	AX235373 Sequence
40	53.6	2.9	2400	6	AX235369	AX235369 Sequence
41	53.2	2.8	3052	10	AF109674	AF109674 Rattus no
42	48.8	2.6	166126	2	AF003686	AP003686 Oryza sat
43	48.4	2.6	2664	9	HSHEPEGF	X62489 H.sapiens D
44	48.4	2.6	2668	9	HSTNX12	X71923 H.sapiens X
45	48.4	2.6	100267	9	HSMMC3W36A	U89337 Homo sapien

ALIGNMENTS

RESULT 1
AX191503
LOCUS AX191503
DEFINITION Sequence 25 from Patent WO0149728.
ACCESSION AX191503
VERSION AX191503.1 GI:15209689
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1775)
AUTHORS Kato,S. and Kimura,T.
TITLE Human proteins having hydrophobic domains and dnas encoding these proteins

linear PAT 15-AUG-2001

JOURNAL Patent: WO 0149728-A 25 12-JUL-2001;
Protegene Inc. (JP) : SAGAMI CHEMICAL RESEARCH CENTER (JP)
FEATURES Location/Qualifiers
1. .1775
/organism="Homo sapiens"
/db_xref="taxon:9606"
62..1402
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC51149.1"
/db_xref="GI:15209690"
/translation="MLHPSPGPGCHLLAVLLALLGTAWAEVWPQLOEQAPMAGALN
RKSEFLLSLHNRLSVQPPADMRRLDWSLSLAQLAARAAALCGITPPLASGLWR
TLQVNMQLLPAGLASFEVYSLWFAEGRYSHAAECARNATCTHTYOLVWATSSQ
LGGRHLCSQAIAEAFVCAVSPGNWVNGKTIIPYKGAWSLCTASVSGCFKAW
DHAGGLCEPRNPMSCQNHRLNISTCHCHCPGPGYGRYCVQRCSLQCVHGRFRE
ECSVCIDIGYGAQCAATKVHPFPHTCDLRIDGCFMVSSEADTYVRAKMKQKRGVL
AOLKSKOVODILAPYLGRLEWTNEVIDSETRFWLGLTYKTAKDSFRWATGEHOAF
TSFAFGPDNHEGNCVELQASAFNNQNRKTRNRYICQFAEHISRWGPGS"
BASE COUNT 360 a 541 c 549 g 325 t
ORIGIN

Query Match		91.7%	Score 1721;	DB 6;	Length 1775;
Best Local Similarity		97.9%	Pred. No. 0;		
Matches 1764;		Conservative	0;	Mismatches 10;	Indels 27; Gaps 1;
QY	63	AAACAAGCCGGTGGCTGACGAGCTGTGCAGGAGCACCTGACGGGCGCCCAACAGACC	122		
Db	2	AAACAAGCCGGTGGCTGACGAGCTGTGCAGGAGTGCCTGACGGGCGCCCAACAGACC	61		
QY	123	ATGTGTCATCAGAGACTCCCTTGGCGGGGGGATCTCTGGCTGTGCTCTCTGGCCCTC	182		
Db	62	ATGTGTCATCAGAGACTCCCTTGGCGGGGGGATCTCTGGCTGTGCTCTCTGGCCCTC	121		
QY	183	CTTGGCACACCTGGGCGAGAGTGTGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCC	242		
Db	122	CTTGGCACACCTGGGCGAGAGTGTGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCC	181		
QY	243	GGAGCCCTGAACGAGGAGAGTTCCTGCTCTCTCCCTGCACACCGGCTGGCGAGC	302		
Db	182	GGAGCCCTGAACGAGGAGAGTTCCTGCTCTCTCCCTGCACACCGGCTGGCGAGC	241		
QY	303	TGGGTCCAGCCCTTGGGCTGACATCGGAGGCTGAGCTGAGTGACAGCTTGCCCAA	362		
Db	242	TGGGTCCAGCCCTTGGGCTGACATCGGAGGCTGAGCTGAGTGACAGCTTGCCCAA	301		
QY	363	CTGGCTCAAGCCAGGCGCCCTCTGTGGAATCCCAACCGGAGCCTGGCATCGGCGTG	422		
Db	302	CTGGCTCAAGCCAGGCGCCCTCTGTGGAATCCCAACCGGAGCCTGGCATCGGCGTG	361		
QY	423	TGGCGCACCTTGAAGTGGCTGGAACATGACGCTGCTGCCCGGGCTTGGCGTCTTT	482		
Db	362	TGGCGCACCTTGAAGTGGCTGGAACATGACGCTGCTGCCCGGGCTTGGCGTCTTT	421		
QY	483	GTTGAAGTGTGACGCTATGTTTGCAGAGGGGACGGTACAGCCACGGGCGAGGAG	542		
Db	422	GTTGAAGTGTGACGCTATGTTTGCAGAGGGGACGGTACAGCCACGGGCGAGGAG	481		
QY	543	TGTGCTCGCAACCCACCTGCACCCACTACACGAGCTCGTGTGGGCCACTCAAGCCAG	602		
Db	482	TGTGCTCGCAACCCACCTGCACCCACTACACGAGCTCGTGTGGGCCACTCAAGCCAG	541		
QY	603	CTGGGCTGTGGGCGCACCTGTGCTCTGCAGGCGACAGCGATAGAGCCTTGTCTGT	662		
Db	542	CTGGGCTGTGGGCGCACCTGTGCTCTGCAGGCGACGCGATAGAGCCTTGTCTGT	601		
QY	663	GCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAACAATCATCCCTATAAGAAG	722		
Db	602	GCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAACAATCATCCCTATAAGAAG	661		
QY	723	GGTGGCTGTGCTGTGCTGTGACAGGCTGTCTCAGGCTGTCTCAAGCCTGGGACCAT	782		
Db	662	GGTGGCTGTGCTGTGCTGTGACAGGCTGTCTCAGGCTGTCTCAAGCCTGGGACCAT	721		

QY	783	GCAGGGGGGCTCTGTGAGTCCCAGGAATCCTTGTGCAATGAGCTGCCAGAACATGGA	842
Db	722	GCAGGGGGGCTCTGTGAGTCCCAGGAATCCTTGTGCAATGAGCTGCCAGAACATGGA	781
QY	843	CGTCTCAACATCAGACACCTGCCACTGTCCACTGTCCCTGGCTACACGGGAGATACG	902
Db	782	CGTCTCAACATCAGACACCTGCCACTGTCCACTGTCCCTGGCTACACGGGAGATACG	841
QY	903	CAGTGTGAGTGCACCTGTGAGTGTGTGCACGGCCGGTTCGGGAGGAGTGTCTCGTC	962
Db	842	CAAGTGTGAGTGCACCTGTGAGTGTGTGCACGGCCGGTTCGGGAGGAGTGTCTCGTC	901
QY	963	GTCTGTGACATCGCTACGGGGAGCCAGTGTGCCACCAAGGTGCATTTCCCTTCAC	1022
Db	902	GTCTGTGACATCGCTACGGGGAGCCAGTGTGCCACCAAGGTGCATTTCCCTTCAC	961
QY	1023	ACCTGTGACCTGAGGATCGACGGAGACTGTCTCATGTGTCTTCAGAGGCGACACCTAT	1082
Db	962	ACCTGTGACCTGAGGATCGACGGAGACTGTCTCATGTGTCTTCAGAGGCGACACCTAT	1021
QY	1083	TACAGAGCCAGGATGAATGTACAGAAAGGCGGGGTGTGGCCCGAGATCAAGAGCCAG	1142
Db	1022	TACAGAGCCAGGATGAATGTACAGAAAGGCGGGGTGTGGCCCGAGATCAAGAGCCAG	1081
QY	1143	AAAGTGCAGGACATCCTCGCTTCTATCTGGCGCGCTGGAGACCAACAGAGGTGACT	1202
Db	1082	AAAGTGCAGGACATCCTCGCTTCTATCTGGCGCGCTGGAGACCAACAGAGGTGACT	1141
QY	1203	GACAGTGTGACCTGCAGACAGGAACTTCTGGATCGGGTCACTTACAAAGACCCCAAGAC	1262
Db	1142	GACAGTGTGACCTGCAGACAGGAACTTCTGGATCGGGTCACTTACAAAGACCCCAAGAC	1201
QY	1263	TCTTCCGCTGGCCACAGGGAGCACCAGGCTTACACAGTTTGGCTTTGGGAGGCT	1322
Db	1202	TCTTCCGCTGGCCACAGGGAGCACCAGGCTTACACAGTTTGGCTTTGGGAGGCT	1261
QY	1323	GACAACACCGGCTGTGGCTGTGCTGTGCTTGGCTTGGCTTGGCTTGGCTTGGCT	1382
Db	1262	GACAACAC- - - - - GGGTTTGGCACTGGTGGAGCTG	1294
QY	1383	CAGGCTTACGCTTCACTGGAACAGCAGCGCTGCAAAACCCGAAACCGTTACATC	1442
Db	1295	CAGGCTTACGCTTCACTGGAACAGCAGCGCTGCAAAACCCGAAACCGTTACATC	1354
QY	1443	TGCCAGTTTGGCCAGGAGCACATCTCCGGTGGGCGCCAGGGTCTCTGACGCTGAC	1502
Db	1355	TGCCAGTTTGGCCAGGAGCACATCTCCGGTGGGCGCCAGGGTCTCTGACGCTGAC	1414
QY	1503	TGGCTCCCTGCGCTGGGAGCACCAGGCTTACCTTACCTGCTGCTGCTGCTGCTG	1562
Db	1415	TGGCTCCCTGCGCTGGGAGCACCAGGCTTACCTTACCTGCTGCTGCTGCTGCTG	1474
QY	1563	AACAAGGCGCAGTTAAGACACATGCTTCAATGCTCAAAAGAGTCTCAGACCTTGCA	1622
Db	1475	AACAAGGCGCAGTTAAGACACATGCTTCAATGCTTCAAAAGAGTCTCAGACCTTGCA	1534
QY	1623	TGCCAAGAGTTGGGCGAGAGAGGAGGCGCAGTGTGGGCGCAGGAGTGTAGTGTAG	1682
Db	1535	TGCCAAGAGTTGGGCGAGAGAGGAGGCGCAGTGTGGGCGCAGGAGTGTAGTGTAG	1594
QY	1683	AAGAAGCTTGGGCGCTTGGCTGTCTTGTATTTGGGAAGATGGGCTTCAATAGATGCG	1742
Db	1595	AAGAAGCTTGGGCGCTTGGCTGTCTTGTATTTGGGAAGATGGGCTTCAATAGATGCG	1654
QY	1743	AGGAGGACACCGCAGTGTGGTCCAAAGAGTGTCTTCCACCTGGCCGAGACCTG	1802
Db	1655	AGGAGGACACCGCAGTGTGGTCCAAAGAGTGTCTTCCACCTGGCCGAGACCTG	1714
QY	1803	TGGGCGAGGAGCTTCCCTGTGGCATGAACCCCGGGGTATTAATTTATGAATCAGCT	1862
Db	1715	TGGGCGAGGAGCTTCCCTGTGGCATGAACCCCGGGGTATTAATTTATGAATCAGCT	1774

D	b	781	GTGGCAGCATCTTACTATGTTGGCTGTGCCAGAGCCCGACCCCTCAGCACCCAGGAGGCCTCC	84
Q	y	798	- - - - -	- - - - -GAGGT 802 - - - - -
D	b	841	TGCCGGCCTGTCTGGGAGGAGACCCTTTTTCGCGAGTGCCCTCCTCTCTGACCAAGGT	900
Q	y	803	CCCCAGAATCCTTGTTCGCATGAGCTGCCAAGAACCATGGACGTTCTCAACATCAGCACCTG	862
D	b	901	CCCAGGAACCTTGTTCGCATGAGCTGCCAAGAACCATGGACGTTCTCAACATCAGCACCTG	960
Q	y	863	CCAATGCCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAAGTCAGGTGCAGCCTGCA	922
D	b	961	CCAATGCCACTGTCCCACTGGCTACACTGCGAGTACTGCCAAGTCGGTGCAGCCTGCA	102
Q	y	923	GTTGTGTCACGGCCGGTTCCGGGAGGAGAGTAGTCTCTGTCGTCTGTGACATCGGCTACGG	982
D	b	1021	GTTGTGTCACGGCCGGTTTCCGGGAGGAGGAGTAGTCTCTGTCGTCTGTGAGCTCGGCTACGG	108
Q	y	983	GGGAGGCCAGTGTGCCACCAAG	1004
D	b	1081	GGGAGGCCAGTGTGCCAGTGAG	1102
RESULT 5				
AX366554				
LOCUS AX366554				
DEFINITION Sequence 321 from Patent WO0206317.				
ACCESSION AX366554				
VERSION AX366554.1				
KEYWORDS GI:18697979				
SOURCE human,				
ORGANISM Homo sapiens				
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE Mitcham,J.L., King,G.E., Algate,P.A., Fling,S.P., Retter,M.W.,				
JOURNAL Fanger,G.R., Reed,S.G., Vedwick,T.S., Carter,D., Hill,P. and				
FEATURES Albone,E.				
source Compositions and methods for the therapy and diagnosis of ovarian				
PATENT: WO 0206317-A 321 24-JAN-2002;				
CORIXA CORPORATION (US)				
Location/Qualifiers				
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Best Local Similarity 99.3%; Pred. No. 1.5e-136;				
Matches 685; Conservative 0; Mismatches 4; Indels 1; Gaps				
Q	y	604	TGGCTGTGGCGGCACCTGTGCTCTCAGCGCCAGACAGCGATAGAAGCCCTTTGTCTGTG	663
D	b	1	TGGCTGTGGCGGCACCTGTGCTCTCAGCGCCAGACAGCGATAGAAGCCCTTTGTCTGTG	60
Q	y	664	CCTACTCCCCGGGAGGCAACTGGGAGTGTAACGGGAAGACAATCATCCCCCTATAAGAAGG	723
D	b	61	CCTACTCCCCGGGAGGCAACTGGGAGTGTAACGGGAAGACAATCATCCCCCTATAAGAAGG	120
Q	y	724	GTGCTTGGTGTTCCTCTGCACAGCCAGTGTCTCAGGCTGCTTCARAGCCTGGACCATG	783
D	b	121	GTGCTTGGTGTTCCTCTGCACAGCCAGTGTCTCAGGCTGCTTCARAGCCTGGACCATG	180
Q	y	784	CAGGGGGCTCTGTGAGTCCCAAGGAATCCTTGTCTCATGAGCTGCGAGAACCATTGGAC	843
D	b	181	CAGGGGGCTCTGTGAGTCCCAAGGAATCCTTGTCTCATGAGCTGCGAGAACCATTGGAC	240
Q	y	844	GTCTCAACATCAGACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATATCGCC	903
D	b	241	GTCTCAACATCAGACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATATCGCC	300


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Qy 904 AAGTGAAGTGCAGCCTGCAGTGTGTGCACGCGCGGTTCGGGAGGAGGAGTGTCTCGTGGC 963
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Qy 1084 ACAG-AGCCAGATGAATGTTCAGAGGAAGCGGGGTGTCTGGCCCAAGTCAAGAGCCAG 1142
Db 481 ACAGAGCCAGATGAATGTTCAGAGGAATGTGGCGGGGTGTGGCCCAAGTCAAGAGCCAG 540
Qy 1143 AAAGTGCAGGACATCTCGCCTTCTATCTGGCGCGCTGGAGACCAACAGGAGTGACT 1202
Db 541 AAAGTGCAGGACATCTCGCCTTCTATCTGGCGCGCTGGAGACCAACAGGAGTGACT 600
Qy 1203 GACAGTGAATTCGAGACCAAGGAACTTCTGGATCGGGCTCACCTACAAAGCCGCAAGGAC 1262
Db 601 GACAGTGAATTCGAGACCAAGGAACTTCTGGATNGGGCTCACCTACAAAGCCGCAAGGAC 660
Qy 1263 TCCTTCGGCTGGCCACAGGGGAGACACAG 1292
Db 661 TCCTTCGGCTGGCCACAGGGGAGACACAG 690

RESULT 6
LOCUS BC008616 1328 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, clone IMAGE:4178394, mRNA, partial cds.
ACCESSION BC008616
VERSION BC008616.1 GI:14250368
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
TITLE 1 (bases 1 to 1328)
JOURNAL Strausberg, R.
Direct Submission
Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalona@bcm.tmc.edu.
Villalona, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Series: IRAK Project: 12 Row: h Column: 4
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.
FEATURES             Location/Qualifiers
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CDS

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BASE COUNT 305 a 381 c 398 g 244 t
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Query Match 29.3%; Score 550; DB 9; Length 1328;
Best Local Similarity 94.1%; Pred. No. 9.9e-110;
Matches 593; Conservative 0; Mismatches 10; Indels 27; Gaps 1;
QY 1236 GGCTCACCTACAGACCGCCAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCC 1295
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QY 1296 TTCACCAAGTTTGGCTTTGGGACGCCGTGACAAACACAGGCGTGGTGGCTGAGTGTGCC 1355
Db 306 TTCACCAAGTTTGGCTTTGGGACGCCGTGACAAACACAGGCGTGGTGGCTGAGTGTGCC 341
QY 1356 ATGGGGTTTGGCAACTCGCTGGAGCTGCAGCTTCAGCTTCAGCTTCAACTGGGAACACCAG 1415
Db 342 ---GGGTTTGGCAACTCGCTGGAGCTGCAGCTTCAGCTTCAACTGGGAACACCAG 398
QY 1416 CGCTGCAAAACCCGAAACCGTTACATCTGCCAGTTTGGCCAGGACACATCTCCCGGTGG 1475
Db 399 CGCTGCAAAACCCGAAACCGTTACATCTGCCAGTTTGGCCAGGACACATCTCCCGGTGG 458
QY 1476 GGCCCGAGGTCCTGAGGCGCTGACCACATGGCTCCCTCGCTGGGAGCACCAGCGCTC 1535
Db 459 GGCCCGAGGTCCTGAGGCGCTGACCACATGGCTCCCTCGCTGGGAGCACCAGCGCTC 518
QY 1536 TGTCTACCTGTCTGCCACCTGTCTGGAACAAGGCCAGGTTTAAGACCATGCTTCATG 1595
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Db 579 TCCAAAGAGTCTCAGACCTTGCACAAATGCCAAGATTTGGGAGAGAGAGGAGGAGGCC 638
QY 1656 CAGTGAGGCGCAGGAGTGTAGTGTAGAAAGCTGGGGCCCTTCGCTTGTGATTG 1715
Db 639 CAGTGAGGCGCAGGAGTGTAGTGTAGAAAGCTGGGGCCCTTCGCTTGTGATTG 698
QY 1716 GGAAGATGGCTTCAATTAGATGGCAGAGAGAGACACCGCCAGTGTGTCCTCCAAAAGGCT 1775
Db 699 GGAAGATGGCTTCAATTAGATGGCAGAGAGAGACACCGCCAGTGTGTCCTCCAAAAGGCT 758
QY 1776 GCTCTCTTCCACCTGGCCAGACCTGTGGGAGAGCGGAGCTTCCCTGTGGCATGAACCC 1835
Db 759 GCTCTCTTCCACCTGGCCAGACCTGTGGGAGAGCGGAGCTTCCCTGTGGCATGAACCC 818
QY 1836 CACGGGTATTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1865
Db 819 CACAGGTTATTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 848

RESULT 7
AC009053
LOCUS AC009053 163427 bp DNA linear PRI 27-JUL-2001
DEFINITION Homo sapiens chromosome 16 clone RP11-252A24, complete sequence.
ACCESSION AC009053
VERSION AC009053.7 GI:15022678
KEYWORDS HTG.
SOURCE Homo sapiens.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 163427)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 163427)
REFERENCE DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 163427)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (27-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Jul 27, 2001 this sequence version replaced gi:9256116.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
SHGC-32349 G27498
SHGC-32146 G27136
SHGC-36058 G30050.
FEATURES source
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/clone="RP11-252A24"
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Best Local Similarity 97.9%; Pred. No. 2.4e-80;
Matches 420; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1437 TACATCTGCCAGTTGCCAGGACACATCTCCGGTGGGGCCAGGGTCTCAGGCCTG 1496
Db 55250 TTCTGCTTCTCCAGCCAGGACACATCTCCGGTGGGGCCAGGGTCTCAGGCCTG 55309
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QY 1737 TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAGAGGCTGCTCTCTTCCACCTGGCCCGAG 1796
Db 55550 TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAGAGGCTGCTCTCTTCCACCTGGCCCGAG 55609
QY 1797 ACCCTGTGGGGCAGCGGAGCTTCCCTGTGTGCATGACACCCACCGGGGTATTAATTATGAA 1856
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Db 55670 TCAGCTGAA 55678
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RESULT 8
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LOCUS Homo sapiens chromosome 16 clone RP11-572F4, complete sequence.
DEFINITION AC009153
ACCESSION AC009153
VERSION AC009153.10 GI:18997244
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 177479)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 177479)
REFERENCE DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 177479)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 177479)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Feb 28, 2002 this sequence version replaced gi:18071320.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
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Best Local Similarity 97.9%; Pred. No. 2.4e-80;
Matches 420; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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Db 144529 TGGCGAAGAGAGGACACCGCCAGTGGTCCAAAAGAGCTGCTCTCTTCCACCTGGCCCGAG 144588
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Db 144649 TCAGCTGAA 144657
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LOCUS Homo sapiens chromosome 16 clone RP11-396D24, *** SEQUENCING IN
PROGRSS ***, 10 unordered pieces.
AC126771
VERSION AC126771.1 GI:21717140
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 197460)
DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 197460)
DOE Joint Genome Institute.
DIRECT SUBMISSION
Submitted (09-JUL-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 558525
Center clone name: RPC1-11_396D24

Summary Statistics
Consensus quality: 191546 bases at least Q40
Consensus quality: 193703 bases at least Q30
Consensus quality: 194840 bases at least Q20
Estimated insert size: 0; null estimation
Estimated insert size: 196580; sum-of-contigs estimation
Quality coverage: 2.1474836E7 in Q20 bases; null estimation
Quality coverage: 8.2 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1600: contig of 1600 bp in length
* 1601 1700: gap of unknown length
* 1701 3466: contig of 1766 bp in length
* 3467 3566: gap of unknown length
* 3567 5709: contig of 2143 bp in length
* 5710 5809: gap of unknown length
* 5810 7800: contig of 1991 bp in length
* 7801 7900: gap of unknown length
* 7901 14727: contig of 6827 bp in length
* 14728 14827: gap of unknown length
* 14828 26876: contig of 12049 bp in length
* 26877 26976: gap of unknown length
* 26977 46712: contig of 19736 bp in length
* 46713 46812: gap of unknown length
* 46813 70129: contig of 23317 bp in length
* 70130 70229: gap of unknown length

* 70230 93612: contig of 23383 bp in length
* 93613 93712: gap of unknown length
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/db_xref="taxon:9606"
/chromosome="16"
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/clone_lib="RPC1 human BAC library 11"
BASE COUNT 50025 a 47482 c 47491 g 51562 t 900 others
ORIGIN
Query Match 22.1%; Score 414.6; DB 2; Length 197460;
Best Local Similarity 97.9%; Pred. No. 2.3e-80;
Matches 420; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1437 TACATCTGCCAGTTTGCCAGGAGCACATCTCCCGTGGGGCCAGGGTCTGAGGCGCTG 1496
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Db 135308 TCAGCTGAA 135316
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LOCUS Homo sapiens chromosome 16 clone RP11-419C5, complete sequence.
DEFINITION AC026468
ACCESSION AC026468
VERSION AC026468.6 GI:16596532
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179675)
DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 179675)
DOE Joint Genome Institute.
DIRECT SUBMISSION
Submitted (22-MAR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 179675)
DOE Joint Genome Institute.
DIRECT SUBMISSION
TITLE


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QY 1677 TCTTAGAAGAAGCTGGGGCCCTTCGCTGCTTTTATTTGGGAAGATGGGCTTCAATTAGA 1736
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Db 179338 ACCCTGTGGGGCAGGGAGCTTCCCTGTGGCATGAACCCACCGGGTATTAAATATTGAA 179279
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Db 179278 TCAGCTGAA 179270
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RESULT 12
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LOCUS Homo sapiens chromosome 16 clone RP11-296110, complete sequence.
AC009060
VERSION AC009060.7 GI:9690317
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 180596)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Unpublished
DOE Joint Genome Institute.
2 (bases 1 to 180596)
Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 180596)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (04-AUG-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Aug 4, 2000 this sequence version replaced gi:92561118.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
STS Content:
SHGC-32944 G29390
WI-6927 G06314
WI-16981 G21928
WI-9564 G06056.
FEATURES
Location/Qualifiers
1..180596
/db_organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-296110"
BASE COUNT 48046 a 43474 c 42543 g 46533 t
ORIGIN

Query Match 21.8%; Score 409.8; DB 9; Length 180596;
Best Local Similarity 97.2%; Pred. No. 2.7e-79;
Matches 417; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1437 TACATCTCCAGTTGCCAGAGACATCTCCCGTGGGGCCAGGCTCTGAGGCGCTG 1496
| | | | |
Db 87744 TTCTGCTCTCTCCAGCCAGAGACATCTCCCGTGGGGCCAGGCTCTGAGGCGCTG 87803
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QY 1497 ACCACATGGCTCCCTCGCTGCGCTGGGAGACACCGGCTCTGCTTACCTGCTGCCACCT 1556
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Db 87804 ACCACATGGCTCCCTCGCTGCGCTGGGAGCACCGGCTCTGCTTACCTGTCGCGCCACCT 87863
QY 1557 GTCTGGAACAGGGCCAGGTTAAGACACCATGTCCTCATGTCCAAAGAGAGTCTCAGACCTT 1616
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Db 87864 GTCTGGAACAGGGCCAGGTTAAGACACCATGTCCTCATGTCCAAAGAGAGTCTCAGACCTT 87923
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QY 1617 GCACATGCCAGAGTTGGGCAGAGAGAGGAGGAGGCCAGTGTAGGGCCAGGGAGTGTAG 1676
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Db 87924 GCACATGCCAGAGTTGGGCAGAGAGAGGAGGAGGCCAGTGTAGGGCCAGGGAGTGTAG 87983
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QY 1677 TGTTAGAAGAGCTGGGGCCCTTCGCTGCTTTTATTTGGGAAGATGGGCTTCAATTAGA 1736
|||||
Db 87984 TGTTAGAAGAGCTGGGGCCCTTCGCTGCTTTTATTTGGGAAGATGGGCTTCAATTAGA 88043
|||||
QY 1737 TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAGAGGCTCTCTTCCACCTGGCCAG 1796
|||||
Db 88044 TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAGAGGCTCTCTTCCACCTGGCCAG 88103
|||||
QY 1797 ACCCTGTGGGGCAGGGAGCTTCCCTGTGGCATGAACCCACCGGGTATTAAATATTGAA 1856
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Db 88104 ACCCTGTGGGGCAGGGAGCTTCCCTGTGGCATGAACCCACCGGGTATTAAATATTGAA 88163
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QY 1857 TCAGCTGAA 1865
|||||
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RESULT 13
AC097265/c
LOCUS AC097265 191108 bp DNA linear HTG 25-OCT-2001
DEFINITION Pan troglodytes clone RP43-119N13, WORKING DRAFT SEQUENCE, 4
unordered pieces.
AC097265
AC097265 GI:16328241
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Pan troglodytes.
Pan troglodytes.
Pan troglodytes.
REFERENCE
1 (bases 1 to 191108)
AUTHORS
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaral, H.C., Are, J.R., Banks, T., Barbata, J.,
Benton, J., Blum, K., Blum, K., Blum, K., Bonn, D., Bouck, J.,
Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.C., Chen, R.,
Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.,
Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,
Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,
Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Louis, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M.,
Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.,
Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N.,
Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokoko, S.,
Oguth, M., Okunolu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L.,
Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M.,
Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoostari, N.,
Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H.,
Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K.,

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Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Unpublished
2 (bases 1 to 204182)
Worley,K.C.
Direct Submission
Submitted (13-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: ZUAY
Center clone name: RP43-35B16
----- Summary Statistics
Sequencing vector: Plasmid; M77789
Chemistry: Dye-Terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 202604 bases at least Q40
Consensus quality: 204032 bases at least Q30
Consensus quality: 205164 bases at least Q20
Estimated insert size: 200244; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 9.4x in Q20 bases; sum-of-contigs estimation

COMMENT

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 48992: contig of 48992 bp in length
* 48993 49092: gap of unknown length
* 49093 90442: contig of 41350 bp in length
* 90443 90542: gap of unknown length
* 90543 124888: contig of 34346 bp in length
* 124889 124988: gap of unknown length
* 124989 145269: contig of 20281 bp in length
* 145270 145369: gap of unknown length
* 145370 173261: contig of 27892 bp in length
* 173262 173362: gap of unknown length
* 173362 186532: contig of 13171 bp in length
* 186533 201672: gap of unknown length
* 201673 201772: contig of 15040 bp in length
* 201773 204182: contig of 2410 bp in length.

FEATURES

source

Location/Qualifiers
1..204182
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-35B16"
BASE COUNT 52711 a 50970 c 50521 g 49254 t 726 others
ORIGIN

Query Match 20.3%; Score 380; DB 2; Length 204182;
Best Local Similarity 93.2%; Pred. No. 8.5e-73;
Matches 414; Conservative 0; Mismatches 15; Indels 15; Gaps 1;

QY 1437 TACATCTCCAGTTTCCAGGAGACACATCTCCCGTGGGGCCAGGCTCTGAGGCGTG 1496

Db 17230 TTCTGCTTCTTCCAGCCAGGAGACATCTCCCGTGGGGCCAGGCTCTGAGGCGTG 17289

QY 1497 ACCACATGGCTCCCTCGCTGCTGGGAGCACCGGCTCTGCTTACTCTGCTGCCACCT 1556

Db 17290 ACCACATGGCTCCCTCGCTGCTGGGAGCACCGGCTCTGCTTACTCTGCTGCCACCT 17349

QY 1557 GTCTGGAACAAGG-----GCCAGTTTAAGACACATGCTCTCATGTCCAAA 1601
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Db 17350 GTCTGGAACAAGGTTCCACCTGTCTGGAACAAGTTAAGACACATGCTCTCATGTCCAAA 17409
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QY 1602 GAGGTCTCAGACCTTGGCACAATGCCAAGTTGGGCGAGAGAGAGGAGGAGGCGGAGTGA 1661
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RESULT 15

AC097331/c

LOCUS

DEFINITION

AC097331

AC097331

AC097331.4

GI:21535856

HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

KEYWORDS

chimpanzee

SOURCE

Pan troglodytes

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (bases 1 to 200409)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

Alsbrooks,S.L., Anaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,

Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,

Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,

Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,

Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,

Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,

Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,

Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,

Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,

Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,

Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,

Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,

Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,

Correll,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,

Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,

Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,

Homs,J., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,

Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,

Karlssoon,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,

Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,

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Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,

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Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,

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Rives,M., Rojas,A., Rojubokan,I., Roife,M., Ruiz,S., Savery,G.,

Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,

Sodergren,E., Sonaika,T., Sparks,A., Stanley,H., Stone,H.,

Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,

Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williams, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 200409)
Worley, K.C.
Direct Submission
Submitted (14-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 200409)
Worley, K.C.
Direct Submission
Submitted (22-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 21, 2002 this sequence version replaced gi:21450389.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: ZUAO
Center clone name: RP43-53A2
----- Summary Statistics
Sequencing vector: Plasmid; M7789
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 187810 bases at least Q40
Consensus quality: 190821 bases at least Q30
Consensus quality: 193098 bases at least Q20
Estimated insert size: 212811; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 9.3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1	39411:	contig of 39411 bp in length
*	39412	39511: gap of unknown length
*	39512	61929: contig of 22418 bp in length
*	61930	62029: gap of unknown length
*	62030	87446: contig of 25417 bp in length
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*	87547	113623: contig of 26077 bp in length
*	113624	113723: gap of unknown length
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*	130749	130848: gap of unknown length
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*	142501	156750: contig of 14250 bp in length
*	156751	156850: gap of unknown length
*	156851	169557: contig of 12707 bp in length
*	169558	169657: gap of unknown length
*	169658	179740: contig of 10083 bp in length
*	179741	179840: gap of unknown length
*	179841	191738: contig of 11898 bp in length
*	191739	191838: gap of unknown length
*	191839	193391: contig of 2153 bp in length
*	194091	194091: gap of unknown length
*	194092	196138: contig of 2047 bp in length
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RESULT 2
US-09-433-248A-3
; Sequence 3, Application US/09433248A
; Patent No. 6355462
; GENERAL INFORMATION:
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Han, Feng
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Disease Resistance Factors
; FILE REFERENCE: BB1252 US NA
; CURRENT APPLICATION NUMBER: US/09/433,248A
; CURRENT FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,242
; PRIOR FILING DATE: 1998-11-05
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (337)
; NAME/KEY: unsure
; LOCATION: (370)
; NAME/KEY: unsure
; LOCATION: (421)
; NAME/KEY: unsure
; LOCATION: (437)
; NAME/KEY: unsure
; LOCATION: (481)
; NAME/KEY: unsure
; LOCATION: (484)
; NAME/KEY: unsure
; LOCATION: (502)
; NAME/KEY: unsure
; LOCATION: (511)
; NAME/KEY: unsure
; LOCATION: (542)
; NAME/KEY: unsure
; LOCATION: (547)
; NAME/KEY: unsure
; LOCATION: (564)
; NAME/KEY: unsure

LOCATION: (571)
US-09-433-248A-3
Query Match 3.6%; Score 47.8; DB 4; Length 582;
Best Local Similarity 50.2%; Pred. No. 0.01;
Matches 118; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
QY 1088 ACTTCGAGACCAAGAACTTCTGGATCGGCTCACCTTACAGACCGCCAGGACTCCTTCC 1147
Db 1 ACATCTCTGAACCGGACCATCGCATGGACACCTCCCAACAAGCCACCTCCGACTACGTCC 60
QY 1148 GCTGGGCGACAGGGGAGCAGCAGGCTTACCAGATTTTCCTTTGGGAGCCCTGACAACC 1207
Db 61 GCGAAGCCATCGGAGGACACGTCGAGCGCCATCTTCGGGTGGCTTCGCGCGGCCCAAGC 120
QY 1208 ACGGGCTGGTGTGCTGAGTGTGCTGATGGGTGTTGGCAACTGCGGTGGAGCTGCAGGCTT 1267
Db 121 CCGGGCTGATGATCTGACCCCGTACGGCGGCGAGATCGGCGAGCGTGGCGGAGGCGGCGA 180
QY 1268 CAGCTGCTTCAACTGGAAACGACGAGCGCTGCAAAACCGGAAACCGTTTACATCTG 1322
Db 181 CGCGTTCCCGCACCGCGCGGCTGCTTACAAACATCCAGTACATGAATCTCTG 235
RESULT 3
US-08-387-942C-18
; Sequence 18, Application US/08387942C
; Patent No. 5939289
; GENERAL INFORMATION:
; APPLICANT: ERTESVAG, HELGA
; APPLICANT: VALLA, SVEIN
; APPLICANT: SKJAK-BRAEK, GUDMUND
; APPLICANT: LARSEN, BJORN
; TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
; TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: P.O. BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,942C
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1809-106P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-387-942C-18
Query Match 3.3%; Score 43.4; DB 2; Length 1155;
Best Local Similarity 49.8%; Pred. No. 0.14;
Matches 110; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 894 CTTCACACCTGTGACCTGAGATCGAGGAGACTGCTTTCATGGTCTTTCAGAGGCGA 953

Db 297 CTTCCGATGAGCGACCTGACCTCGACGCAACCGGACCACTGTCGCCAAGTCGA 356
QY 954 CACCTATTACAGCAGCAGATGAATGTGAGAGAAAGGGGGTGTGCGCCAGATCAA 1013
Db 357 CGGCTGGTTCAACGGCTACATCCCGGCCAGGACGCGCGGATCGGAGCTGACCCCTGGA 416
QY 1014 GAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGCGCGCTGAGACCAACCAACGA 1073
Db 417 GCGGTGGAATCCGGAGATGTCGGCTACGGTTTCGACCCCGACGAGACCATCAA 476
QY 1074 GGTGACTGACAGTACTTCTGAGACCAAGAACTTCTGGATCG 1114
Db 477 CCGTACGATCCGACAGCGTGGCCGACGACCAACAGCCTCG 517

RESULT 4

US-08-387-942C-1

; Sequence 1, Application US/08387942C

; Patent No. 5939289

; GENERAL INFORMATION:

; APPLICANT: ERTESVAG, HELGA

; APPLICANT: VALLA, SVEIN

; APPLICANT: SKJAK-BRAEK, GUDMUND

; APPLICANT: LARSEN, BJORN

; TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES

; TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; STREET: P.O. BOX 747

; CITY: FALLS CHURCH

; STATE: VA

; COUNTRY: USA

; ZIP: 22042

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/387,942C

; FILING DATE: 09-MAY-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: MOREY JR, GERALD M.

; REGISTRATION NUMBER: 28,977

; REFERENCE/DOCKET NUMBER: 1809-106P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-205-8000

; TELEFAX: 703-205-8050

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12588 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORIGINAL SOURCE:

; ORGANISM: Azotobacter vinelandii

; STRAIN: E

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 290..1951

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 2227..6438

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 6702..9695

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 9973..12588

US-08-387-942C-1

Query Match 3.3%; Score 43.4; DB 2; Length 12588;

Best Local Similarity 49.8%; Pred. No. 0.27;

Matches 110; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 894 CTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTTTCATGGTGTCTTTCAGAGCAGA 953
Db 2523 CTTCCGATGATGACGACCTGACCTCGACGGGAACCGGCAACCTGTCCGCCAAGTCGA 2582
QY 954 CACCTATTACAGACCGAGGATGAATGTGAGAGAAAGGGGGTGTGCGCCAGATCAA 1013
Db 2583 CGGCTGGTTCAACGGCTACATCCCGGCCAGGACGCGCGGATCGGAGCTGACCCCTGGA 2642
QY 1014 GAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGCGCGCGCTGAGACCAACCAACGA 1073
Db 2643 GCGGTGGAATCCCGGAGATGTCGGGTACGGTTTCGACCCCGACGAGACCATCAA 2702
QY 1074 GGTGACTGACAGTACTTCTGAGACCAAGAACTTCTGGATCG 1114
Db 2703 CCGTACGATCCGACAGCGTGGCCGACGACCAACAGCCTCG 2743

RESULT 5

PCT-US95-03747-1

; Sequence 1, Application PC/TUS9503747

; GENERAL INFORMATION:

; APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION

; TITLE OF INVENTION: Brevicin, A Glial Cell Proteoglycan

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell and Flores

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/03747

; FILING DATE: 27-MAR-1995

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Imbra, Richard J.

; REGISTRATION NUMBER: 37,643

; REFERENCE/DOCKET NUMBER: FP-LJ 1453

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3259 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 112..2848

PCT-US95-03747-1

Query Match 3.2%; Score 42.6; DB 5; Length 3259;

Best Local Similarity 53.0%; Pred. No. 0.28;

Matches 115; Conservative 0; Mismatches 99; Indels 3; Gaps 1;

QY 822 CGAGAGGAGTGTCTGTCGGTGTGTGACATCGGTACGGGGGAGCCAGTGTGCCACCAA 881
Db 2106 CGAGAGGGGGTCCCGCTGTGTTGCTGCTATGGGGGGACCTGTGCGATGTGG 2165
QY 882 GGTGCATTTTCCTTCCACACCTGTGACCTGAGGATCGAGGAGACTGCTTCATGTGTC 941

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Db 2166 CTTCCACTTCTGCAGCCCGGTTGGAC---GCTTCCAGGGTGCCTGTACAAGCACTT 2222
Qy 942 TTCAGAGGACACACCTATTACAGAGCCAGGATCAAAATGTACAGAGAAAGCGGGTGTCT 1001
Db 2223 TTCTGCCGGAAGGAGCTGGAGAGCGGAGAGACAAAGTCGCGGATGTACGCGGCACCT 2282
Qy 1002 GCGCCAGATCAGAGCCAGCAAAAGTGCAGGACATCCTC 1038
Db 2283 GCGCAGCATCAGCACGCGGAGGAGAAAGGACTTCATC 2319

RESULT 6
US-08-404-665-3
; Sequence 3, Application US/08404665
; Patent No. 5591583
; GENERAL INFORMATION:
; APPLICANT: Reid, Robert A.
; APPLICANT: Ackley, Rhonda L.
; APPLICANT: Hemperly, John J.
; TITLE OF INVENTION: HUMAN RESTRICTIN AND NUCLEIC ACID
; TITLE OF INVENTION: SEQUENCES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,665
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3341
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4724 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-404-665-3

Query Match 3.1%; Score 40.8; DB 1; Length 4724;
Best Local Similarity 52.3%; Pred. No. 0.85;
Matches 90; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy 705 CTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTGTCCCTGGCTA 764
Db 987 CTGCAGTGGCCAGGCAACTTTAGCTTTGAGTCTGTGGCTGCATCTGCACGAGGCTG 1046
Qy 765 CACGGGCAGATCTGCGAAGTGAAGTGCACCTGTGTCAGTGTGTCACGCGCGGTTCGCGGA 824
Db 1047 GTTTGGCAAGAATTGTCGAGGCGCCCTACTCCCGCTGGTGTCTCCAGCGGGGGTGTG 1106
Qy 825 GGAGGAGTCTCGTGTGTCACATCGCTACGGGGGAGCCAGTGTGCC 876
Db 1107 TGTGGATGCCAGTGTCTGTGACAGCGAGTACAGCGGGGATGACTGTTC 1158

RESULT 7
US-08-404-671-3
; Sequence 3, Application US/08404671
```

```
; Patent No. 5635360
; GENERAL INFORMATION:
; APPLICANT: Reid, Robert A.
; APPLICANT: Ackley, Rhonda L.
; APPLICANT: Hemperly, John J.
; TITLE OF INVENTION: HUMAN RESTRICTIN AND NUCLEIC ACID
; TITLE OF INVENTION: SEQUENCES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,671
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3341
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4724 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-404-671-3

Query Match 3.1%; Score 40.8; DB 1; Length 4724;
Best Local Similarity 52.3%; Pred. No. 0.85;
Matches 90; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy 705 CTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTGTCCCTGGCTA 764
Db 987 CTGCAGTGGCCAGGCAACTTTAGCTTTGAGTCTGTGGCTGCATCTGCACGAGGCTG 1046
Qy 765 CACGGGCAGATCTGCGAAGTGAAGTGCACCTGTGTCAGTGTGTCACGCGCGGTTCGCGGA 824
Db 1047 GTTTGGCAAGAATTGTCGAGGCGCCCTACTCCCGCTGGTGTCTCCAGCGGGGGTGTG 1106
Qy 825 GGAGGAGTCTCGTGTGTCACATCGCTACGGGGGAGCCAGTGTGCC 876
Db 1107 TGTGGATGCCAGTGTCTGTGACAGCGAGTACAGCGGGGATGACTGTTC 1158

RESULT 8
US-08-404-781-3
; Sequence 3, Application US/08404781
; Patent No. 5681931
; GENERAL INFORMATION:
; APPLICANT: Reid, Robert A.
; APPLICANT: Ackley, Rhonda L.
; APPLICANT: Hemperly, John J.
; TITLE OF INVENTION: HUMAN RESTRICTIN AND NUCLEIC ACID
; TITLE OF INVENTION: SEQUENCES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
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ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,781
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3341
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4724 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-404-781-3

Query Match 3.1%; Score 40.8; DB 1; Length 4724;
Best Local Similarity 52.3%; Pred. No. 0.85;
Matches 90; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
QY 705 CTGCCAGAACATGGACGCTCAACATGACGACCTGCCACTGACCTGCTCCCTCGGCTA 764
DB 987 CTGCAGTGGCCAGGCAACTTTAGCTTGTAGTCTGTGGCTGCATCTGCACGAAGGCTG 1046
QY 765 CACGGCGCAGATCTGCCAAGTGAAGTGCAGCCCTGCACTGTGTGACGCGCGGTTCCCGGA 824
DB 1047 GTTTGGCAAGAAATGTCGAGGCCCTACTGCCGCTGGGTTGTCTCCAGCGGGGGGTG 1106
QY 825 GAGGAGTCTGTGCTGTGACATCGGCTACGGGGGAGCCAGTGTGCC 876
DB 1107 TGTGGATGCCAGTGCATCTGTGACAGCGAGTACAGCGGGGATGACTGTTC 1158

RESULT 9
US-08-387-942C-17
Sequence 17, Application US/08387942C
Patent No. 5939289
GENERAL INFORMATION:
APPLICANT: ERTESVAG, HELGA
APPLICANT: VALLA, SVEIN
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
ENCODING MANNURONAN C-5-EPIMERASE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22042

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,942C
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1809-106P
TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1176 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-387-942C-17

Query Match 3.0%; Score 39.4; DB 2; Length 1176;
Best Local Similarity 52.1%; Pred. No. 1.3;
Matches 88; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY 1011 CAAGAGCCAGAAAGTGCAGGACATCTCGCTTTCTATCTCTGGGCGGCTGAGACCAACAA 1070
DB 873 CGACAAACGCGAGGCGCGCTGCGGAGGTCTCTGCTGCTTCGACGATACCGC 932
QY 1071 CGAGGTGACTGACAGTCTTCGAGACAGGAGAACTTCTGGATCGGCTCACTACAGAC 1130
DB 933 CGGGCGTCCGACCTACTACAGACCTTGAACACCCGGATCGAGGGCAACCACTCAG 992
QY 1131 CCCCAGGACTCTTCCGCTGGGCCACAGGGGAGCACCAGGCTTCCAC 1179
DB 993 CGGCTCGGCCAACTCCACCTACGGCATCAGGAGCGCAACGCGGCACC 1041

RESULT 10
US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 3.0%; Score 39.2; DB 4; Length 4403765;
Best Local Similarity 53.2%; Pred. No. 12;
Matches 83; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 279 CCCGAGCTGGCATCCGGCGCTGTGGCGCACCTGCAAGTGGGCTGGAACATGCAGCTGCT 338
DB 3994090 CCGGTCAGCGCGCGCGCGCTGCGGCGCCAGGAGGCGCCCGCGCAACAGCACCG 3994031
QY 339 GCCCGCGGCTTGGCTCTTTGTTGAAGTGGTACGCTATGTTTGCAGAGGGGAGCG 398
DB 3994030 GCGCGCGGCTCGGTCGCTCAAGATGCTGGTGGCTTCTGTGGCGGTGTAGGGGTTCACAG 3993971
QY 399 GTACAGCCACGCGGCGGAGAGTGTGCTCGCAACGC 434
DB 3993970 GCACCACCGCGCGCGGCTGGTGGATCGCCAGGC 3993935
RESULT 11
US-08-387-942C-21

; Sequence 21, Application US/08387942C
; Patent No. 5939289
; GENERAL INFORMATION:
; APPLICANT: ERTESVAG, HELGA
; APPLICANT: VALLA, SVEIN
; APPLICANT: SKJAK-BRAEK, GUDMUND
; APPLICANT: LARSEN, BJORN
; TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
; TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: P.O. BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,942C
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1809-106P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-387-942C-21

Query Match 2.9%; Score 38.6; DB 2; Length 1155;
Best Local Similarity 48.4%; Pred. No. 2;
Matches 107; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 894 CTTCCACACCTGTGACCTGAGGATCGACGAGACTGCTTTCATGTGTCTTCAGAGGCAGA 953
DB 297 CTTGGCATGAGCGACTGACCTCGACGCAACCGGCAACCTGTCCGCCAAGGTGCA 356

QY 954 CACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGCGGGTGTCTGGCCCCAGATCAA 1013
DB 357 CGGCTGTTCAACGGCTACATTCCCGCCAGGACGGTCCGATCGCGACGTGACCCCTGA 416

QY 1014 GAGCCAGAAGTCAGACATCTCTGCGCTCTATCTGGGCGCGCTGGAGACCAACCAAGA 1073
DB 417 GCGGGTGGAAATCCGGGAATGTCGGTTACGGTTTCGATCCGCACGACGACCATCAA 476

QY 1074 GTGACTGACAGTGACTTCGAGACCAAGAACTTCTGGATCG 1114
DB 477 CCGTACGATCCGCGACAGCTGGCCACGACACACGGGCTCG 517

RESULT 12
US-09-387-574-9
; Sequence 9, Application US/09387574
; Patent No. 6188951
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Kinney, Tony
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Plant Geranylgeranyl Transferases
; FILE REFERENCE: BB-1239

; CURRENT APPLICATION NUMBER: US/09/387,574
; CURRENT FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: 60/098,743
; EARLIER FILING DATE: September 1, 1998
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-387-574-9

Query Match 2.8%; Score 37.4; DB 4; Length 2335;
Best Local Similarity 51.5%; Pred. No. 4.6;
Matches 86; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 1059 GGAGACCACCAACGAGGTGACTGACAGTCTTCGAGACCAAGAACTTCTGGATCGGGCT 1118
DB 675 GGACACCACCTCCAGCTCAGGAGAGAAGAACTACTCTTCAGGTTCTTCAAGCTTGTGCA 734

QY 1119 CACCTACAAGACCGCCCAAGGACTCCTCCGCTGGGCCACAGGGGAGCACACCGCCTTAC 1178
DB 735 GGCCACCATTCGCGCTCGGCTGCGGCGCGCCGCGGCGGGAAGGAGGCGCTCCGG 794

QY 1179 CAGTTTTCCTTTGGGAGCCTGACAAACACCGGCTGGTGTGCTGA 1225
DB 795 TAGGCTGCCGATGAGGACCTCGACCTCCCTTCGCGAATTCCTCA 841

RESULT 13
US-09-668-096-9
; Sequence 9, Application US/09668096
; Patent No. 6312954
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Kinney, Tony
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Plant Geranylgeranyl Transferases
; FILE REFERENCE: BB1239 US NA DIV
; CURRENT APPLICATION NUMBER: US/09/668,096
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/098,743
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 09/387,534
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-668-096-9

Query Match 2.8%; Score 37.4; DB 4; Length 2335;
Best Local Similarity 51.5%; Pred. No. 4.6;
Matches 86; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 1059 GGAGACCACCAACGAGGTGACTGACAGTCTTCGAGACCAAGAACTTCTGGATCGGGCT 1118
DB 675 GGACACCACCTCCAGCTCAGGAGAGAAGAACTACTCTTCAGGTTCTTCAAGCTTGTGCA 734

QY 1119 CACCTACAAGACCGCCCAAGGACTCCTCCGCTGGGCCACAGGGGAGCACACCGCCTTAC 1178
DB 735 GGCCACCATTCGCGCTCGGCTGCGGCGCGCCGCGGCGGGAAGGAGGCGCTCCGG 794

QY 1179 CAGTTTTCCTTTGGGAGCCTGACAAACACCGGCTGGTGTGCTGA 1225
DB 795 TAGGCTGCCGATGAGGACCTCGACCTCCCTTCGCGAATTCCTCA 841

RESULT 14
US-09-470-443-7
; Sequence 7, Application US/09470443

Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Lerman, John D.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-470-443-7

Query Match 2.8%; Score 37.2; DB 4; Length 1070;
Best Local Similarity 46.0%; Pred. No. 4.2;
Matches 126; Conservative 0; Mismatches 148; Indels 0; Gaps 0;
QY 250 GCCAGGCGACCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCTGTGGCGCAC 309
Db 743 GGTGG 802
QY 310 CTGCAAGTGGGCTGGAAATGCAATGCACTGCTGCCCGCGGGCTTGGCGTCTCTTTGTTGAAGTG 369
Db 803 CTGTGCTGTGTGCTGCGGCTTCTACCGCTGCTGCCCGGGGGGGGGGGGGGGGGGG 862
QY 370 GTGAGCCTATGTTTTCAGAGGGGCGAGCGGTACAGCCAGCGGCGAGGAGTGTGCTGCG 429
Db 863 TTCCCCCAGCAGCAGCAGTAAAGTGGCTGCGGCGGGCGGAGAGCCCGGGAGCCTTGC 922
QY 430 AAGCGCACCTGCACCCACTACAGCAGCTGTGTGGGCCACCTCAAGCAGCTGGGCTGT 489
Db 923 GCGCCGCTGTGCGGG 982
QY 490 GGGCGGCACCTGTGCTGTGCGAGGCGCAGACAGCGA 523
Db 983 GCTGGGTCCGGCTGCCCGCTGCCCGGGGGGGGGA 1016

RESULT 15
US-08-173-497-1
; Sequence 1, Application US/08173497
; Patent No. 5437958
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van Der Vieren, Monica
; TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
; TITLE OF INVENTION: Subunit
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,497
; FILING DATE:

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5437958and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/31363
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3726 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..3485
US-08-173-497-1
Query Match 2.8%; Score 37.2; DB 1; Length 3726;
Best Local Similarity 56.6%; Pred. No. 5.9;
Matches 69; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 297 CCTGTGGCGCACCCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCCGGGGCTTGGCGTC 356
Db 2375 CGTGGGGAGCTCCCTGGAGCTCAACGTGATTGTGTGGAAACGAGGTGAGGATTC 2434
QY 357 CTTTGTGAAGTGGTTCAGCCTATGTTTGCAGAGGGGCGAGGTTACAGCCACGCGGAGG 416
Db 2435 CTACGGAACCGTGGTTCAGCCTCTACTATCCAGCAGGGCTGTGCACGCGGGTGTTCAGG 2494
QY 417 AG 418
Db 2495 AG 2496
Search completed: December 28, 2002, 21:38:49
Job time : 1461.06 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 21:39:38 ; Search time 4743 Seconds
(without alignments)
11511.040 Million cell updates/sec

Title: US-09-944-896-49
Perfect score: 1876
Sequence: 1 ctctttgtccaccagccca.....tcagctgaaaaaaaaaaaaa 1876

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 10

Total number of hits satisfying chosen parameters: 2077837

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.ov.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pin.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	1029	54.9	1775	6	AX191503	Sequence
2	1008	53.7	1341	6	AX191493	Sequence
3	485	25.9	690	6	AX366554	Sequence
4	483	25.7	3293	9	HS804652	Sequence
5	414	22.1	163427	9	AC009053	Homo sapi
6	414	22.1	177479	9	AC009153	Homo sapi
7	414	22.1	197460	2	AC126771	Homo sapi
8	336	17.9	179675	9	AC026468	Homo sapi
9	336	17.9	190595	9	AC009022	Homo sapi
10	323	17.2	1328	9	BC008616	Homo sapi
11	287	15.3	191108	2	AC097265	Pan trogl
12	285	15.2	180596	9	AC009060	Homo sapi
13	195	10.4	200409	2	AC097331	Pan trogl
14	195	10.4	204182	2	AC097271	Pan trogl
15	190	10.1	205044	2	AC009125	Homo sapi
16	123	6.6	79023	2	AC021951	Homo sapi
17	115	6.1	2900	9	AB060195	Macaca fa
18	115	6.1	200409	2	AC097331	Pan trogl
19	109	5.8	205044	2	AC009125	Homo sapi
20	95	5.1	2340	9	AK096051	Homo sapi
21	79	4.2	79023	2	AC021951	Homo sapi
22	44	2.3	200755	2	AC093451	Mus muscu
23	34	1.8	197326	2	AC098076	Rattus no
24	23	1.2	12977	1	AE005865	Caulobact
25	22	1.2	98517	9	HS36623	Human DNA
26	22	1.2	110000	2	HS171M.1	Continuation (2 of
27	22	1.2	134151	2	AC079318	Homo sapi
28	22	1.2	165645	2	AC125935	Rattus no
29	22	1.2	178413	2	AL805954	Mus muscu
30	22	1.2	189456	9	AC079905	Homo sapi
31	22	1.2	191494	10	AL591488	Mouse DNA
32	22	1.2	205272	2	AL353591	Homo sapi
33	22	1.2	208613	2	AC093464	Mus muscu
34	22	1.2	223898	2	AC124604	Mus muscu
35	22	1.2	264522	2	AC090437	Mus muscu
36	22	1.2	340000	9	HS21C102	Homo sapi
37	21	1.1	1050	9	BC033766	Homo sapi
38	21	1.1	5061	1	RL431175	Rhizobium
39	21	1.1	7215	9	HSU22027	Human cytoc
40	21	1.1	7216	6	A47885	Sequence 3
41	21	1.1	7216	6	AR069321	Sequence
42	21	1.1	8778	9	HSU22028	Human cytoc
43	21	1.1	8779	6	A47886	Sequence 4
44	21	1.1	8779	6	AR069322	Sequence
45	21	1.1	30826	9	AL807743	Human DNA
46	21	1.1	73198	9	HSU2127L3	Human DNA
47	21	1.1	95359	9	AC078903	Homo sapi
48	21	1.1	105448	9	AC010494	Homo sapi
49	21	1.1	119707	2	AL773521	Sus scrofa
50	21	1.1	126895	2	AL773562	Sus scrofa
51	21	1.1	129402	9	AC011510	Homo sapi
52	21	1.1	131112	9	AL157712	Human DNA
53	21	1.1	141589	9	HS117P20	Homo sapi
54	21	1.1	150835	2	AC122336	Mus muscu
55	21	1.1	151630	2	AC012527	Homo sapi
56	21	1.1	154169	9	AC008962	Homo sapi
57	21	1.1	155132	2	AC080148	Homo sapi
58	21	1.1	155526	2	AC013371	Homo sapi
59	21	1.1	157285	2	AC099319	Felis cat
60	21	1.1	157493	2	AC027068	Homo sapi
61	21	1.1	164011	2	AC125556	Rattus no
62	21	1.1	168532	2	AC119698	Rattus no
63	21	1.1	169089	9	AC008537	Homo sapi
64	21	1.1	173085	2	AC127524	Homo sapi
65	21	1.1	173127	2	AC125141	Mus muscu

66	21	1.1	173251	2	AC058798	Homo sapi	AC058798	c 139	20	1.1	165228	9	CNS01DWS	AL138479	Human chr
67	21	1.1	173804	9	HS1030M6	Human DNA	AL035089	140	20	1.1	165704	9	AC012507	AC012507	Homo sapi
c 68	21	1.1	176034	2	AC123323	Rattus no	AC123323	c 141	20	1.1	166697	2	AC115290	AC115290	Mus muscu
c 69	21	1.1	176054	2	AC022377	Homo sapi	AC022377	c 142	20	1.1	167026	9	AP002783	AP002783	Homo sapi
c 70	21	1.1	176059	2	AC037464	Homo sapi	AC037464	c 143	20	1.1	167849	2	AC017001	AC017001	Homo sapi
71	21	1.1	178548	9	AC018831	Homo sapi	AC018831	c 144	20	1.1	167871	2	AC099705	AC099705	Mus muscu
c 72	21	1.1	178886	2	AC116832	Mus muscu	AC116832	c 145	20	1.1	168703	4	AC091759	AC091759	Sus scro
73	21	1.1	179237	2	AC111287	Rattus no	AC111287	c 146	20	1.1	169784	2	AC072042	AC072042	Homo sapi
74	21	1.1	183231	9	AC113785	Rattus no	AC113785	c 147	20	1.1	170064	2	AC095307	AC095307	Rattus no
c 75	21	1.1	186968	9	AC007917	Homo sapi	AC007917	c 148	20	1.1	170261	2	AC008542	AC008542	Homo sapi
c 76	21	1.1	190033	2	AC019349	Homo sapi	AC019349	c 149	20	1.1	170517	2	AC069526	AC069526	Homo sapi
c 77	21	1.1	196044	9	AC018505	Homo sapi	AC018505	c 150	20	1.1	170668	9	AC104012	AC104012	Homo sapi
78	21	1.1	198597	9	AC026218	Homo sapi	AC026218	c 151	20	1.1	170925	2	AC111655	AC111655	Rattus no
c 79	21	1.1	200836	2	AC011965	Homo sapi	AC011965	c 152	20	1.1	171585	2	AC127472	AC127472	Sus scro
80	21	1.1	202844	9	AC090956	Homo sapi	AC090956	c 153	20	1.1	172489	2	AC128579	AC128579	Rattus no
81	21	1.1	207722	2	AL732526	Mus muscu	AL732526	c 154	20	1.1	172677	2	AC096039	AC096039	Rattus no
c 82	21	1.1	209876	9	AC011599	Homo sapi	AC011599	c 155	20	1.1	172953	9	AC067721	AC067721	Homo sapi
c 83	21	1.1	219337	2	AC073291	Mus muscu	AC073291	c 156	20	1.1	173391	9	AC090063	AC090063	Homo sapi
c 84	21	1.1	220678	2	AC023857	Homo sapi	AC023857	c 157	20	1.1	175115	9	AC069246	AC069246	Homo sapi
c 85	21	1.1	223407	2	AC023387	Homo sapi	AC023387	c 158	20	1.1	175245	2	AC130090	AC130090	Homo sapi
86	21	1.1	229402	9	AC069271	Homo sapi	AC069271	c 159	20	1.1	175368	9	CNS01DWF	AC130090	Homo sapi
c 87	21	1.1	237613	2	AC025769	Homo sapi	AC025769	c 160	20	1.1	176174	9	AC007483	AC007483	Homo sapi
c 88	21	1.1	245520	2	AC127341	Mus muscu	AC127341	c 161	20	1.1	176355	9	AC025518	AC025518	Homo sapi
89	20	1.1	777	6	E06782	cdNA contai	E06782	c 162	20	1.1	176417	2	AC024160	AC024160	Homo sapi
c 90	20	1.1	1189	10	BC021951	Mus muscu	BC021951	c 163	20	1.1	177555	2	AC130192	AC130192	Sus scro
91	20	1.1	1526	9	IR2068071	Homo sapi	IR2068071	c 164	20	1.1	177784	9	AC027465	AC027465	Homo sapi
92	20	1.1	3952	10	BC034508	Homo sapi	BC034508	c 165	20	1.1	179217	2	AC099748	AC099748	Bos tauru
93	20	1.1	7035	10	AC030238	Mus muscu	AC030238	c 166	20	1.1	179270	2	AC110145	AC110145	Rattus no
c 94	20	1.1	9596	4	BT0300468	Rattus no	AB0300238	c 167	20	1.1	180487	2	AC113228	AC113228	Bos tauru
c 95	20	1.1	32415	10	HAMSHCA		AJ300468	c 168	20	1.1	181650	2	AC124478	AC124478	Mus muscu
c 96	20	1.1	40158	2	AC103711	Homo sapi	L15351	c 169	20	1.1	182171	9	AC066589	AC066589	Homo sapi
c 97	20	1.1	57963	9	AC023494	Homo sapi	AC023494	c 170	20	1.1	182573	2	AC110879	AC110879	Oryctolag
98	20	1.1	60761	2	AC068568	Homo sapi	AC068568	c 171	20	1.1	182717	2	AC079823	AC079823	Homo sapi
c 99	20	1.1	64175	2	AC113068	Homo sapi	AC113068	c 172	20	1.1	182909	9	AC026130	AC026130	Homo sapi
c 100	20	1.1	65861	2	AC116124	Mus muscu	AC116124	c 173	20	1.1	183224	9	AC022206	AC022206	Homo sapi
c 101	20	1.1	65861	2	AC116124	Mus muscu	AC116124	c 174	20	1.1	183594	2	AL732473	AL732473	Mus muscu
c 102	20	1.1	96183	8	TS18		AC007060	c 175	20	1.1	183692	9	AC073413	AC073413	Homo sapi
c 103	20	1.1	97165	2	AC096257	Rattus no	AC096257	c 176	20	1.1	183774	9	AC092420	AC092420	Homo sapi
c 104	20	1.1	97346	2	AC017201	Drosophil	AC017201	c 177	20	1.1	183833	9	AL161646	AL161646	Human DNA
c 105	20	1.1	105495	9	AC105999	Homo sapi	AC105999	c 178	20	1.1	184234	2	AC091758	AC091758	Sus scro
c 106	20	1.1	105496	9	AF165142	Homo sapi	AF165142	c 179	20	1.1	185221	9	AC087474	AC087474	Homo sapi
c 107	20	1.1	107777	2	AC104971	Homo sapi	AC104971	c 180	20	1.1	185761	2	AC108814	AC108814	Mus muscu
c 108	20	1.1	110000	2	HSS17IM_2		Continuation (3 of	c 181	20	1.1	186870	2	AC116170	AC116170	Homo sapi
c 109	20	1.1	110000	2	AE014181_2		Continuation (3 of	c 182	20	1.1	187038	2	AC021179	AC021179	Homo sapi
c 110	20	1.1	110000	10	AE014181_2		Continuation (3 of	c 183	20	1.1	187117	9	AC016749	AC016749	Homo sapi
c 111	20	1.1	123224	9	AC011414	Homo sapi	AC011414	c 184	20	1.1	188946	2	AL645608	AL645608	Homo sapi
c 112	20	1.1	123547	9	AC015857	Homo sapi	AC015857	c 185	20	1.1	189076	2	AC023788	AC023788	Homo sapi
c 113	20	1.1	124510	9	AC027306	Homo sapi	AC027306	c 186	20	1.1	190023	9	AC011669	AC011669	Homo sapi
c 114	20	1.1	128757	9	AL359837	Human DNA	AL359837	c 187	20	1.1	190283	9	AC091560	AC091560	Homo sapi
c 115	20	1.1	130177	9	HSB6279B7	Human DNA	AL078644	c 188	20	1.1	190705	2	AC091931	AC091931	Homo sapi
c 116	20	1.1	130364	9	AC116316	Homo sapi	AC116316	c 189	20	1.1	193264	9	AC090885	AC090885	Homo sapi
c 117	20	1.1	130388	9	AC025434	Homo sapi	AC025434	c 190	20	1.1	194624	9	AC008742	AC008742	Homo sapi
c 118	20	1.1	131355	2	AC089989	Rattus no	AC089989	c 191	20	1.1	194880	2	AC091929	AC091929	Homo sapi
c 119	20	1.1	134249	2	AC026734	Homo sapi	AC026734	c 192	20	1.1	196931	9	AC022867	AC022867	Homo sapi
c 120	20	1.1	137539	2	AC130193	Felis cat	AC130193	c 193	20	1.1	197838	2	AC115785	AC115785	Mus muscu
c 121	20	1.1	138036	9	AC008752	Homo sapi	AC008752	c 194	20	1.1	198230	9	AC092662	AC092662	Homo sapi
c 122	20	1.1	144432	2	AF276983	Homo sapi	AF276983	c 195	20	1.1	200000	2	AC004630	AC004630	Homo sapi
c 123	20	1.1	146019	2	AC120631	Rattus no	AC120631	c 196	20	1.1	200620	2	AL772207	AL772207	Mus muscu
c 124	20	1.1	148370	10	AC091514	Rattus no	AC091514	c 197	20	1.1	203519	10	AC112258	AC112258	Mus muscu
c 125	20	1.1	148412	9	AC010654	Homo sapi	AC010654	c 198	20	1.1	203519	10	AC112258	AC112258	Mus muscu
c 126	20	1.1	151608	2	AC123290	Rattus no	AC123290	c 199	20	1.1	209612	2	AC096124	AC096124	Rattus no
c 127	20	1.1	152855	2	AC103224	Rattus no	AC103224	c 200	20	1.1	210070	2	AC067951	AC067951	Homo sapi
c 128	20	1.1	153764	9	AL355350	Human DNA	AL355350	c 201	20	1.1	210954	9	AC003684	AC003684	Homo sapi
c 129	20	1.1	153975	2	AC084243	Homo sapi	AC084243	c 202	20	1.1	214971	2	AC094543	AC094543	Rattus no
c 130	20	1.1	156826	2	AC055767	Homo sapi	AC055767	c 203	20	1.1	216180	2	AC124347	AC124347	Mus muscu
c 131	20	1.1	157835	3	AC009356	Drosophil	AC009356	c 204	20	1.1	216866	2	AC122873	AC122873	Mus muscu
c 132	20	1.1	159613	3	AC007226	Homo sapi	AC007226	c 205	20	1.1	217346	9	AC012363	AC012363	Homo sapi
c 133	20	1.1	159640	3	AC008230	Drosophil	AC008230	c 206	20	1.1	223289	2	AC112142	AC112142	Mus muscu
c 134	20	1.1	160307	9	AC0018359	Homo sapi	AC0018359	c 207	20	1.1	232055	2	AL806527	AL806527	Mus muscu
c 135	20	1.1	160754	9	AC007613	Homo sapi	AC007613	c 208	20	1.1	237477	10	AL663026	AL663026	Mouse DNA
c 136	20	1.1	161153	10	AC090887	Mus muscu	AC090887	c 209	20	1.1	246998	2	AC103311	AC103311	Rattus no
c 137	20	1.1	161649	2	AC023652	Homo sapi	AC023652	c 210	20	1.1	247876	2	AL844873	AL844873	Mus muscu
c 138	20	1.1	164963	9	AC090833	Homo sapi	AC090833	c 211	20	1.1	250788	2	AC125523	AC125523	Mus muscu
c 139	20	1.1	164963	9	AC090833	Homo sapi	AC090833	c 211	20	1.1	258223	3	AE003807	AE003807	Drosophil

212	1.1	309159	2	AC074271	Homo sapi	285	19	1.0	37914	2	AC063959	Mus muscu
213	1.1	331801	1	NMA4Z2491	Alu162755 Neisseria	c 286	19	1.0	38944	8	SPBP3562	Alu163702 S.pombe c
c 214	1.1	340000	2	HS21C102	Alu163302 Homo sapi	c 287	19	1.0	40611	9	AC021090	AC021090 Homo sapi
215	1.1	348189	2	AC119567	AC119567 Homo sapi	c 288	19	1.0	40953	2	AC020347	AC020347 Drosophil
c 216	1.0	500	6	AX474820	AX474820 Sequence	289	19	1.0	44913	8	SPU23729	SPU23729 Schizosacch
217	1.0	758	9	HS420455	AJ420455 Homo sapi	290	19	1.0	45333	8	HSU10618A	HSU10618A Human DNA
c 218	1.0	758	9	HSGLRA206	AF053492 Homo sapi	c 291	19	1.0	46783	2	AC096502	AC096502 Rattus no
219	1.0	768	10	S70302	S70302 cytokine re	c 292	19	1.0	48173	2	AL583849	AL583849 Human DNA
220	1.0	802	10	BC013334	BC013334 Mus muscu	c 293	19	1.0	50488	9	AL133231	AL133231 Human DNA
221	1.0	912	10	MMELA2R	X04573 Mouse mRNA	294	19	1.0	51815	2	AC068454	AC068454 Homo sapi
c 222	1.0	917	10	BC026552	BC026552 Mus muscu	c 295	19	1.0	53628	2	AC124004	AC124004 Mus muscu
223	1.0	934	10	AY074084	AY074084 Mus muscu	c 296	19	1.0	55707	2	AC101785	AC101785 Mus muscu
224	1.0	1008	9	BC000509	BC000509 Homo sapi	c 297	19	1.0	57000	9	AB038162	AB038162 Homo sapi
c 225	1.0	1013	9	AF024690	AF024690 Homo sapi	c 298	19	1.0	57700	2	AC099868	AC099868 Mus muscu
226	1.0	1021	10	AF151108	AF151108 Mus muscu	c 299	19	1.0	59460	2	AC130298	AC130298 Homo sapi
227	1.0	1078	9	BC016277	BC016277 Homo sapi	c 300	19	1.0	62180	2	AP000441	AP000441 Homo sapi
228	1.0	1129	6	AX464088	AX464088 Sequence	301	19	1.0	64108	2	AC101983	AC101983 Mus muscu
229	1.0	1242	9	HSU86070	U86070 Homo sapien	302	19	1.0	64569	9	AC117433	AC117433 Homo sapi
230	1.0	1325	9	AF131814	AF131814 Homo sapi	303	19	1.0	65943	2	AC124996	AC124996 Mus muscu
231	1.0	1444	9	BC002793	BC002793 Homo sapi	304	19	1.0	66092	2	AC125435	AC125435 Homo sapi
232	1.0	1507	9	HSU52464	U52464 Human P2 pu	305	19	1.0	66254	9	AL137791	AL137791 Human DNA
233	1.0	1559	9	AF007891	AF007891 Homo sapi	c 306	19	1.0	66974	2	AC130566	AC130566 Homo sapi
c 234	1.0	1549	8	HVGLN2	U16000 Hordeum vul	c 307	19	1.0	67119	2	AC100327	AC100327 Mus muscu
235	1.0	1556	9	BC000571	BC000571 Homo sapi	c 308	19	1.0	67131	2	AC103791	AC103791 Homo sapi
c 236	1.0	1571	9	HSP2Y6	X97058 H.sapiens m	c 309	19	1.0	68409	2	AC105975	AC105975 Mus muscu
c 237	1.0	1600	8	HVGLN2R	X53580 Barley gln	c 310	19	1.0	70548	9	HSAP003625	HSAP003625 Homo sapi
c 238	1.0	1647	9	AF218005	AF218005 Homo sapi	c 311	19	1.0	71573	2	AC105408	AC105408 Mus muscu
c 239	1.0	1667	6	AX250017	AX250017 Sequence	c 312	19	1.0	71715	2	AC105650	AC105650 Homo sapi
240	1.0	1691	6	AX250019	AX250019 Sequence	313	19	1.0	73065	8	NCB1308	AC124808 Rattus no
241	1.0	1724	9	AF265209	AF265209 Homo sapi	c 314	19	1.0	82016	2	AC016110	AC016110 Homo sapi
242	1.0	1725	9	HUMENICMA	L35240 Human enig	c 315	19	1.0	83504	2	AC114641	AC114641 Mus muscu
243	1.0	1832	9	AF007892	AF007892 Homo sapi	c 316	19	1.0	84877	10	AL672018	AL672018 Mouse DNA
244	1.0	1944	9	AF227216S1	AF227216 Homo sapi	c 317	19	1.0	85097	3	AC026301	AC026301 Caenorhab
245	1.0	1980	10	BC027199	BC027199 Mus muscu	c 318	19	1.0	86173	9	AL160004	AL160004 Human DNA
246	1.0	2110	1	ABGHPA	DI4440 A. pasteurii	c 319	19	1.0	86421	9	AC108118	AC108118 Homo sapi
247	1.0	2152	10	BC008638	BC008638 Mus muscu	c 320	19	1.0	88662	2	AC021501	AC021501 Homo sapi
c 248	1.0	2246	10	BC008989	BC008989 Mus muscu	c 321	19	1.0	89134	2	AP004162	AP004162 Oryza sat
c 249	1.0	2260	6	AY071207	AY071207 Sequence	c 322	19	1.0	89267	9	AC1359079	AC1359079 Human DNA
250	1.0	2295	3	AY060938	AY060938 Drosophil	c 323	19	1.0	90601	9	AC087308	AC087308 Homo sapi
251	1.0	2298	9	AB070146	AB070146 Macaca fa	c 324	19	1.0	91192	9	AC073072	AC073072 Homo sapi
252	1.0	2308	10	RATKINLA	M75146 Rat kinesin	c 325	19	1.0	92567	2	AC103425	AC103425 Rattus no
253	1.0	2338	9	BC007952	BC007952 Homo sapi	c 326	19	1.0	93667	2	AC107039	AC107039 Pan trogl
254	1.0	2352	9	AF007893	AF007893 Homo sapi	c 327	19	1.0	94000	9	AP000562	AP000562 Homo sapi
255	1.0	2386	10	RATKINLC	M75148 Rat kinesin	c 328	19	1.0	94255	8	AP0003090	AP0003090 Homo sapi
256	1.0	2409	9	BC009391	BC009391 Homo sapi	c 329	19	1.0	95582	8	AP004943	AP004943 Lotus jap
257	1.0	2486	6	AX098605	AX098605 Sequence	c 330	19	1.0	96953	9	AC079621	AC079621 Homo sapi
258	1.0	2490	1	SPU5974	AJ005974 Shewanell	c 331	19	1.0	97146	9	AL135929	AL135929 Human DNA
259	1.0	2571	3	AB066348	AB066348 Crassost	c 332	19	1.0	97512	9	AL139351	AL139351 Human DNA
260	1.0	2818	8	AF019614	AF019614 Solanum t	c 333	19	1.0	98240	9	AC006021	AC006021 Homo sapi
261	1.0	2928	9	AB071049	AB071049 Macaca fa	c 334	19	1.0	98713	2	AC002511	AC002511 Human DNA
262	1.0	2996	9	HUMGMCsFRB	M59941 Human GM-CS	c 335	19	1.0	98951	2	AC090069	AC090069 Homo sapi
263	1.0	3079	9	AK092663	AK092663 Homo sapi	c 336	19	1.0	104705	9	AC079412	AC079412 Homo sapi
c 264	1.0	3318	6	AX250079	AX250079 Sequence	c 337	19	1.0	106169	9	AC073534	AC073534 Homo sapi
c 265	1.0	3345	9	AF178985	AF178985 Homo sapi	c 338	19	1.0	106616	2	AC099002	AC099002 Rattus no
266	1.0	3371	5	CHRCORNE	DI6541 Gallus gall	c 339	19	1.0	10733	9	AC008472	AC008472 Homo sapi
267	1.0	4169	6	AX250159	AX250159 Sequence	c 340	19	1.0	108625	9	AL356773	AL356773 Human DNA
268	1.0	4442	9	BC013645	BC013645 Homo sapi	341	19	1.0	108669	2	AC011675	AC011675 Homo sapi
269	1.0	6984	10	AF042317	AF042317 Mus muscu	342	19	1.0	109877	2	AC123276	AC123276 Rattus no
270	1.0	7185	10	MMU04999	U04999 Mus musculu	c 343	19	1.0	110000	2	AC097795_2	AC097795_2 Continuation (3 of
271	1.0	10029	1	AE011108	AE011108 Xanthomon	c 344	19	1.0	110000	2	AC026388_0	AC026388_0 Mus muscu
c 272	1.0	1508	1	AE011748	AE011748 Homo sapi	345	19	1.0	110000	9	HSAP6345_0	HSAP6345_0 Homo sapi
273	1.0	13284	2	AC019860	AC019860 Drosophil	c 346	19	1.0	110000	10	AE014174_2	AE014174_2 Continuation (3 of
274	1.0	13638	9	AC005573	AC005573 Homo sapi	347	19	1.0	110104	9	AC011348	AC011348 Homo sapi
c 275	1.0	19809	2	AC017750	AC017750 Drosophil	348	19	1.0	111324	9	AC000377	AC000377 Human Chr
276	1.0	24276	9	AC091800	AC091800 Homo sapi	c 349	19	1.0	112010	2	AC122588	AC122588 Rattus no
277	1.0	29759	9	AL133392	AL133392 Human DNA	c 350	19	1.0	112067	9	AC008894	AC008894 Homo sapi
c 278	1.0	31224	2	AC024693	AC024693 Homo sapi	c 351	19	1.0	112098	2	AC119347	AC119347 Rattus no
c 279	1.0	35100	6	AR065851	AR065851 Sequence	352	19	1.0	112098	2	AC119347	AC119347 Rattus no
c 280	1.0	35100	6	AR127849	AR127849 Sequence	353	19	1.0	112098	2	AC119347	AC119347 Rattus no
c 281	1.0	35100	6	AR127849	AR127849 Sequence	354	19	1.0	112098	2	AC119347	AC119347 Rattus no
c 282	1.0	35872	8	AF325196	AF325196 Triticum	c 355	19	1.0	112098	2	AC119347	AC119347 Rattus no
c 283	1.0	37770	9	AC010513	AC010513 Homo sapi	c 356	19	1.0	112098	2	AC119347	AC119347 Rattus no
c 284	1.0	37784	9	AC002997	AC002997 Human DNA	c 357	19	1.0	112098	2	AC119347	AC119347 Rattus no

358	19	1.0 112389	2	AC073598	AC073598 Homo sapi	431	19	1.0 152631	9	AC117432	AC117432 Homo sapi
c 359	19	1.0 113196	9	HSJ697K14	AL121829 Human DNA	c 432	19	1.0 152732	2	AC074204	Mus muscu
360	19	1.0 113213	9	AC008490	Homo sapi	433	19	1.0 152901	2	AC055781	Homo sapi
361	19	1.0 113474	2	AC013932	AC013932 Drosophil	c 434	19	1.0 152951	2	AC123392	Rattus no
c 362	19	1.0 115252	2	AC102851	Mus muscu	435	19	1.0 153659	2	AC124057	Homo sapi
363	19	1.0 115732	9	AC104566	Homo sapi	c 436	19	1.0 154967	2	AC124057	Homo sapi
364	19	1.0 117559	9	AC092279	Homo sapi	437	19	1.0 155035	2	AC120282	Rattus no
365	19	1.0 119689	9	AC126304	Rattus no	438	19	1.0 155035	2	AC096239	Rattus no
c 366	19	1.0 126707	2	AL773521	Sus scrofa	439	19	1.0 155074	9	AC003693	Human chr
c 367	19	1.0 126708	2	HS469K11	AL449209 Homo sapi	c 440	19	1.0 155125	9	AC003693	Human chr
c 368	19	1.0 120793	2	AF322450	Homo sapi	c 441	19	1.0 155125	9	AC024561	Homo sapi
369	19	1.0 120948	2	AL123596	Medicago	442	19	1.0 155536	9	AC004112	Homo sapi
370	19	1.0 123256	2	AL356602	Homo sapi	443	19	1.0 155589	9	AC084879	Homo sapi
c 371	19	1.0 123391	9	HSJ902P15	AL096888 Human DNA	c 444	19	1.0 155723	2	AC103599	Mus muscu
c 372	19	1.0 125000	9	AB017602	Homo sapi	445	19	1.0 155925	2	AP004814	Oryza sat
c 373	19	1.0 126809	2	AC128053	AC128053 Rattus no	446	19	1.0 157102	2	AC016409	Homo sapi
c 374	19	1.0 127683	9	AC003683	AC003683 Homo sapi	c 447	19	1.0 157481	9	AC093512	Homo sapi
375	19	1.0 127701	2	AC091302	AC091302 Oryza sat	c 448	19	1.0 157656	2	AC104124	Homo sapi
c 376	19	1.0 129102	2	AC103927	Mus muscu	449	19	1.0 157739	9	AP001623	Homo sapi
c 377	19	1.0 129120	2	HS187B23	AL031280 Human DNA	450	19	1.0 158249	2	AC121929	Mus muscu
c 378	19	1.0 129197	2	AC101726	AC101726 Mus muscu	451	19	1.0 158320	2	AC055727	Homo sapi
c 379	19	1.0 129440	9	AC004806	AC004806 Homo sapi	c 452	19	1.0 158395	9	AC079600	Homo sapi
c 380	19	1.0 129654	9	AL157765	Human DNA	c 453	19	1.0 158535	9	AC093368	Homo sapi
381	19	1.0 130831	2	AC027568	AC027568 Homo sapi	c 454	19	1.0 158862	2	AC122964	Rattus no
382	19	1.0 131611	9	AC005099	AC005099 Homo sapi	c 455	19	1.0 159281	9	HS406M12	Human DNA
c 383	19	1.0 132323	9	AL116615	AC116615 Homo sapi	456	19	1.0 159284	2	AC084369	Homo sapi
c 384	19	1.0 132933	9	AL137002	Human DNA	c 457	19	1.0 159602	9	CNS01DRH	Human chr
c 385	19	1.0 132948	9	HS349A12	AL033520 Human DNA	c 458	19	1.0 159637	2	AC007990	Homo sapi
c 386	19	1.0 133544	9	AC100748	AC100748 Homo sapi	c 459	19	1.0 159836	2	AF236875	Homo sapi
c 387	19	1.0 133661	14	U93872	Kaposi's sa	460	19	1.0 159922	2	AC128830	Rattus no
c 388	19	1.0 134979	9	AC018720	AC018720 Homo sapi	461	19	1.0 160219	2	AC111053	Homo sapi
c 389	19	1.0 135033	9	AC009955	AC009955 Homo sapi	c 462	19	1.0 160259	2	AC111945	Rattus no
c 390	19	1.0 135062	9	AC026691	AC026691 Homo sapi	463	19	1.0 160405	9	AC092324	Homo sapi
c 391	19	1.0 135300	9	AC008163	AC008163 Homo sapi	c 464	19	1.0 160436	2	AC040953	Homo sapi
c 392	19	1.0 135430	9	AC112131	AC112131 Homo sapi	465	19	1.0 161530	2	AC015529	Homo sapi
c 393	19	1.0 136933	3	AC005891	AC005891 Drosophil	466	19	1.0 161753	2	AF186997	Homo sapi
c 394	19	1.0 137508	14	KSU75698	U75698 Kaposi's sa	c 467	19	1.0 162149	2	AC023574	Homo sapi
c 395	19	1.0 137833	9	CNS01DV6	AL133455 Human chr	468	19	1.0 162477	2	AC103957	Homo sapi
c 396	19	1.0 137862	2	AL356780	AL356780 Homo sapi	c 469	19	1.0 162539	2	AL354753	Homo sapi
c 397	19	1.0 138502	2	AC128093	AC128093 Rattus no	470	19	1.0 162921	3	AC007853	Drosophil
c 398	19	1.0 138547	2	AC021456	AC021456 Homo sapi	c 471	19	1.0 163166	2	AC124463	Mus muscu
399	19	1.0 139117	2	AC068147	AC068147 Homo sapi	472	19	1.0 163253	2	AC093312	Oryza sat
400	19	1.0 139253	9	AC091899	AC091899 Homo sapi	473	19	1.0 163338	9	AL162426	Human DNA
401	19	1.0 139629	2	AP003809	AP003809 Oryza sat	474	19	1.0 163577	2	AC107571	Rattus no
c 402	19	1.0 139857	2	AC120315	AC120315 Rattus no	c 475	19	1.0 163838	2	AC069241	Homo sapi
403	19	1.0 141591	9	AC079467	AC079467 Homo sapi	c 476	19	1.0 164508	2	AC104130	Homo sapi
c 404	19	1.0 141717	2	AP004457	AP004457 Oryza sat	c 477	19	1.0 164522	9	AC026191	Homo sapi
c 405	19	1.0 141794	2	AC093455	AC093455 Homo sapi	478	19	1.0 164834	2	AC105633	Rattus no
c 406	19	1.0 141978	2	AC102006	AC102006 Mus muscu	c 479	19	1.0 165081	2	AC113484	Mus muscu
407	19	1.0 142156	2	AP004399	AP004399 Oryza sat	c 480	19	1.0 165120	2	AC069430	Homo sapi
c 408	19	1.0 142451	4	AC091542	AC091542 Felis cat	481	19	1.0 165639	2	AC016267	Homo sapi
c 409	19	1.0 142527	9	AL589843	AL589843 Human DNA	c 482	19	1.0 166183	9	CNS01RH2	Human chr
c 410	19	1.0 143111	2	AC121938	AC121938 Mus muscu	483	19	1.0 166229	2	AC022070	Homo sapi
411	19	1.0 143785	2	AC092334	AC092334 Homo sapi	484	19	1.0 166465	2	AP002351	Homo sapi
c 412	19	1.0 144068	2	AC079236	AC079236 Homo sapi	c 485	19	1.0 166517	9	AL732604	Human DNA
c 413	19	1.0 144124	2	AC117252	AC117252 Mus muscu	486	19	1.0 166572	2	AC091508	Felis cat
414	19	1.0 144260	9	AC006998	AC006998 Homo sapi	c 487	19	1.0 166660	9	AC008073	Homo sapi
415	19	1.0 145173	9	AC005599	AC005599 Homo sapi	488	19	1.0 166937	9	AC025679	Homo sapi
c 416	19	1.0 145242	2	AC018823	AC018823 Homo sapi	c 489	19	1.0 166978	9	AC004098	Homo sapi
c 417	19	1.0 145380	9	AL357129	AL357129 Human DNA	c 490	19	1.0 167286	2	AC115907	Mus muscu
c 418	19	1.0 145762	9	AP001626	AP001626 Homo sapi	491	19	1.0 167439	2	AC130273	Papio cyn
419	19	1.0 146776	2	AC093486	AC093486 Homo sapi	492	19	1.0 167544	3	AC093095	Drosophil
420	19	1.0 148517	2	AC011147	AC011147 Homo sapi	493	19	1.0 167579	9	AC026161	Homo sapi
c 421	19	1.0 148572	2	AC130911	AC130911 Rattus no	c 494	19	1.0 167760	9	AC022994	Homo sapi
c 422	19	1.0 149266	2	AC116022	AC116022 Homo sapi	495	19	1.0 167914	2	AC055870	Homo sapi
423	19	1.0 150260	9	AC034186	AC034186 Homo sapi	c 496	19	1.0 168055	9	AC090796	Homo sapi
c 424	19	1.0 150348	2	AC097387	AC097387 Rattus no	497	19	1.0 168582	2	AC079534	Mus muscu
c 425	19	1.0 151019	9	AC026796	AC026796 Homo sapi	c 498	19	1.0 168593	2	AC103080	Rattus no
c 426	19	1.0 151804	2	AC008161	AC008161 Mus muscu	499	19	1.0 169083	2	AL355346	Homo sapi
c 427	19	1.0 152077	9	HS130G2	AL008627 Human DNA	c 500	19	1.0 169246	9	AC091815	Homo sapi
c 428	19	1.0 152135	9	AC011199	AC011199 Homo sapi	c 501	19	1.0 169588	2	AC107100	Rattus no
c 429	19	1.0 152258	2	AC116838	AC116838 Mus muscu	c 502	19	1.0 170155	2	AC068353	Homo sapi
c 430	19	1.0 152283	9	AC024083	AC024083 Homo sapi	c 503	19	1.0 170268	2	AC026834	Homo sapi

504	19	1.0 170343	2	AC015939	AC015939 Mus muscu	c 577	19	1.0 184516	2	AC117100	AC117100 Rattus no
505	19	1.0 170343	2	AP005185	Oryza sat	c 578	19	1.0 185136	2	AC120615	AC120615 Rattus no
506	19	1.0 170450	2	AC105379	Trypanoso	c 579	19	1.0 185574	9	AC073341	AC073341 Homo sapi
507	19	1.0 170856	2	AC068160	Homo sapi	c 580	19	1.0 185930	2	AC102735	AC102735 Mus muscu
508	19	1.0 171115	2	AC102661	AC102661 Mus muscu	c 581	19	1.0 186048	2	AC074190	AC074190 Homo sapi
509	19	1.0 171390	9	AC027315	AC027315 Homo sapi	c 582	19	1.0 186855	2	AC118611	AC118611 Mus muscu
510	19	1.0 171491	2	AC022606	AC022606 Homo sapi	c 583	19	1.0 187002	2	AC109218	AC109218 Mus muscu
511	19	1.0 171495	2	AC122450	AC122450 Mus muscu	c 584	19	1.0 187032	9	AC114289	AC114289 Homo sapi
512	19	1.0 171727	2	AC117809	AC117809 Mus muscu	c 585	19	1.0 187343	2	AC016688	AC016688 Homo sapi
513	19	1.0 171751	3	AC023697	Drosophil	c 586	19	1.0 187418	2	AC090580	AC090580 Homo sapi
514	19	1.0 171858	2	AC011672	AC011672 Homo sapi	c 587	19	1.0 187533	2	AC125827	AC125827 Rattus no
515	19	1.0 172105	2	AC021197	AC021197 Homo sapi	c 588	19	1.0 187773	9	AC011040	AC011040 Mus muscu
516	19	1.0 172105	9	AC093135	Pan trogl	c 589	19	1.0 187888	9	AC011467	AC011467 Homo sapi
517	19	1.0 172155	9	AC018653	AC018653 Homo sapi	c 590	19	1.0 188601	2	AC022254	AC022254 Homo sapi
518	19	1.0 172282	2	AC111367	AC111367 Rattus no	c 591	19	1.0 188820	2	AC097299	AC097299 Rattus no
519	19	1.0 172367	2	AC118989	Canis fam	c 592	19	1.0 188833	9	HS268H5	AC097299 Rattus no
520	19	1.0 172588	2	AC007430	AC007430 Homo sapi	c 593	19	1.0 188868	9	AC023232	AC023232 Homo sapi
521	19	1.0 172588	2	AC129153	AC129153 Rattus no	c 594	19	1.0 188921	2	AC025122	AC025122 Homo sapi
522	19	1.0 172863	2	AC125073	AC125073 Mus muscu	c 595	19	1.0 189139	2	AC021663	AC021663 Homo sapi
523	19	1.0 172942	2	AC016899	AC016899 Homo sapi	c 596	19	1.0 189875	9	AC011239	AC011239 Homo sapi
524	19	1.0 173839	9	AC026005	AC026005 Homo sapi	c 597	19	1.0 190223	9	AL355137	AL355137 Human DNA
525	19	1.0 173873	2	AC097818	AC097818 Rattus no	c 598	19	1.0 190265	2	AC123818	AC123818 Mus muscu
526	19	1.0 174086	2	AC110010	AC110010 Homo sapi	c 599	19	1.0 190811	9	AC025569	AC025569 Homo sapi
527	19	1.0 174162	2	AC024611	AC024611 Mus muscu	c 600	19	1.0 191037	2	AC131053	AC131053 Homo sapi
528	19	1.0 174257	2	AC117639	AC117639 Mus muscu	c 601	19	1.0 191211	2	AC091561	AC091561 Homo sapi
529	19	1.0 174278	2	AC016330	AC016330 Homo sapi	c 602	19	1.0 191234	2	AC018681	AC018681 Homo sapi
530	19	1.0 174445	9	AC051642	AC051642 Homo sapi	c 603	19	1.0 192337	2	AC117628	AC117628 Mus muscu
531	19	1.0 174714	9	AC025280	AC025280 Homo sapi	c 604	19	1.0 193460	2	AC113198	AC113198 Mus muscu
532	19	1.0 175099	10	AL606863	AL606863 Mouse DNA	c 605	19	1.0 193991	2	AC115701	AC115701 Mus muscu
533	19	1.0 175137	2	AC115339	AC115339 Rattus no	c 606	19	1.0 194215	2	AC024422	AC024422 Homo sapi
534	19	1.0 175629	9	AC097173	AC097173 Homo sapi	c 607	19	1.0 194308	3	AC009377	AC009377 Drosophili
535	19	1.0 176060	2	AC099364	AC099364 Rattus no	c 608	19	1.0 194893	9	AC024382	AC024382 Homo sapi
536	19	1.0 176174	9	AC007483	AC007483 Homo sapi	c 609	19	1.0 194943	9	AC105252	AC105252 Homo sapi
537	19	1.0 176233	2	AC102885	AC102885 Mus muscu	c 610	19	1.0 195197	9	AC020911	AC020911 Homo sapi
538	19	1.0 176562	2	AC130272	AC130272 Papio cyn	c 611	19	1.0 195339	2	AC125721	AC125721 Rattus no
539	19	1.0 176584	2	AC062010	AC062010 Homo sapi	c 612	19	1.0 196378	2	AC117504	AC117504 Homo sapi
540	19	1.0 177158	2	AC121433	AC121433 Rattus no	c 613	19	1.0 196671	9	AC073479	AC073479 Homo sapi
541	19	1.0 177385	9	AC010885	AC010885 Homo sapi	c 614	19	1.0 196980	2	AC122405	AC122405 Mus muscu
542	19	1.0 177807	9	AC093759	AC093759 Homo sapi	c 615	19	1.0 196988	9	AP002761	AP002761 Homo sapi
543	19	1.0 178343	2	AC024049	AC024049 Homo sapi	c 616	19	1.0 197650	2	AL391243	AL391243 Homo sapi
544	19	1.0 178804	9	AC113134	AC113134 Homo sapi	c 617	19	1.0 198046	2	AL731670	AL731670 Mus muscu
545	19	1.0 178965	9	AL353753	AL353753 Human DNA	c 618	19	1.0 198470	9	AC046170	AC046170 Homo sapi
546	19	1.0 179013	9	AC022370	AC022370 Homo sapi	c 619	19	1.0 199226	2	AC114446	AC114446 Rattus no
547	19	1.0 179027	9	AC128987	AC128987 Rattus no	c 620	19	1.0 199240	2	AC010287	AC010287 Homo sapi
548	19	1.0 179202	9	AC114493	AC114493 Homo sapi	c 621	19	1.0 199287	2	AC068659	AC068659 Homo sapi
549	19	1.0 179222	2	AC118451	AC118451 Rattus no	c 622	19	1.0 200498	2	AP000944	AP000944 Homo sapi
550	19	1.0 179612	10	AC121970	AC121970 Mus muscu	c 623	19	1.0 201858	2	AC025712	AC025712 Homo sapi
551	19	1.0 180069	2	AC017041	AC017041 Homo sapi	c 624	19	1.0 202918	2	AC115800	AC115800 Mus muscu
552	19	1.0 180072	9	AC017092	AC017092 Homo sapi	c 625	19	1.0 202918	2	AL35075	AL35075 Human chr
553	19	1.0 180241	2	AC102757	AC102757 Mus muscu	c 626	19	1.0 205379	10	AL591174	AL591174 Mouse DNA
554	19	1.0 180399	2	AC079252	AC079252 Homo sapi	c 627	19	1.0 206512	2	AC015544	AC015544 Homo sapi
555	19	1.0 180629	2	AC104075	AC104075 Homo sapi	c 628	19	1.0 207739	2	AC113528	AC113528 Mus muscu
556	19	1.0 180774	2	AC061979	AC061979 Homo sapi	c 629	19	1.0 208197	9	AC009107	AC009107 Homo sapi
557	19	1.0 181016	9	AC068273	AC068273 Homo sapi	c 630	19	1.0 209947	2	AC122932	AC122932 Mus muscu
558	19	1.0 181132	3	AC008206	AC008206 Drosophili	c 631	19	1.0 210539	2	AC116733	AC116733 Mus muscu
559	19	1.0 181511	9	AC015555	AC015555 Homo sapi	c 632	19	1.0 212265	2	AC120520	AC120520 Canis fam
560	19	1.0 181663	9	AC092415	AC092415 Homo sapi	c 633	19	1.0 213965	2	AL353721	AL353721 Homo sapi
561	19	1.0 181716	2	AC113230	AC113230 Sus scrof	c 634	19	1.0 214659	2	AC125221	AC125221 Mus muscu
562	19	1.0 181991	9	AC025882	AC025882 Homo sapi	c 635	19	1.0 215287	2	AC079432	AC079432 Mus muscu
563	19	1.0 182165	9	AC093429	AC093429 Homo sapi	c 636	19	1.0 216303	10	AL627445	AL627445 Mouse DNA
564	19	1.0 182567	2	AC064818	AC064818 Homo sapi	c 637	19	1.0 216574	2	AL831731	AL831731 Mus muscu
565	19	1.0 182698	2	AC064818	AC064818 Homo sapi	c 638	19	1.0 218230	2	AC090390	AC090390 Homo sapi
566	19	1.0 182855	9	AC009292	AC009292 Homo sapi	c 639	19	1.0 218799	2	AC091328	AC091328 Homo sapi
567	19	1.0 183099	2	AC025288	AC025288 Homo sapi	c 640	19	1.0 219306	2	AC122458	AC122458 Mus muscu
568	19	1.0 183204	2	AC018906	AC018906 Homo sapi	c 641	19	1.0 219471	2	AL772341	AL772341 Mus muscu
569	19	1.0 183774	9	AC092420	AC092420 Homo sapi	c 642	19	1.0 220501	2	AL806521	AL806521 Mus muscu
570	19	1.0 183915	2	AC073967	AC073967 Homo sapi	c 643	19	1.0 221372	9	AL390778	AL390778 Human DNA
571	19	1.0 183946	2	AC009164	AC009164 Homo sapi	c 644	19	1.0 221673	2	AC012183	AC012183 Homo sapi
572	19	1.0 184235	2	AC111852	AC111852 Rattus no	c 645	19	1.0 222082	2	AC123031	AC123031 Mus muscu
573	19	1.0 184361	2	AC022597	AC022597 Homo sapi	c 646	19	1.0 222577	2	AC124718	AC124718 Mus muscu
574	19	1.0 184486	2	AC128991	AC128991 Rattus no	c 647	19	1.0 222973	2	AC093403	AC093403 Mus muscu
575	19	1.0 184508	2	AC125702	AC125702 Rattus no	c 648	19	1.0 223150	2	AC104396	AC104396 Mus muscu
576	19					c 649	19	1.0 223281	2	AC101671	AC101671 Mus muscu

796	18	1.0	1221	6	E02929	E02929 DNA sequenc	18	1.0	1455	1	RTH270259	AJ270259 Ralstonia
797	18	1.0	1222	9	HUMSCMLA	D43768 Homo sapien	18	1.0	1455	1	UBO28235	U28235 blood disea
798	18	1.0	1223	10	BC022601	BC022601 Mus muscu	18	1.0	1457	1	AX117557	AX117557 Chromobac
799	18	1.0	1224	6	AX280901	AX280901 Sequence	18	1.0	1457	1	AX117557	AX117557 Chromobac
800	18	1.0	1224	6	AX463099	AX463099 Sequence	18	1.0	1458	1	AX117558	AX117558 Chromobac
801	18	1.0	1230	6	AX468692	AX468692 Sequence	18	1.0	1458	1	AX117560	AX117560 Chromobac
802	18	1.0	1230	6	AX468692	AX468692 Sequence	18	1.0	1458	1	AX117561	AX117561 Chromobac
803	18	1.0	1232	3	AF302228	AF302228 Drosophil	18	1.0	1458	1	AX117562	AX117562 Chromobac
804	18	1.0	1234	3	AF118935	AF118935 Drosophil	18	1.0	1459	1	AB008503	AB008503 Ultramicr
805	18	1.0	1258	8	AF366456	AF366456 Allium ce	18	1.0	1459	1	AB008504	AB008504 Ultramicr
806	18	1.0	1259	8	AY092975	AY092975 Arabidops	18	1.0	1459	1	AB008505	AB008505 Ultramicr
807	18	1.0	1260	1	AF390082	AF390082 Ralstonia	18	1.0	1459	1	AX117552	AX117552 Chromobac
808	18	1.0	1264	10	MMSUBPREC	X62934 M.musculus	18	1.0	1459	1	AX117554	AX117554 Chromobac
809	18	1.0	1275	1	AF089859	AF089859 Aquabacte	18	1.0	1459	1	AX117559	AX117559 Chromobac
810	18	1.0	1288	17	AF119895	AF119895 Homo sapi	18	1.0	1460	1	IR1902571	IR1902571 Homo sapi
811	18	1.0	1318	8	AB028194	AB028194 Arabidops	18	1.0	1461	1	AX117556	AX117556 Chromobac
812	18	1.0	1330	9	BC021729	BC021729 Homo sapi	18	1.0	1461	1	AB017487	AB017487 Chromobac
813	18	1.0	1332	6	AX403382	AX403382 Sequence	18	1.0	1462	1	AY043379	AY043379 Ralstonia
814	18	1.0	1332	6	AX454566	AX454566 Sequence	18	1.0	1462	1	BSU282220	BSU282220 Burkholderi
815	18	1.0	1332	6	AX464310	AX464310 Sequence	18	1.0	1464	3	AY043378	AY043378 Ralstonia
816	18	1.0	1332	6	AX491044	AX491044 Sequence	18	1.0	1464	3	AF517544	AF517544 Aedes aeg
817	18	1.0	1359	1	PSERRBC	L37367 Pseudomonas	18	1.0	1465	1	PP16SRRNA	PP16SRRNA
818	18	1.0	1382	9	AF230929	AF230929 Homo sapi	18	1.0	1466	9	HUMNK1A	HUMNK1A
819	18	1.0	1390	9	BC005075	BC005075 Homo sapi	18	1.0	1466	9	AB004790	AB004790 Burkholde
820	18	1.0	1413	1	AB015048	AB015048 Leptothri	18	1.0	1468	1	AF385538	AF385538 Beta prot
821	18	1.0	1416	10	BC024441	BC024441 Mus muscu	18	1.0	1470	1	PS09216SR	PS09216SR
822	18	1.0	1418	1	AF035050	AF035050 Homo sapi	18	1.0	1470	1	PS11616SR	PS11616SR
823	18	1.0	1423	9	BC011833	BC011833 Homo sapi	18	1.0	1470	1	AB024604	AB024604 Ralstonia
824	18	1.0	1425	10	BC025912	BC025912 Mus muscu	18	1.0	1471	1	AB024605	AB024605 Ralstonia
825	18	1.0	1431	1	AF207891	AF207891 Ralstonia	18	1.0	1471	1	AB024606	AB024606 Ralstonia
826	18	1.0	1431	1	AF207892	AF207892 Ralstonia	18	1.0	1471	1	AB024607	AB024607 Ralstonia
827	18	1.0	1431	1	AF207893	AF207893 Ralstonia	18	1.0	1471	1	AB024608	AB024608 Ralstonia
828	18	1.0	1431	1	AF207894	AF207894 Ralstonia	18	1.0	1471	1	AB024609	AB024609 Ralstonia
829	18	1.0	1431	1	AF207895	AF207895 Ralstonia	18	1.0	1471	1	AB017489	AB017489 Beta prot
830	18	1.0	1431	1	AF207896	AF207896 Ralstonia	18	1.0	1474	1	PS01716SR	PS01716SR
831	18	1.0	1431	1	AF207897	AF207897 Ralstonia	18	1.0	1474	1	CHRRDA	CHRRDA
832	18	1.0	1431	1	BSU28232	BSU28232 Burkholderi	18	1.0	1475	9	IR2073509	IR2073509
833	18	1.0	1434	1	UBU28234	UBU28234 blood disea	18	1.0	1476	9	AF390930	AF390930
834	18	1.0	1435	1	AF453507	AF453507 Unculture	18	1.0	1479	3	AY071151	AY071151 Drosophil
835	18	1.0	1436	1	AF488779	AF488779 Ralstonia	18	1.0	1482	10	BC0328927	BC0328927
836	18	1.0	1437	1	BSU28227	BSU28227 Burkholderi	18	1.0	1485	10	BC0039335	BC0039335 Mus muscu
837	18	1.0	1437	1	BSU28229	BSU28229 Burkholderi	18	1.0	1486	9	PL16SRA62	PL16SRA62
838	18	1.0	1441	1	BSU27985	BSU27985 Burkholderi	18	1.0	1486	9	S62045	S62045
839	18	1.0	1441	1	BSU27986	BSU27986 Burkholderi	18	1.0	1487	1	AF368759	AF368759 Pseudomon
840	18	1.0	1441	1	BSU28221	BSU28221 Burkholderi	18	1.0	1487	1	BSU27983	BSU27983 Burkholderi
841	18	1.0	1441	1	BSU28222	BSU28222 Burkholderi	18	1.0	1488	1	PL16SR220	PL16SR220
842	18	1.0	1441	1	BSU28228	BSU28228 Burkholderi	18	1.0	1490	1	PBB11585	PBB11585 Beta proteo
843	18	1.0	1444	10	BC005413	BC005413 Mus muscu	18	1.0	1490	1	PS15816SR	PS15816SR
844	18	1.0	1445	1	PSU28237	PSU28237 Pseudomonas	18	1.0	1492	1	AB024934	AB024934 Spingomo
845	18	1.0	1445	1	PSU28238	PSU28238 Pseudomonas	18	1.0	1492	1	AF293003	AF293003 Unculture
846	18	1.0	1446	1	AF529336	AF529336 Unculture	18	1.0	1493	1	AF154097	AF154097 Unculture
847	18	1.0	1446	1	BSU27984	BSU27984 Burkholderi	18	1.0	1493	1	AF177943	AF177943 Tepidmon
848	18	1.0	1446	1	BSU27987	BSU27987 Burkholderi	18	1.0	1494	1	AB024305	AB024305 Matsuebac
849	18	1.0	1446	1	BSU28222	BSU28222 Burkholderi	18	1.0	1497	1	AY005032	AY005032 Burkholde
850	18	1.0	1446	1	BSU28225	BSU28225 Burkholderi	18	1.0	1499	1	AY043380	AY043380 Ralstonia
851	18	1.0	1446	1	BSU28226	BSU28226 Burkholderi	18	1.0	1500	9	BC004229	BC004229 Homo sapi
852	18	1.0	1446	1	BSU28230	BSU28230 Burkholderi	18	1.0	1503	1	AF236014	AF236014 Beta prot
853	18	1.0	1446	1	BSU28231	BSU28231 Burkholderi	18	1.0	1508	9	BC005830	BC005830 Homo sapi
854	18	1.0	1446	1	BSU28233	BSU28233 Burkholderi	18	1.0	1513	1	AB021375	AB021375 Pseudomon
855	18	1.0	1446	1	UBU28236	UBU28236 Burkholderi	18	1.0	1513	1	AB021403	AB021403 Pseudomon
856	18	1.0	1447	1	AF479337	AF479337 Glacial i	18	1.0	1516	9	AF182076	AF182076 Homo sapi
857	18	1.0	1447	9	AF147782	AF147782 Homo sapi	18	1.0	1519	9	BC006311	BC006311 Homo sapi
858	18	1.0	1449	1	RTH270258	AJ270258 Ralstonia	18	1.0	1525	1	AB006750	AB006750 Unidentif
859	18	1.0	1450	1	RPI270260	AJ270260 Ralstonia	18	1.0	1525	1	AF385534	AF385534 Leptothri
860	18	1.0	1450	1	RTH270257	AJ270257 Ralstonia	18	1.0	1526	3	AY119176	AY119176 Drosophil
861	18	1.0	1451	1	BSU17553	BSU17553 Chromobac	18	1.0	1529	9	BC007248	BC007248 Homo sapi
862	18	1.0	1452	1	BSU28224	BSU28224 Burkholderi	18	1.0	1530	9	AX014310	AX014310 Sequence
863	18	1.0	1453	1	AY117555	AY117555 Chromobac	18	1.0	1534	6	BC014009	BC014009 Homo sapi
864	18	1.0	1453	1	AY117558	AY117558 Chromobac	18	1.0	1537	1	AB045276	AB045276 Ralstonia
865	18	1.0	1453	1	RTH270256	AJ270256 Ralstonia	18	1.0	1537	1	AF280433	AF280433 Ralstonia
866	18	1.0	1454	1	AY117563	AY117563 Chromobac	18	1.0	1540	1	AF125877	AF125877 Dehydroab
867	18	1.0	1454	1	AY117566	AY117566 Chromobac	18	1.0	1540	1	AF125877	AF125877 Dehydroab
868	18	1.0	1455	1	AY117571	AY117571 Chromobac	18	1.0	1540	1	AF125877	AF125877 Dehydroab

942	18	1.0	1545	10	BC022771	BC022771 Mus muscu
943	18	1.0	1546	9	AK093399	AK093399 Homo sapi
944	18	1.0	1547	10	RATSPRA	RATSPRA Rattus norv
945	18	1.0	1548	9	AF175387	AF175387 Homo sapi
946	18	1.0	1549	6	AR177374	AR177374 Sequence
947	18	1.0	1550	9	AK025991	AK025991 Homo sapi
948	18	1.0	1551	10	BC011100	BC011100 Mus muscu
949	18	1.0	1552	3	AY075570	AY075570 Drosophi
950	18	1.0	1553	9	BC010095	BC010095 Homo sapi
951	18	1.0	1554	9	AF042080	AF042080 Homo sapi
952	18	1.0	1555	8	AF367333	AF367333 Arabidops
953	18	1.0	1556	9	BC017797	BC017797 Homo sapi
954	18	1.0	1557	9	AF102848	AF102848 Homo sapi
955	18	1.0	1558	9	BC019588	BC019588 Homo sapi
956	18	1.0	1559	9	HUMSPRLONG	HUMSPRLONG Homo sapi
957	18	1.0	1560	9	HSCSP940	HSCSP940 Human SP-40
958	18	1.0	1561	9	AX202086	AX202086 Sequence
959	18	1.0	1562	6	IL17171	IL17171 Sequence 27
960	18	1.0	1563	10	AF176527	AF176527 Mus muscu
961	18	1.0	1564	9	BC010514	BC010514 Homo sapi
962	18	1.0	1565	3	LM030455	LM030455 Leishmania
963	18	1.0	1566	9	BC014962	BC014962 Homo sapi
964	18	1.0	1567	9	AB060881	AB060881 Macaca fa
965	18	1.0	1568	9	HSU97144	HSU97144 Homo sapien
966	18	1.0	1569	9	AK026144	AK026144 Homo sapi
967	18	1.0	1570	6	HUMCYPC17	HUMCYPC17 Human cyto
968	18	1.0	1571	6	AX468690	AX468690 Sequence
969	18	1.0	1572	6	HUMSUBPRA	HUMSUBPRA Human subst
970	18	1.0	1573	9	HSAN9985	HSAN9985 Homo sapi
971	18	1.0	1574	6	AR194170	AR194170 Sequence
972	18	1.0	1575	3	AY070856	AY070856 Drosophi
973	18	1.0	1576	6	AX283089	AX283089 Sequence
974	18	1.0	1577	6	AX283091	AX283091 Sequence
975	18	1.0	1578	4	AF176914	AF176914 Oryctolag
976	18	1.0	1579	4	AF332576	AF332576 Oryctolag
977	18	1.0	1580	6	AK023724	AK023724 Homo sapi
978	18	1.0	1581	6	AX058194	AX058194 Sequence
979	18	1.0	1582	6	AR176410	AR176410 Sequence
980	18	1.0	1583	6	AX365695	AX365695 Sequence
981	18	1.0	1584	9	AF097494	AF097494 Homo sapi
982	18	1.0	1585	10	BC003809	BC003809 Mus muscu
983	18	1.0	1586	6	AX154562	AX154562 Sequence
984	18	1.0	1587	10	AF311288	AF311288 Rattus no
985	18	1.0	1588	6	AX092418	AX092418 Sequence
986	18	1.0	1589	6	AX463956	AX463956 Sequence
987	18	1.0	1590	10	BC034854	BC034854 Mus muscu
988	18	1.0	1591	6	AX399254	AX399254 Sequence
989	18	1.0	1592	9	HSMB02906	HSMB02906 Homo sapi
990	18	1.0	1593	10	BC003727	BC003727 Mus muscu
991	18	1.0	1594	10	BC012960	BC012960 Mus muscu
992	18	1.0	1595	6	AX053103	AX053103 Sequence
993	18	1.0	1596	9	HSU31814	HSU31814 Human trans
994	18	1.0	1597	6	AX083354	AX083354 Sequence
995	18	1.0	1598	6	AX399256	AX399256 Sequence
996	18	1.0	1599	6	E02020	E02020 cDNA encodi
997	18	1.0	1600	6	E05489	E05489 cDNA encodi
998	18	1.0	1601	10	BC030409	BC030409 Mus muscu
999	18	1.0	1602	4	RBCY450DA	RBCY450DA Rabbit cyto
1000	18	1.0	1603	9	BC011603	BC011603 Homo sapi
RESULT 1	AX191503	Sequence 25 from Patent WO0149728.	1775 bp	DNA	linear	PAT 15-AUG-2001
LOCUS	AX191503					
DEFINITION	Sequence 25 from Patent WO0149728.					
ACCESSION	AX191503					
VERSION	AX191503.1	GI:15209689				
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1775) Kato,S. and Kimura,T. Human proteins having hydrophobic domains and dnas encoding these proteins Patent: WO 0149728-A 25 12-JUL-2001; Protegene Inc. (JP) : SAGAMI CHEMICAL RESEARCH CENTER (JP)						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						
CDS						
BASE COUNT	360 a	541 c	549 g	325 t		
ORIGIN						
Query Match	54.9%;	Score 1029;	DB 6;	Length 1775;		
Best Local Similarity	99.7%;	Pred. No. 0;				
Matches 1229;	Conservative	0;	Mismatches	4;	Indels	0;
Gaps	0;					
QY	102	CCTGACGGCCCAACAGACCCATGCTGCATCCAGAGACCTCCCTCGCGGGGCGCATCTC	161			
Db	41	CTGACGGCCCAACAGACCCATGCTGCATCCAGAGACCTCCCTCGCGGGGCGCATCTC	100			
QY	162	CTGGCTGTGCTCCTGGCCCTCTCTGGGACACCATCTGGGACAGGTGTGCCACCCAGCTG	221			
Db	101	CTGGCTGTGCTCCTGGCCCTCTCTGGGACACCATCTGGGACAGGTGTGCCACCCAGCTG	160			
QY	222	CAGGACGAGCTCCGATGCGCGGAGCCCTGAACAGGAGGAGTCTTCTGCTCTCTCC	281			
Db	161	CAGGACGAGCTCCGATGCGCGGAGCCCTGAACAGGAGGAGTCTTCTGCTCTCTCC	220			
QY	282	CTGCACACCGCTCGCGAGCTGGGTCCAGCCCTCGGCTGACATCGGAGGCTGGAC	341			
Db	221	CTGCACACCGCTCGCGAGCTGGGTCCAGCCCTCGGCTGACATCGGAGGCTGGAC	280			
QY	342	TGGAGTGACAGCTGGCCCAACCTGGCTCAAGCCAGGCGAGCCCTCTGGAATCCCAAC	401			
Db	281	TGGAGTGACAGCTGGCCCAACCTGGCTCAAGCCAGGCGAGCCCTCTGGAATCCCAAC	340			
QY	402	CCGAGCTGCGATCCGCGCTGTGGCGACCCCTCGAAGTGGGTGGAACATGACGCTGCTG	461			
Db	341	CCGAGCTGCGATCCGCGCTGTGGCGACCCCTCGAAGTGGGTGGAACATGACGCTGCTG	400			
QY	462	CCCGCGGGCTTGGCGTCTTTTGTGTAAGTGTGACCCCTATGTTTTCAGAGGGGAGCGG	521			
Db	401	CCCGCGGGCTTGGCGTCTTTTGTGTAAGTGTGACCCCTATGTTTTCAGAGGGGAGCGG	460			
QY	522	TACAGCCACCGCGGAGAGAGTGTGCTGCGAACCCGACCTGCACCCACTACACGAGCTC	581			
Db	461	TACAGCCACCGCGGAGAGAGTGTGCTGCGAACCCGACCTGCACCCACTACACGAGCTC	520			
QY	582	GTGTGGGCCACCTCAAGCCAGCTGGGTGTGGGGGGGACCTGTGCTCTGACGGCCAGACA	641			
Db	521	GTGTGGGCCACCTCAAGCCAGCTGGGTGTGGGGGGGACCTGTGCTCTGACGGCCAGACA	580			
QY	642	GCATAGAACCTTTGCTGTGCTTACTTCCCGGAGGCAACTGGGAGGTCAACGGGAAG	701			
Db	581	GCATAGAACCTTTGCTGTGCTTACTTCCCGGAGGCAACTGGGAGGTCAACGGGAAG	640			
QY	702	ACATATCATCCCTATAGAAAGGGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGC	761			

Db	641	ACAATCATCCCTATAAAGAGGTGCTGGTGTGCTCTGACAGCCAGTGTCTCAGGC	700
Qy	762	TGCTTCAAAGCTGGAGCATCAGGGGGTCTGTGAGTCCCCAGGAATCCTTGTGC	821
Db	701	TGCTTCAAAGCTGGAGCATCAGGGGGTCTGTGAGTCCCCAGGAATCCTTGTGC	760
Qy	822	ATGAGCTGCCAAGACCATGGAGCTCAACATFACAGCACTGCCACTGTCCCCCT	881
Db	761	ATGAGCTGCCAAGACCATGGAGCTCAACATFACAGCACTGCCACTGTCCCCCT	820
Qy	882	GGCTACAGGGCAGATCTGCCAAGTGAAGTGCAGCTGCAGTGTGACAGCGGGTTC	941
Db	821	GGCTACAGGGCAGATCTGCCAAGTGAAGTGCAGCTGCAGTGTGACAGCGGGTTC	880
Qy	942	CGGAGGAGGAGTGTCTGCTGCTGTGACATCGCTACGGGGGAGCCAGTGTGCCACC	1001
Db	881	CGGAGGAGGAGTGTCTGCTGCTGTGACATCGCTACGGGGGAGCCAGTGTGCCACC	940
Qy	1002	AAGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGAGGAGTGTTCATGTG	1061
Db	941	AAGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGAGGAGTGTTCATGTG	1000
Qy	1062	TCTTACAGGAGAGCTATTACAGAGCCAGGATGAATGTACAGAGAAAGCGGGTG	1121
Db	1001	TCTTACAGGAGAGCTATTACAGAGCCAGGATGAATGTACAGAGAAAGCGGGTG	1060
Qy	1122	CTGGCCAGATCAGAGCCAGAAAGTGCAGGACATCTCGCTTCTATCTGGGCGCGTG	1181
Db	1061	CTGGCCAGATCAGAGCCAGAAAGTGCAGGACATCTCGCTTCTATCTGGGCGCGTG	1120
Qy	1182	GAGACCAACAGAGTGTGACAGTGTGACAGTGTGACAGCAGGAACTTCTGATCGGGT	1241
Db	1121	GAGACCAACAGAGTGTGACAGTGTGACAGTGTGACAGCAGGAACTTCTGATCGGGT	1180
Qy	1242	ACCTACAGACCCAGGAGTCTCTCCGCTGGCCACAGGGAGCAGGAGCCCTTACC	1301
Db	1181	ACCTACAGACCCAGGAGTCTCTCCGCTGGCCACAGGGAGCAGGAGCCCTTACC	1240
Qy	1302	ACCTTGTGCTTGGGAGCTGTACACACCGG	1334
Db	1241	AGTTTGGCTTGGGAGCTGTACACACCGG	1273
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DEFINITION	Sequence 15 from Patent W00149728.	linear	PAT 15-AUG-2001
ACCESSION	AX191493		
VERSION	AX191493.1	GI:15209675	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 1341)		
JOURNAL	Kato, S. and Kimura, T.		
FEATURES	Human proteins having hydrophobic domains and dnas encoding these		
source	Patent: WO 0149728-A 15 12-JUL-2001;		
BASE COUNT	Protegene Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)		
ORIGIN	Location/Qualifiers		
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	260 a 420 c 414 g 247 t		
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Matches 1208; Conservative 0; Mismatches 4; Indels 0; Gaps 0;			
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Db	1	ATGTCGATCCAGAGACCTCCCTGGCGGGGGATCTCTTGGCTGTCTCTGGCCCTC	60
Qy	183	CTTGGCCACCACTGGGAGAGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCC	242
Db	61	CTTGGCCACCACTGGGAGAGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCC	120
Qy	243	GGAGCCCTGAACAGGAAGAGAGTGTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCT	302
Db	121	GGAGCCCTGAACAGGAAGAGAGTGTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCT	180
Qy	303	TGGTCTCAGCCCTCGGCTGACATCGGAGGCTGGAGTGTGGAGTGTGGAGTGTGGAG	362
Db	181	TGGTCTCAGCCCTCGGCTGACATCGGAGGCTGGAGTGTGGAGTGTGGAGTGTGGAG	240
Qy	363	CTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCGAGCTGGCATCCGGCTG	422
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Qy	423	TGGCGCACCTGCAAGTGGGCTGGAACATGCAGCTGTGCGCGGGGCTTGGCGTCTTT	482
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Qy	483	GTTGAAGTGTCTAGCCCTATGTTTGCAGAGGGGAGCGGTACAGCCAGCGCGGAGGAG	542
Db	361	GTTGAAGTGTCTAGCCCTATGTTTGCAGAGGGGAGCGGTACAGCCAGCGCGGAGGAG	420
Qy	543	TGTGCTCGCAACCCCACTGCACCCACTACACGAGCTGTGTGGGCGCACCTCAAGCCAG	602
Db	421	TGTGCTCGCAACCCCACTGCACCCACTACACGAGCTGTGTGGGCGCACCTCAAGCCAG	480
Qy	603	CTGGGCTGTGGGCGCACCTGTCTCTGAGGCGGAGGAGTCAACGGGAGGAGTCAATCAT	662
Db	481	CTGGGCTGTGGGCGCACCTGTCTCTGAGGCGGAGGAGTCAACGGGAGGAGTCAATCAT	540
Qy	663	GCCTACTCTCCCGGAGGCAACTGGGAGTCAACGGGAGGAGTCAATCATCATATAAGAG	722
Db	541	GCCTACTCTCCCGGAGGCAACTGGGAGTCAACGGGAGGAGTCAATCATCATATAAGAG	600
Qy	723	GGTGGCTGTGGGCGCACCTGTCTCTGAGGCGGAGGAGTCAACGGGAGGAGTCAATCAT	782
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Qy	783	GCAGGGGGCTCTGTGAGTCTCCAGGAGTCAACGGGAGGAGTCAATCATCATATAAGAG	842
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Qy	963	GTCTGTGACATCGGCTACGGGGAGGAGTGTGCCACCAAGGAGTCAATTTTCCCTCCAC	1022
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Qy	1023	ACCTGTGAGCTGAGGATCGAGGAGTGTCTTCTGAGGAGGAGGAGTCAATTTTCCCTCC	1082
Db	901	ACCTGTGAGCTGAGGATCGAGGAGTGTCTTCTGAGGAGGAGGAGTCAATTTTCCCTCC	960
Qy	1083	TACAGAGCCAGGATGAATGTACAGAGGAGGAGGAGTGTCTTCTGAGGAGGAGGAGTCA	1142
Db	961	TACAGAGCCAGGATGAATGTACAGAGGAGGAGGAGTGTCTTCTGAGGAGGAGGAGTCA	1020
Qy	1143	AAAGTGAGGAGATCTCTGCGCTTCTATCTGGGCGGCTGGAGACCAACAGGAGTCAAT	1202
Db	1021	AAAGTGAGGAGATCTCTGCGCTTCTATCTGGGCGGCTGGAGACCAACAGGAGTCAAT	1080
Qy	1203	GACAGTGTGAGGAGGAGGAGTCTGAGTGTGGGCTCACTTACAGAGGAGGAGGAGTCA	1262

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Db 1081 GACAGTGAAGTTCAGACACAGGAACTTCTGGATCGGGTCACTACAGACCGCCCAAGGAC 1140
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Qy 1323 GACAACACGGG 1334
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RESULT 3
LOCUS AX366554 690 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 321 from Patent WO0206317.
ACCESSION AX366554
VERSION AX366554.1 GI:18697979
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Mitcham,J.L., King,G.E., Algate,P.A., Eling,S.P., Retter,M.W.,
Fanger,G.R., Reed,S.G., Vedvick,T.S., Carter,D., Hill,P. and
Albone,E.
TITLE Compositions and methods for the therapy and diagnosis of ovarian
cancer
JOURNAL Patent: WO 0206317-A 321 24-JAN-2002;
CORIAX CORPORATION (US)
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/db_xref="taxon:9606"
BASE COUNT 148 a 197 c 212 g 131 t 2 others
ORIGIN
Query Match 25.9%; Score 485; DB 6; Length 690;
Best Local Similarity 100.0%; Pred. No. 2.1e-272; Indels 0; Gaps 0;
Matches 485; Conservative 0; Mismatches 0;

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Qy 664 CCTACTCCCGGAGGCAACTGGAGGTCAACGGGAAGACAATCATCCCTATAGAAGG 723
Db 61 CCTACTCCCGGAGGCAACTGGAGGTCAACGGGAAGACAATCATCCCTATAGAAGG 120
Qy 724 GTGCTGTGTCTCTGCAGGCGAGTCTCTCAGGCTGCTTCAAGGCTGGGACCATG 783
Db 121 GTGCTGTGTCTCTGCAGGCGAGTCTCTCAGGCTGCTTCAAGGCTGGGACCATG 180
Qy 784 CAGGGGGGCTGTGTAGGTCCCGAGAAATCTTGTGTGATGAGTGTGCAGAACCATGAC 843
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Qy 844 GTCTCAACATCAGACCTGCCACTGCCACGTCCCTGTGCTACACGGGAGATAGTCC 903
Db 241 GTCTCAACATCAGACCTGCCACTGCCACGTCCCTGTGCTACACGGGAGATAGTCC 300
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Db 361 TCTGTGACATCGGCTACGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCACA 420
Qy 1024 CTTGTACCTTGAGATCGACGGAGAGTGTCTCATGGTGTCTTCAGAGGAGACACTATT 1083
Db 421 CTTGTACCTTGAGATCGACGGAGAGTGTCTCATGGTGTCTTCAGAGGAGACACTATT 480

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Qy 1084 ACAGA 1088
Db 481 ACAGA 485

RESULT 4
LOCUS HSM804652 3293 bp mRNA linear PRI 10-JUL-2002
DEFINITION Homo sapiens mRNA; cDNA DKFZp686E1934 (from clone DKFZp686E1934).
ACCESSION AL833339
VERSION AL833339.1 GI:21733974
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3293)
AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Weill,B., Amid,C. and
Wiemann,S.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZp686E1934) is available at the RZPD in Berlin. Please contact
the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
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DH10B; sites SfiIA + SfiIB"
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polyA_signal 3171..3176
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BASE COUNT 783 a 946 c 967 g 597 t
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Best Local Similarity 99.0%; Pred. No. 3.2e-271;
Matches 983; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 7 TGTCCACGACCCAGCCTGACTCTCTGGAGATTGTGAATAGCTTCCATCCAGCTTGAGAAAC 66
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Qy 67 AAGCCGGGTGGCTGAGCAGGCTGTGCACGAGGACCTGACGGGGCCCAACAGACCATGC 126
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Qy 127 TGCATCCAGAGACTTCCCTTGGCCGGGGCATCTCTGGCTGTGCTTCCCTGGCCCTCTTG 186
Db 198 TGCATCCAGAGACTTCCCTTGGCCGGGGCATCTCTGGCTGTGCTTCCCTGGCCCTCTTG 257
Qy 187 GCACCACTTGGCAGAGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGAG 246
Db 258 GCACCGGCTGGCAGAGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGAG 317
Qy 247 CCCTGAACAGAGAGAGATTCTTGTCTCTTCCCTGCACAAACCCCTTCCGAGCTGGG 306
Db 318 CCCTGAACAGAGAGAGATTCTTGTCTCTTCCCTGCACAAACCCCTTCCGAGCTGGG 377
Qy 307 TCCAGCCCCCTGCCGCTGACATGGGAGCTGGAGTGGAGTGGACAGCTGGCCCAACTGG 366
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Qy 367 CTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCGAGCCTTGGCATCCGCGCTGTGGC 426

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Db 438 CTCACGACGAGGAGCCCTCTGTGGAAACCCCAACCCGAGCCTGGCGTCCGGCCGTCGC 497
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 QY 487 AAGTGGTCAAGCTATGTTTGGAGAGGGGCGACGCGTACACCCACGCGGAGAGAGTGTG 546
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 QY 907 TGAGGTGACGCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 966
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RESULT 5
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 VERSION HTG.
 KEYWORDS Homo sapiens.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 163427)
 TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
 JOURNAL Direct Submission
 UNPUBLISHED
 2 (bases 1 to 163427)
 TITLE DOE Joint Genome Institute.
 JOURNAL Direct Submission
 UNPUBLISHED
 3 (bases 1 to 163427)
 TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
 JOURNAL Direct Submission
 UNPUBLISHED
 Submitted (27-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
 On Jul 27, 2001 this sequence version replaced gi:9256116.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing completed at Stanford Human Genome Center

RESULT 6
 AC009153
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 DEFINITION AC009153
 ACCESSION AC009153.10 GI:18997244
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 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 177479)
 TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
 JOURNAL Direct Submission
 UNPUBLISHED
 2 (bases 1 to 177479)
 TITLE DOE Joint Genome Institute.
 JOURNAL Direct Submission
 UNPUBLISHED
 3 (bases 1 to 177479)
 TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
 JOURNAL Direct Submission
 UNPUBLISHED
 Submitted (05-JAN-2002) DOE Joint Genome Institute, 2800 Mitchell

www-shgc.stanford.edu
 Quality: Phrap Quality >=40 99.8% of Sequence;
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 SHGC-32349 G27498
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 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 177479)
 TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
 JOURNAL Direct Submission
 UNPUBLISHED
 2 (bases 1 to 177479)
 TITLE DOE Joint Genome Institute.
 JOURNAL Direct Submission
 UNPUBLISHED
 3 (bases 1 to 177479)
 TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
 JOURNAL Direct Submission
 UNPUBLISHED
 Submitted (05-JAN-2002) DOE Joint Genome Institute, 2800 Mitchell

Direct Submission
Submitted (09-JUL-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 558525
Center clone name: RPCI-11_396D24

Summary Statistics
Consensus quality: 191546 bases at least Q40
Consensus quality: 193703 bases at least Q30
Consensus quality: 194840 bases at least Q20
Estimated insert size: 0; null estimation
Quality coverage: 2.1474836E7 in Q20 bases; null estimation
Quality coverage: 8.2 in Q20 bases; sum-of-contigs estimation.
* NOTE: this is a 'working draft' sequence. It currently
* consists of 10 contigs, the true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1700: gap of unknown length
* 1701: contig of 1766 bp in length
* 3467: gap of unknown length
* 3567: contig of 2143 bp in length
* 5710: gap of unknown length
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* 7900: gap of unknown length
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Drive, Walnut Creek, CA 94598, USA
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Direct Submission
Submitted (28-FEB-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Feb 28, 2002 this sequence version replaced gi:18071320.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
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Best Local Similarity 100.0%; Pred. No. 1.1e-230;
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DEFINITION PROGRESS ***, 10 unordered pieces.
AC126771
AC126771.1 GI:21717140
VERSION HTG; HTGS_PHASE1.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 197460)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL unpublished
REFERENCE 2 (bases 1 to 197460)
AUTHORS DOE Joint Genome Institute.

QY 1632 TTGGCAGAGAGAGGAGGAGCCAGTGTAGGCCAGGGAGTGTAGTGTATTAGAGAAAGCTG 1691
 |||||
 Db 135083 TTGGCAGAGAGAGGAGGAGCCAGTGTAGGCCAGGGAGTGTAGTGTATTAGAGAAAGCTG 135142
 |||||
 QY 1692 GCGCCCTTCGCTGCTTTTCATGCGAAGATGGCTCAATTAGATGCGCCAGGAGAGGA 1751
 |||||
 Db 135143 GGGCCCTTCGCTGCTTTTGAATGGGAAGATGGCTCAATTAGATGCGCCAGGAGAGGA 135202
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 QY 1752 CACCGCCAGTGTCTCAAAAAGGCTGTCTCTTCCACCTGGCCAGAGCCCTGTGGGGCAGC 1811
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 Db 135203 CACCGCCAGTGTCTCAAAAAGGCTGTCTCTTCCACCTGGCCAGAGCCCTGTGGGGCAGC 135262
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 QY 1812 GGAGCTTCCCTGTGGCATGAACCCAGGGGTATTAAATTATGAATCAGCTGAA 1865
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 Db 135263 GGAGCTTCCCTGTGGCATGAACCCAGGGGTATTAAATTATGAATCAGCTGAA 135316
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RESULT 8
 AC026468/c
 LOCUS AC026468 179675 bp DNA linear PRI 02-NOV-2001
 DEFINITION Homo sapiens chromosome 16 clone RP11-419C5, complete sequence.
 ACCESSION AC026468
 VERSION AC026468.6 GI:16596532
 KEYWORDS HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS 1 (bases 1 to 179675)
 TITLE DOE Joint Genome Institute.
 JOURNAL Sequencing of Human Chromosome 16
 REFERENCE 2 (bases 1 to 179675)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (22-MAR-2000) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE 3 (bases 1 to 179675)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (02-NOV-2001) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 On Nov 2, 2001 this sequence version replaced gi:14589452.

COMMENT
 Sequence Quality Assessment:
 This entry has been annotated with sequence quality
 estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than
 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the
 GenBank flat file format but are available as part
 of this entry's ASN.1 file.

Sequence Quality Assessment:
 This entry has been annotated with sequence quality
 estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than
 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the
 GenBank flat file format but are available as part
 of this entry's ASN.1 file.

FEATURES
 source
 1. .179675
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosomes="16"
 /clone="RP11-419C5"
 BASE COUNT 49567 a 43464 c 41958 g 44686 t
 ORIGIN

Query Match 17.9%; Score 336; DB 9; Length 179675;

Best Local Similarity 99.7%; Pred. No. 7.4e-185;
 Matches 386; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1452 GCCCAGGAGCAGCATCTCCGGTGGGCCCGAGGCTCTGAGGCTGACACATGGCTCCCT 1511
 |||||
 Db 37319 GCCCAGGAGCAGCATCTCCGGTGGGCCCGAGGCTCTGAGGCTGACACATGGCTCCCT 37260
 |||||
 QY 1512 GCGCTCGCCCTGGGAGCAGCGGCTCTGCTTACCTGTGTGCCACCTGTCTGGACAAAGGC 1571
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 Db 37259 GCGCTCGCCCTGGGAGCAGCGGCTCTGCTTACCTGTGTGCCACCTGTCTGGACAAAGGC 37200
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 QY 1572 CAGGTTAAGACACACATGCTCATGTGTCCTCAAGAGGCTCTCAGACCTTGCACAATGCCAGAAG 1631
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 Db 37199 CAGGTTAAGACACACATGCTCATGTGTCCTCAAGAGGCTCTCAGACCTTGCACAATGCCAGAAG 37140
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 QY 1632 TTGGCAGAGAGAGCAGGAGGAGCCAGTGTAGGGCCAGGGAGTGTAGTGTATTAGAGAAAGCTG 1691
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 Db 37139 TTGGCAGAGAGAGCAGGAGGAGCCAGTGTAGGGCCAGGGAGTGTAGTGTATTAGAGAAAGCTG 37080
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 QY 1692 GGGCCCTTCGCTGCTTTTGTATGGGAAGATGGGCTTCAATTAGATGGCCGAGAGAGGA 1751
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 Db 37079 GGGCCCTTCGCTGCTTTTGTATGGGAAGATGGGCTTCAATTAGATGGCCGAGAGAGGA 37020
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 QY 1752 CACCGCCAGTGTCTCAAAAAGGCTGTCTTCCACCTGGCCAGAGCCCTGTGGGGCAGC 1811
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 Db 37019 CACCGCCAGTGTCTCAAAAAGGCTGTCTTCCACCTGGCCAGAGCCCTGTGGGGCAGC 36960
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 QY 1812 GGAGCTTCCCTGTGGCATGAACCCAC 1838
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 Db 36959 GGAGCTTCCCTGTGGCATGAACCCAC 36933
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RESULT 9
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 LOCUS AC009022 190595 bp DNA linear PRI 07-FEB-2002
 DEFINITION Homo sapiens chromosome 16 clone RP11-106J23, complete sequence.
 ACCESSION AC009022
 VERSION AC009022.9 GI:18581696
 KEYWORDS HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 190595)
 AUTHORS DOE Joint Genome Institute.
 TITLE Sequencing of Human Chromosome 16
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 190595)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE 3 (bases 1 to 190595)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (07-FEB-2002) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 On Feb 7, 2002 this sequence version replaced gi:16924076.

COMMENT
 Sequence Quality Assessment:
 This entry has been annotated with sequence quality
 estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than
 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the
 GenBank flat file format but are available as part
 of this entry's ASN.1 file.

Sequence Quality Assessment:
 This entry has been annotated with sequence quality
 estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than

1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

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     source            1..190595
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="16"
                        /clone="RP11-106J23"
     misc_feature      91050..91410
                        /note="unresolved tandem repeat"
BASE COUNT           51435 a 43243 c 43697 g 52220 t
ORIGIN
Query Match          17.9%   Score 336;   DB 9;   Length 190595;
Best Local Similarity 99.7%;   Pred. No. 7.4e-185;
Matches 386;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY 1452 GCCCAGGACACATCTCCCGTGGGGCCAGGGTCTTGAGGCTGACACATGGCTCCCT 1511
|||||
Db 179683 GCCCAGGACACATCTCCCGTGGGGCCAGGGTCTTGAGGCTGACACATGGCTCCCT 179624

QY 1512 CGCTGCGCTGGGAGCAGCGCTCTGTTACTGTCTGCTGCCACCTGTCTGGAACAAGGC 1571
|||||
Db 179623 CGCTGCGCTGGGAGCAGCGCTCTGTTACTGTCTGCTGCCACCTGTCTGGAACAAGGC 179564

QY 1572 CAGTTAAGACACATCGCTCATGTCCAAAGAGGTCTCAGACCTTGCCAAATGCCAGAAG 1631
|||||
Db 179563 CAGTTAAGATCATATGCTCATGTCCAAAGAGGTCTCAGACCTTGCCAAATGCCAGAAG 179504

QY 1632 TTGGGACAGAGAGGCGAGGAGGCGCAGTGAGGGCCAGGAGTGTAGTGTAGAAAGCTTG 1691
|||||
Db 179503 TTGGGACAGAGAGGCGAGGAGGCGCAGTGAGGGCCAGGAGTGTAGTGTAGAAAGCTTG 179444

QY 1692 GGGCCCTTCGCCCTCTTTGATTTGGGAGATGGCGCTTCAATAGATGGCGAAGGAGGA 1751
|||||
Db 179443 GGGCCCTTCGCCCTCTTTGATTTGGGAGATGGCGCTTCAATAGATGGCGAAGGAGGA 179384

QY 1752 CACCGCAGTGGTCCAAAAGGCTCTCTTCCACCTGGCCAGCCCTGTGGGCGAGC 1811
|||||
Db 179383 CACCGCAGTGGTCCAAAAGGCTCTCTTCCACCTGGCCAGCCCTGTGGGCGAGC 179324

QY 1812 GGAGCTTCCTGTGGCATGAACCCAC 1838
|||||
Db 179323 GGAGCTTCCTGTGGCATGAACCCAC 179297

RESULT 10
BC008616
LOCUS
DEFINITION Homo sapiens, clone IMAGE:4178394, mRNA, linear PRI 12-JUL-2001
ACCESSION BC008616
VERSION BC008616.1 GI:14250368
KEYWORDS
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1328)
Strausberg,R.
Direct Submission
Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cdna Library Preparation: Life Technologies, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

FEATURES             Location/Qualifiers
     source            1..1328
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:4178394"
                        /tissue_type="Brain, anaplastic oligodendroglioma with
                        1p/19q loss"
                        /clone_lib="NCI_CGAP_Brn67"
                        /lab_host="DH10B"
                        /note="Vector: pCMV-SPORT6"
                        <1..473
                        /codon_start=3
                        /product="Unknown (protein for IMAGE:4178394)"
                        /protein_id="AAH08616.1"
                        /db_xref="GI:14250369"
                        /translation="RVRGCDAPPCRNPGWRLPADGKGLRAWSPERGOLLTPFPGR
                        GPREHMAASAGKRGKGSWOOTPGSEWNLIDYPGPLTYTKAKDSFRWATGSHQAF
                        TSFAGGDPATHGFGNCVLEQASAAFNWNRQKTRNRYICQFAHEISRWGGPS"
BASE COUNT           305 a 381 c 398 g 244 t
ORIGIN
Query Match          17.2%   Score 323;   DB 9;   Length 1328;
Best Local Similarity 99.7%;   Pred. No. 3e-177;
Matches 373;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY 1359 GGGTTTGCAACTGGTGGAGCTGCAGGCTTCAGCTGCCTCACTGGAAGCAGCAGGC 1418
|||||
Db 342 GGGTTTGCAACTGGTGGAGCTGCAGGCTTCAGCTGCCTCACTGGAAGCAGCAGGC 401

QY 1419 TGCAAAACCCGAACCGTTACATCTGCCAGTTTGCCAGGACACATCTCCGGTGGGC 1478
|||||
Db 402 TGCAAAACCCGAACCGTTACATCTGCCAGTTTGCCAGGACACATCTCCGGTGGGC 461

QY 1479 CCAGGGTCTGAGGCTGACACATGGCTCCCTCGCTCGCCCTGGGAGCAGCCGCTCTGC 1538
|||||
Db 462 CCAGGGTCTGAGGCTGACACATGGCTCCCTCGCTCGCCCTGGGAGCAGCCGCTCTGC 521

QY 1539 TTACCTGTCTGCCACCTGTCTGGAACAAGGCCAGGTTAAGACCATGCTCATGTCC 1598
|||||
Db 522 TTACCTGTCTGCCACCTGTCTGGAACAAGGCCAGGTTAAGACCATGCTCATGTCC 581

QY 1599 AAAGAGGTCTCAGACCTTGCCACAATGCCAAGTTGGGAGAGAGGAGGAGGCCAG 1658
|||||
Db 582 AAAGAGGTCTCAGACCTTGCCACAATGCCAAGTTGGGAGAGAGGAGGAGGCCAG 641

QY 1659 TGAGGGCCAGGAGTGTAGTTAGAAAGCTGGGGCCCTTCGCCCTGCTTTTATTGGGA 1718
|||||
Db 642 TGAGGGCCAGGAGTGTAGTTAGAAAGCTGGGGCCCTTCGCCCTGCTTTTATTGGGA 701

QY 1719 AGATGGGCTTCAAT 1732
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Db 702 AGATGGGCTTCAAT 715

RESULT 11
AC097265/c
LOCUS
DEFINITION Pan troglodytes clone RP43-119N13, WORKING DRAFT SEQUENCE, 4
```

DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalon@bcm.tmc.edu
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 12 Row: h Column: 4
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.

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FEATURES             Location/Qualifiers
     source            1..1328
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:4178394"
                        /tissue_type="Brain, anaplastic oligodendroglioma with
                        1p/19q loss"
                        /clone_lib="NCI_CGAP_Brn67"
                        /lab_host="DH10B"
                        /note="Vector: pCMV-SPORT6"
                        <1..473
                        /codon_start=3
                        /product="Unknown (protein for IMAGE:4178394)"
                        /protein_id="AAH08616.1"
                        /db_xref="GI:14250369"
                        /translation="RVRGCDAPPCRNPGWRLPADGKGLRAWSPERGOLLTPFPGR
                        GPREHMAASAGKRGKGSWOOTPGSEWNLIDYPGPLTYTKAKDSFRWATGSHQAF
                        TSFAGGDPATHGFGNCVLEQASAAFNWNRQKTRNRYICQFAHEISRWGGPS"
BASE COUNT           305 a 381 c 398 g 244 t
ORIGIN
```

```
Query Match          17.2%   Score 323;   DB 9;   Length 1328;
Best Local Similarity 99.7%;   Pred. No. 3e-177;
Matches 373;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY 1359 GGGTTTGCAACTGGTGGAGCTGCAGGCTTCAGCTGCCTCACTGGAAGCAGCAGGC 1418
|||||
Db 342 GGGTTTGCAACTGGTGGAGCTGCAGGCTTCAGCTGCCTCACTGGAAGCAGCAGGC 401

QY 1419 TGCAAAACCCGAACCGTTACATCTGCCAGTTTGCCAGGACACATCTCCGGTGGGC 1478
|||||
Db 402 TGCAAAACCCGAACCGTTACATCTGCCAGTTTGCCAGGACACATCTCCGGTGGGC 461

QY 1479 CCAGGGTCTGAGGCTGACACATGGCTCCCTCGCTCGCCCTGGGAGCAGCCGCTCTGC 1538
|||||
Db 462 CCAGGGTCTGAGGCTGACACATGGCTCCCTCGCTCGCCCTGGGAGCAGCCGCTCTGC 521

QY 1539 TTACCTGTCTGCCACCTGTCTGGAACAAGGCCAGGTTAAGACCATGCTCATGTCC 1598
|||||
Db 522 TTACCTGTCTGCCACCTGTCTGGAACAAGGCCAGGTTAAGACCATGCTCATGTCC 581

QY 1599 AAAGAGGTCTCAGACCTTGCCACAATGCCAAGTTGGGAGAGAGGAGGAGGCCAG 1658
|||||
Db 582 AAAGAGGTCTCAGACCTTGCCACAATGCCAAGTTGGGAGAGAGGAGGAGGCCAG 641

QY 1659 TGAGGGCCAGGAGTGTAGTTAGAAAGCTGGGGCCCTTCGCCCTGCTTTTATTGGGA 1718
|||||
Db 642 TGAGGGCCAGGAGTGTAGTTAGAAAGCTGGGGCCCTTCGCCCTGCTTTTATTGGGA 701

QY 1719 AGATGGGCTTCAAT 1732
|||||
Db 702 AGATGGGCTTCAAT 715
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RESULT 11
AC097265/c
LOCUS
DEFINITION Pan troglodytes clone RP43-119N13, WORKING DRAFT SEQUENCE, 4

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

unordered pieces.
AC097265
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Pan troglodytes.
Pan troglodytes.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 191108)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burckett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Louiweg,H., Lozada,M., Mapua,P., Martin,R., Lucier,R., Luna,R.,
Me,J., Maheshwari,M., Mapua,P., Martin,R., Lucier,R., Luna,R.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Ogduh,N., Okwunu,G., Oragunye,N., Owiedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojask,A., Rojubokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N.,
Sisson,I., Sodergren,E., Sonaik,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczky,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

REFERENCE AUTHORS

Direct Submission
2 (bases 1 to 191108)
Worley,K.C.
Submitted (13-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 23, 2001 this sequence version replaced gi:16258969.
----- Genome Center
Center: Baylor College of Medicine
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: ZUAR
Center clone name: RP43-119N13
----- Summary Statistics
Sequencing vector: Plasmid; M7789
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 191814 bases at least Q40
Consensus quality: 193054 bases at least Q30
Consensus quality: 194113 bases at least Q20
Estimated insert size: 193275; sum-of-contigs estimation

TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

Direct Submission
2 (bases 1 to 191108)
Worley,K.C.
Submitted (13-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 23, 2001 this sequence version replaced gi:16258969.
----- Genome Center
Center: Baylor College of Medicine
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: ZUAR
Center clone name: RP43-119N13
----- Summary Statistics
Sequencing vector: Plasmid; M7789
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 191814 bases at least Q40
Consensus quality: 193054 bases at least Q30
Consensus quality: 194113 bases at least Q20
Estimated insert size: 193275; sum-of-contigs estimation

COMMENT

Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 9.3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 121806: contig of 121806 bp in length
* 121807 121906: gap of unknown length
* 121907 172531: contig of 50625 bp in length
* 172532 172631: gap of unknown length
* 172632 180970: contig of 8339 bp in length
* 180971 181070: gap of unknown length
* 181071 191108: contig of 10038 bp in length.
FEATURES
Location/Qualifiers
1.191108
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-119N13"
BASE COUNT 49835 a 45817 c 45055 g 50100 t 301 others
ORIGIN
Query Match 15.3%; Score 287; DB 2; Length 191108;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1452 GCCCAGGAGACATCTCCCGTGGGGCCCGGCTGAGGCTGACCATGGTCCCT 1511
|||||
Db 54247 GCCCAGGAGACATCTCCCGTGGGGCCCGGCTGAGGCTGACCATGGTCCCT 54188
QY 1512 CGCCTGCCCTGGGAGCACCAGCTCTGCTTACCTGTCTGCCACCTGTCTGGAACAGGCG 1571
Db 54187 CGCCTGCCCTGGGAGCACCAGCTCTGCTTACCTGTCTGCCACCTGTCTGGAACAGGCG 54128
QY 1572 CAGGTTAAGACCATCATGCTTCCAAAGAGTCTCAGACCTTGCCACAATGCCAGAAG 1631
|||||
Db 54127 CAGGTTAAGACCATCATGCTTCCAAAGAGTCTCAGACCTTGCCACAATGCCAGAAG 54068
QY 1632 TTCCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1691
Db 54067 TTCCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 54008
QY 1692 GGSCCCTTCGCTCTGCTTTTGGGAGAGTGGGCTTCAATTAGATG 1738
|||||
Db 54007 GGSCCCTTCGCTCTGCTTTTGGGAGAGTGGGCTTCAATTAGATG 53961
RESULT 12
AC009060
LOCUS
DEFINITION
AC009060
ACCESSION
VERSION
AC009060.7 GI:9690317
KEYWORDS
HTG.
SOURCE
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 180596)
DOE Joint Genome Institute and Stanford Human Genome Center.
REFERENCE
AUTHORS
DOE Joint Genome Institute
JOURNAL
Direct Submission
REFERENCE
2 (bases 1 to 180596)
DOE Joint Genome Institute.
AUTHORS
Direct Submission
TITLE
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

```

REFERENCE
AUTHORS    3 (bases 1 to 180596)
TITLE      DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL    Direct Submission
           Submitted (04-AUG-2000) DOE Joint Genome Institute, 2800 Mitchell
           Drive, Walnut Creek, CA 94598, USA
COMMENT    On Aug 4, 2000 this sequence version replaced gi:9256118.
           Draft Sequence produced by DOE Joint Genome Institute
           www.jgi.doe.gov
           Finishing Completed at Stanford Human Genome Center
           www.shgc.stanford.edu
           Quality: Phrap Quality >=40 99.9% of Sequence;
           Estimated Total Number of Errors is 0.2.
           STS Content:
           SHGC-32944 G29390
           WI-6927 G06314
           WI-16981 G21928
           WI-9564 G06056.
FEATURES
source      Location/Qualifiers
            1..180596
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="16"
            /clone="RP11-296110"
BASE COUNT 48046 a 43474 c 42543 g 46533 t
ORIGIN
Query Match      15.2%; Score 285; DB 9; Length 180596;
Best Local Similarity 99.5%; Pred. No. 6.7e-155;
Matches 385; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1452 GCCCAGGACACATCTCCCGTGGGGCCAGGCTCTGAGGCTGACACATGGCTCCCT 1511
|
Db 87759 GCCCAGGACACATCTCCCGTGGGGCCAGGCTCTGAGGCTGACACATGGCTCCCT 87818
|
QY 1512 CGCTGCTCCCTGGGAGCAGCGCTGCTTACTGCTGCCACCTCTGCGAACAGGGC 1571
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Db 87819 CGCTGCTCCCTGGGAGCAGCGCTGCTTACTGCTGCCACCTCTGCGAACAGGGC 87878
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QY 1632 TTGGGACAGAGAGCAGGAGGCGCAGTGAGGCGCAGGAGTGAGTGTAGAGAGCTG 1691
|
Db 87939 TTGGGACAGAGAGCAGGAGGCGCAGTGAGGCGCAGGAGTGAGTGTAGAGAGCTG 87998
|
QY 1692 GGGCCCTTCGCTGCTTTTGTGGAAGATGGGCTTCAATAGATGGCGAAGAGGAGGA 1751
|
Db 87999 GGGCCCTTCGCTGCTTTTGTGGAAGATGGGCTTCAATAGATGGCGAAGAGGAGGA 88058
|
QY 1752 CACCGCCAGTGGTCCAAAAGAGCTGCTCTCTCCACCTGGCCAGACCCCTGTGGGGCAGC 1811
|
Db 88059 CACCGCCAGTGGTCCAAAAGAGCTGCTCTCTCCACCTGGCCAGACCCCTGTGGGGCAGC 88118
|
QY 1812 GGAGCTTCCCTGTGGCATGAACCCAC 1838
|
Db 88119 GGAGCTTCCCTGTGGCATGAACCCAC 88145
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RESULT 13
AC097331 Pan troglodytes clone RP43-53A2, WORKING DRAFT SEQUENCE, 14
LOCUS      200409 bp DNA linear HTG 22-JUN-2002
DEFINITION
unordered pieces.
ACCESSION AC097331
VERSION AC097331.4 GI:21535856
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE chimpanzee.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 200409)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,

```

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Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
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Devilla,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.H.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
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Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karissom,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louisseg,H.,
Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
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Nguyen,N., Nickerson,E., Nwokwenkwo,S., Ogih,H., Okwuonu,G.,
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Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savary,G.,
Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,I.,
Sodergren,E., Sonalke,I., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 200409)
Worley,K.C.
Direct Submission
Submitted (14-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 200409)
Worley,K.C.
Direct Submission
Submitted (22-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jun 21, 2002 this sequence version replaced gi:21450389.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: ZUAQ
Center clone name: RP43-53A2
----- Summary Statistics
Sequencing vector: Plasmid; M7789
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 187810 bases at least Q40
Consensus quality: 190821 bases at least Q30
Consensus quality: 193098 bases at least Q20
Estimated insert size: 212811; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-gel estimation
Quality coverage: 9.3x in Q20 bases; sum-of-contigs estimation
-----

```


Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 9.4x in Q20 bases; sum-of-ctnigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hsc.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

1 48992: contig of 48992 bp in length
* 48993 49092: gap of unknown length
* 49093 90442: contig of 41350 bp in length
* 90443 90542: gap of unknown length
* 90543 124888: contig of 34346 bp in length
* 124889 124988: gap of unknown length
* 124989 145269: contig of 20281 bp in length
* 145270 145369: gap of unknown length
* 145370 173261: contig of 27892 bp in length
* 173262 173361: gap of unknown length
* 173362 186532: contig of 13171 bp in length
* 186533 186632: gap of unknown length
* 186633 201672: contig of 15040 bp in length
* 201673 201772: gap of unknown length
* 201773 204182: contig of 2410 bp in length.

FEATURES
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1. 204182
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-35B16"

BASE COUNT 52711 a 50970 c 50521 g 49254 t 726 others

ORIGIN
Query Match 10.4%; Score 195; DB 2; Length 204182;
Best Local Similarity 99.6%; Pred. No. 4.9e-102;
Matches 245; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCCTTTTGTCCACGACCCAGCCCTGACCTCTGGAGATTGTGAATAGCTCCATCCAGCCCTG 60

Db 5214 CTCCTTTTGTCCACGACCCAGCCCTGACCTCTGGAGATTGTGAATAGCTCCATCCAGCCCTG 5273

QY 61 AGAAACAAGCGGGTGGCTGAGCCAGGCTGTGACGGAGCCTGTGACGGGCCCAACAGAC 120

Db 5274 AGAAACAAGCGGGTGGCTGAGCCAGGCTGTGACGGAGCCTGTGACGGGCCCAACAGAC 5333

QY 121 CCATGCTGCATCCAGAGACCTCCCTGCGGGGGGCGATCTCTGGCTGTGCTCTGGGCC 180

Db 5334 CCATGCTGCATCCAGAGACCTCCCTGCGGGGGGCGATCTCTGGCTGTGCTCTGGGCC 5393

QY 181 TCCTTGGCACCACTGGGACAGGTTGGCCACCCAGCTGAGGAGCGGCTCCGATGG 240

Db 5394 TCCTTGGCACCACTGGGACAGGTTGGCCACCCAGCTGAGGAGCGGCTCCGATGG 5453

QY 241 CCGGAG 246

Db 5454 CCGGAG 5459

RESULT 15

AC009125/c

LOCUS

DEFINITION

AC009125

AC009125

VERSION

AC009125.5

KEYWORDS

HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE

Homo sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 205044)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 205044)
DOE Joint Genome Institute.
Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jun 21, 2000 this sequence version replaced gi:7689944.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 595469
Center clone name: RPCI-11_492H8

Summary Statistics

Consensus quality: 156671 bases at least Q40
Consensus quality: 183548 bases at least Q30
Consensus quality: 188961 bases at least Q20
Estimated insert size: 189500; agarose-fp estimation
Quality coverage: 3.4 in Q20 bases; sum-of-ctnigs estimation
Quality coverage: 3.23 in Q20 bases; sum-of-ctnigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 60 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1059: contig of 1059 bp in length
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* 1160 2165: contig of 1006 bp in length
* 2166 2265: gap of unknown length
* 2266 3328: contig of 1063 bp in length
* 3329 3428: gap of unknown length
* 3429 4435: contig of 1007 bp in length
* 4436 4535: gap of unknown length
* 4536 5539: contig of 1004 bp in length
* 5540 5639: gap of unknown length
* 5640 6729: contig of 1090 bp in length
* 6730 6829: gap of unknown length
* 6830 8057: contig of 1228 bp in length
* 8058 8157: gap of unknown length
* 8158 9286: contig of 1129 bp in length
* 9287 9386: gap of unknown length
* 9387 10700: contig of 1314 bp in length
* 10701 10800: gap of unknown length
* 10801 11829: contig of 1029 bp in length
* 11830 11929: gap of unknown length
* 11930 13279: contig of 1350 bp in length
* 13280 13379: gap of unknown length
* 13380 14619: contig of 1240 bp in length
* 14620 14719: gap of unknown length
* 14720 15934: contig of 1215 bp in length
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* 16035 17350: contig of 1316 bp in length
* 17351 17450: gap of unknown length
* 17451 19063: contig of 1613 bp in length
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* 19164 20431: contig of 1268 bp in length
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* 20532 21622: contig of 1091 bp in length
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* 21723 23188: contig of 1466 bp in length
* 23189 23288: gap of unknown length
* 23289 24522: contig of 1234 bp in length
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* 32894 32993: gap of unknown length
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* 36130 36229: gap of unknown length
* 36230 38136: contig of 1907 bp in length
* 38137 38236: gap of unknown length
* 38237 39974: contig of 1738 bp in length
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* 40075 41564: contig of 1490 bp in length
* 41565 41664: gap of unknown length
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* 43567 43666: gap of unknown length
* 43668 45289: contig of 1623 bp in length
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* 45390 47644: contig of 2255 bp in length
* 47645 47744: gap of unknown length
* 47745 50582: contig of 2838 bp in length
* 50583 50682: gap of unknown length
* 50684 53054: contig of 2372 bp in length
* 53055 53154: gap of unknown length
* 53155 54755: contig of 1601 bp in length
* 54756 54855: gap of unknown length
* 54856 57563: contig of 2708 bp in length
* 57564 57663: gap of unknown length
* 57664 59769: contig of 2106 bp in length
* 59770 59869: gap of unknown length
* 59870 61957: contig of 2088 bp in length
* 61958 62057: gap of unknown length
* 62059 65392: contig of 3335 bp in length
* 65393 65492: gap of unknown length
* 65493 68420: contig of 2928 bp in length
* 68421 68520: gap of unknown length
* 68521 71229: contig of 2709 bp in length
* 71230 71329: gap of unknown length
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* 73729 77868: contig of 4140 bp in length
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* 81038 81137: gap of unknown length
* 81138 83328: contig of 2192 bp in length
* 83329 83429: gap of unknown length
* 83430 86409: contig of 2981 bp in length
* 86410 86509: gap of unknown length
* 86510 90134: contig of 3625 bp in length
* 90135 90234: gap of unknown length
* 90235 93916: contig of 3682 bp in length
* 93917 94016: gap of unknown length
* 94017 97118: contig of 3702 bp in length
* 97119 97818: gap of unknown length
* 97820 100965: contig of 3147 bp in length
* 100966 101065: gap of unknown length
* 101066 105156: contig of 4091 bp in length
* 105157 105257: gap of unknown length
* 105258 110076: contig of 4820 bp in length
* 110077 110177: gap of unknown length
* 110178 114320: contig of 4144 bp in length
* 114321 114420: gap of unknown length
* 114421 120993: contig of 6573 bp in length
* 120994 121094: gap of unknown length
* 121095 127991: contig of 6898 bp in length
* 127992 128091: gap of unknown length
* 128092 136414: contig of 8323 bp in length

* 136415 136514: gap of unknown length
* 136515 150305: contig of 13791 bp in length
* 150306 150405: gap of unknown length
* 150406 163992: contig of 13587 bp in length
* 163993 164092: gap of unknown length
* 164093 186975: contig of 22883 bp in length
* 186976 187075: gap of unknown length
* 187076 205044: contig of 17969 bp in length.

FEATURES
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Location/Qualifiers
1. .205044
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/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-492H8"
/clone_lib="RPC1 human BAC library 11"
BASE COUNT 54631 a 45103 c 45331 g 53992 t 5987 others
ORIGIN

Query Match 10.1%; Score 190; DB 2; Length 205044;
Best Local Similarity 99.6%; Pred. No. 4-2e-99;
Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 338 GGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCC 397
Db 96233 GGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCC 96174
QY 398 AACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCTCAAGTGGGCTGGAACATGCAGCT 457
Db 96173 AACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCTCAAGTGGGCTGGAACATGCAGCT 96114
QY 458 GCTGCCCGCGGGCTTGGCGCTCTTTGTTGAAGTGGTTCAGCTATGTTTCAGAGGGGCA 517
Db 96113 GCTGCCCGCGGGCTTGGCGCTCTTTGTTGAAGTGGTTCAGCTATGTTTCAGAGGGGCA 96054
QY 518 GCGGTACAGCCAGCGCGGAGAGAGTGTCTGCAAGCCAGCCACTGCACCCACTACAGCA 577
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RESULT 16
AC021951

LOCUS Homo sapiens clone RP11-396D24, LOW-PASS SEQUENCE SAMPLING. HTG 13-JUL-2000
DEFINITION Homo sapiens clone RP11-396D24, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC021951
VERSION AC021951.2 GI:9154380
KEYWORDS HTG; HTGS_PHASE0.

SOURCE
Homo sapiens.ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORSTITLE
1 (bases 1 to 79023)JOURNAL
Homo sapiens, clone RP11-396D24REFERENCE
AUTHORS

2 (bases 1 to 79023)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepe, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Dearlano, K., Dewar, K., Domino, M., Doyle, M., Fenebor, J.,
Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hago, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lechoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., Olliver, J., Peterson, K.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,

Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (22-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6730807.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L5885

Center clone name: 396_D_24

* NOTE: This record contains 79 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads.
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1
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* 1010 1922: contig of 913 bp in length
* 1923 2022: gap of 100 bp
* 2023 2941: contig of 919 bp in length
* 2942 3041: gap of 100 bp
* 3042 3960: contig of 919 bp in length
* 3961 4060: gap of 100 bp
* 4061 4972: contig of 912 bp in length
* 4973 5072: gap of 100 bp
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* 5967 6065: gap of 100 bp
* 6067 6967: contig of 901 bp in length
* 6968 7067: gap of 100 bp
* 7068 7964: contig of 897 bp in length
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* 8949 9048: gap of 100 bp
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* 15911 16010: gap of 100 bp
* 16011 16901: contig of 891 bp in length
* 16902 17001: gap of 100 bp
* 17002 17897: contig of 896 bp in length
* 17898 17997: gap of 100 bp
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* 18893 18992: gap of 100 bp
* 18993 19883: contig of 891 bp in length
* 19884 19983: gap of 100 bp
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* 20886 20985: gap of 100 bp
* 20986 21899: contig of 914 bp in length

* 21900 21999: gap of 100 bp
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* 22920 23019: gap of 100 bp
* 23020 23928: contig of 909 bp in length
* 23929 24028: gap of 100 bp
* 24029 24922: contig of 894 bp in length
* 24923 25022: gap of 100 bp
* 25023 25916: contig of 894 bp in length
* 25917 26016: gap of 100 bp
* 26017 26914: contig of 898 bp in length
* 26915 27014: gap of 100 bp
* 27015 27910: contig of 896 bp in length
* 27911 28010: gap of 100 bp
* 28011 28929: contig of 919 bp in length
* 28930 29029: gap of 100 bp
* 29030 29902: contig of 873 bp in length
* 29903 30002: gap of 100 bp
* 30003 30896: contig of 894 bp in length
* 30897 30996: gap of 100 bp
* 30997 31881: contig of 885 bp in length
* 31882 31981: gap of 100 bp
* 31982 32866: contig of 885 bp in length
* 32867 32965: gap of 100 bp
* 32967 33869: contig of 903 bp in length
* 33870 33969: gap of 100 bp
* 33970 34888: contig of 919 bp in length
* 34889 34988: gap of 100 bp
* 34989 35880: contig of 892 bp in length
* 35881 35980: gap of 100 bp
* 35981 36880: contig of 900 bp in length
* 36881 36980: gap of 100 bp
* 36981 37874: contig of 894 bp in length
* 37875 37974: gap of 100 bp
* 37975 38862: contig of 888 bp in length
* 38863 38962: gap of 100 bp
* 38963 39874: contig of 912 bp in length
* 39875 39974: gap of 100 bp
* 39975 40899: contig of 925 bp in length
* 40900 40999: gap of 100 bp
* 41000 41911: contig of 912 bp in length
* 41912 42011: gap of 100 bp
* 42012 42921: contig of 910 bp in length
* 42922 43021: gap of 100 bp
* 43022 43934: contig of 913 bp in length
* 43935 44034: gap of 100 bp
* 44035 44952: contig of 918 bp in length
* 44953 45052: gap of 100 bp
* 45053 45950: contig of 898 bp in length
* 45951 46050: gap of 100 bp
* 46051 46928: contig of 878 bp in length
* 46929 47028: gap of 100 bp
* 47029 47925: contig of 897 bp in length
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* 49023 49923: contig of 901 bp in length
* 49924 50023: gap of 100 bp
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* 51009 51918: contig of 910 bp in length
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* 55015 55924: contig of 910 bp in length
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* 56910 57009: gap of 100 bp
* 57010 57902: contig of 893 bp in length
* 57903 58002: gap of 100 bp

AUTHORS
TITLE
JOURNAL
COMMENT

DOE Joint Genome Institute.
Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jun 21, 2000 this sequence version replaced gi:7689944.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 595469
Center clone name: RPCI-11_492H8

Summary Statistics

Consensus quality: 156671 bases at least Q40
Consensus quality: 183548 bases at least Q30
Consensus quality: 188961 bases at least Q20
Estimated insert size: 189500; agarose-fp estimation
Estimated insert size: 199144; sum-of-contigs estimation
Quality coverage: 3.4 in Q20 bases; agarose-fp estimation
Quality coverage: 3.23 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 60 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1059: contig of 1059 bp in length
1060 1159: gap of unknown length
1160 2165: contig of 1006 bp in length
2166 2265: gap of unknown length
2266 3328: contig of 1063 bp in length
3329 3429: gap of unknown length
3430 4435: contig of 1007 bp in length
4436 4536: gap of unknown length
4537 5539: contig of 1004 bp in length
5540 5640: gap of unknown length
5641 6730: contig of 1090 bp in length
6731 6829: gap of unknown length
6830 8057: contig of 1228 bp in length
8058 8157: gap of unknown length
8158 9286: contig of 1129 bp in length
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9388 10701: contig of 1314 bp in length
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21623 21722: gap of unknown length
21723 23188: contig of 1466 bp in length
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27394 28954: contig of 1562 bp in length

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30864 32893: contig of 2030 bp in length
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32994 34228: contig of 1235 bp in length
34229 34328: gap of unknown length
34330 36129: contig of 1801 bp in length
36130 36229: gap of unknown length
36230 38136: contig of 1907 bp in length
38137 38236: gap of unknown length
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40075 41564: contig of 1490 bp in length
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41666 43566: contig of 1902 bp in length
43567 43666: gap of unknown length
43668 45289: contig of 1623 bp in length
45290 45389: gap of unknown length
45390 47644: contig of 2255 bp in length
47645 47744: gap of unknown length
47745 50582: contig of 2838 bp in length
50583 50683: gap of unknown length
50684 53054: contig of 2372 bp in length
53055 54755: contig of 1601 bp in length
54756 54855: gap of unknown length
54856 57563: contig of 2708 bp in length
57564 57663: gap of unknown length
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62059 65392: contig of 3335 bp in length
65393 65492: gap of unknown length
65493 68420: contig of 2928 bp in length
68421 71229: contig of 2709 bp in length
71230 71329: gap of unknown length
71330 73628: contig of 2299 bp in length
73629 73728: gap of unknown length
73729 77868: contig of 4140 bp in length
77869 77968: gap of unknown length
77969 81036: contig of 3068 bp in length
81037 81136: gap of unknown length
81137 83328: contig of 2192 bp in length
83329 83428: gap of unknown length
83429 86409: contig of 2981 bp in length
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90135 90234: gap of unknown length
90235 93916: contig of 3682 bp in length
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97719 100965: contig of 3147 bp in length
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110177 114320: contig of 4144 bp in length
114321 114420: gap of unknown length
114421 120993: contig of 6573 bp in length
120994 121093: gap of unknown length
121094 127991: contig of 6898 bp in length
127992 128091: gap of unknown length
128092 136414: contig of 8323 bp in length
136415 136514: gap of unknown length
136515 150305: contig of 13791 bp in length
150306 150406: gap of unknown length
150407 163992: contig of 13587 bp in length
163993 164092: gap of unknown length

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* 164093 186975: contig of 22883 bp in length
* 186976 187075: gap of unknown length
* 187076 205044: contig of 17969 bp in length.
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/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-492H8"
/clone_lib="RPCI human BAC library 11"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.6e-51;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 798 GAGGTCCCGAGGATCTGTGCGATGAGTCCGACAGACCAACGAGGAGTCTCAACATCAGC 857
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Db 43774 GAGGTCCCGAGGATCTGTGCGATGAGTCCGACAGACCAACGAGGAGTCTCAACATCAGC 43833
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QY 858 ACCTGCCACTGCCACTGTCCCTCGGTACACGGCGAGATAGTCCCAAG 906
|||||
Db 43834 ACCTGCCACTGCCACTGTCCCTCGGTACACGGCGAGATAGTCCCAAG 43882
|||||

RESULT 20
AC096051 2340 bp mRNA linear PRI 15-JUL-2002
LOCUS
DEFINITION Homo sapiens cDNA FLJ3732 fis, clone KIDNE2010750.
ACCESSION AK096051
VERSION AK096051.1 GI:21755444
KEYWORDS oligo capping; fis (full insert sequence);
SOURCE Homo sapiens kidney cDNA to mRNA, clone_lib:KIDNE2
clone:KIDNE2010750.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K.,
Arita,M., Mutsaers,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B.,
Suzuki,Y., Sugano,S., Nagahara,K., Masuho,Y., Nagai,K. and
Isogai,T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 2340)
Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
Kazusa-Kanata, Kisarazu, Chiba 252-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
Location/Qualifiers
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/tissue_type="kidney"
/clone_lib="KIDNE2"
/note="cloning vector: pME18SFL3"
180..641
/note="unnamed protein product"

FEATURES
source
CDS
* NOTE: This record contains 79 individual
* sequencing reads that have not been assembled into
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* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

* 1
* 910 1009: contig of 909 bp in length
* 1010 1009: gap of 100 bp
* 1010 1922: contig of 913 bp in length
* 1923 2022: gap of 100 bp
* 2023 2941: contig of 919 bp in length
* 2942 3041: gap of 100 bp
* 3042 3960: contig of 919 bp in length
* 3961 4060: gap of 100 bp
* 4061 4972: contig of 912 bp in length
* 4973 5072: gap of 100 bp
* 5073 5966: contig of 894 bp in length
* 5967 6066: gap of 100 bp
* 6067 6967: contig of 901 bp in length
* 6968 7067: gap of 100 bp
* 7068 7984: contig of 897 bp in length
* 7965 8064: gap of 100 bp
* 8065 8948: contig of 884 bp in length
* 8949 9048: gap of 100 bp
* 9049 9945: contig of 897 bp in length
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* 10046 10941: contig of 896 bp in length
* 10942 11041: gap of 100 bp
* 11042 11974: contig of 933 bp in length
* 11975 12074: gap of 100 bp
* 12075 12953: contig of 879 bp in length
* 12954 13053: gap of 100 bp
* 13054 13940: contig of 887 bp in length
* 13941 14040: gap of 100 bp
* 14041 14924: contig of 884 bp in length
* 14925 15024: gap of 100 bp
* 15025 15910: contig of 886 bp in length
* 15911 16010: gap of 100 bp
* 16011 16901: contig of 891 bp in length
* 16902 17001: gap of 100 bp
* 17002 17897: contig of 896 bp in length
* 17898 17997: gap of 100 bp
* 17998 18892: contig of 895 bp in length
* 18893 18992: gap of 100 bp
* 18993 19883: contig of 891 bp in length
* 19884 19983: gap of 100 bp
* 19984 20885: contig of 902 bp in length
* 20886 20985: gap of 100 bp
* 20986 21899: contig of 914 bp in length
* 21900 21999: gap of 100 bp
* 22000 22919: contig of 920 bp in length
* 22920 23019: gap of 100 bp
* 23020 23928: contig of 909 bp in length
* 23929 24028: gap of 100 bp
* 24029 24922: contig of 894 bp in length
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* 25023 25916: contig of 894 bp in length
* 25917 26016: gap of 100 bp
* 26017 26914: contig of 898 bp in length
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* 27015 27910: contig of 896 bp in length
* 27911 28010: gap of 100 bp
* 28011 28929: contig of 919 bp in length
* 28930 29029: gap of 100 bp
* 29030 29902: contig of 873 bp in length
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* 30003 30896: contig of 894 bp in length
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* 31882 31881: contig of 885 bp in length
* 31882 31981: gap of 100 bp

* 31982 32866: contig of 885 bp in length
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* 32967 33869: contig of 903 bp in length
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* 33970 34888: contig of 919 bp in length
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* 36981 37874: contig of 894 bp in length
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* 37975 38862: contig of 888 bp in length
* 38863 38962: gap of 100 bp
* 38963 39874: contig of 912 bp in length
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* 41000 41911: contig of 912 bp in length
* 41912 42011: gap of 100 bp
* 42012 42921: contig of 910 bp in length
* 42922 43021: gap of 100 bp
* 43022 43934: contig of 913 bp in length
* 43935 44034: gap of 100 bp
* 44035 44952: contig of 918 bp in length
* 44953 45052: gap of 100 bp
* 45053 45950: contig of 898 bp in length
* 45951 46050: gap of 100 bp
* 46051 46928: contig of 878 bp in length
* 46929 47028: gap of 100 bp
* 47029 47925: contig of 897 bp in length
* 47926 48025: gap of 100 bp
* 48026 48922: contig of 897 bp in length
* 48923 49022: gap of 100 bp
* 49023 49923: contig of 901 bp in length
* 49924 50023: gap of 100 bp
* 50024 50908: contig of 885 bp in length
* 50909 51008: gap of 100 bp
* 51009 51918: contig of 910 bp in length
* 51919 52018: gap of 100 bp
* 52019 52934: contig of 916 bp in length
* 52935 53034: gap of 100 bp
* 53035 53922: contig of 888 bp in length
* 53923 54022: gap of 100 bp
* 54023 54914: contig of 892 bp in length
* 54915 55014: gap of 100 bp
* 55015 55924: contig of 910 bp in length
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* 56025 56909: contig of 885 bp in length
* 56910 57009: gap of 100 bp
* 57010 57902: contig of 893 bp in length
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* 58003 58884: contig of 882 bp in length
* 58885 58984: gap of 100 bp
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* 61907 62006: gap of 100 bp
* 62007 62901: contig of 895 bp in length
* 62902 63001: gap of 100 bp
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* 64888 64987: gap of 100 bp
* 64988 65885: contig of 898 bp in length
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* 65986 66885: contig of 900 bp in length
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* 68878 68977: gap of 100 bp
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 * 69972 70884: contig of 913 bp in length
 * 70885 70984: gap of 100 bp

Query Match 4.2%; Score 79; DB 2; Length 79023;
 Best Local Similarity 100.0%; Pred. No. 6.6e-34;
 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 421 TGTGGCGCACCCTGCAAGTGGCTGGACATGCGAGCTGCTCCCGCGGCTTGGCGTCT 480
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 Db 53193 TGTGGCGCACCCTGCAAGTGGCTGGACATGCGAGCTGCTCCCGCGGCTTGGCGTCT 53134
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 481 TTGTTGAAGTGGTCAGCT 499
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 Db 53133 TTGTTGAAGTGGTCAGCT 53115

RESULT 22
 AC093451/c
 LOCUS
 DEFINITION Mus musculus chromosome 8 clone rp23-340n2 strain C57BL/6J, WORKING
 DRAFT SEQUENCE, 4 ordered pieces.

ACCESSION
 VERSION AC093451.19 GI:22325019
 KEYWORDS HTG: HTGS_PHASE2; HTGS_DRAFT.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 200755)

TITLE Prescott, A. and Roe, B.A.
 JOURNAL Mus musculus BAC Clone rp23-340n2
 Unpublished

REFERENCE
 AUTHORS 2 (bases 1 to 200755)
 TITLE Prescott, A. and Roe, B.A.
 JOURNAL Submitted (24-AUG-2001) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA

REFERENCE
 AUTHORS 3 (bases 1 to 200755)
 TITLE Prescott, A. and Roe, B.A.
 JOURNAL Direct Submission

COMMENT
 Submitted (20-AUG-2002) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 On Aug 20, 2002 this sequence version replaced gi:22213237.

----- Genome Center
 Center: Department of Chemistry And Biochemistry
 The University of Oklahoma
 Center code:UOKNOR

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.

* This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 33810: contig of 33810 bp in length
 * 33811 33910: gap of unknown length
 * 33911 70420: contig of 36510 bp in length
 * 70421 70520: gap of unknown length
 * 70521 132973: contig of 62453 bp in length
 * 132974 133074: gap of unknown length
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 /strain="C57BL/6J"

/db_xref="taxon:10090"
 /chromosome="8"
 /clone="rp23-340n2"
 /clone_lib="RPCI - 23 Female (C57BL/6J) Mouse BAC Library"
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 ORIGIN

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 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1170 CTGGGCGCCTGGAGACACCAACGAGGTGACTGACAGTGACTT 1213
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RESULT 23
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 LOCUS
 DEFINITION Rattus norvegicus clone CH230-122N13, *** SEQUENCING IN PROGRESS
 ***, 70 unordered pieces.

ACCESSION
 VERSION AC098076.4 GI:21729308
 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

1 (bases 1 to 197326)

Muzny, D.M., Adams, C., Ali-Osman, F.R., Allen, C.,
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 Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
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 Williams, G., Williamson, A., Wleczka, R., Woodson, S., Worley, K.,
 Wu, C., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G. and Gibbs, R.

Direct Submission
 Unpublished
 2 (bases 1 to 197326)

AUTHORS
TITLE

Worley, K.C.
Direct Submission
Submitted (23-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 197326)

REFERENCE
AUTHORS
TITLE
JOURNAL

Worley, K.C.
Direct Submission
Submitted (12-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:17967675.

COMMENT

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GGRF
Center clone name: CH230-122N13
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 131850 bases at least Q40
Consensus quality: 140067 bases at least Q30
Consensus quality: 146790 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 70 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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1268 1367: gap of unknown length
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2732 2833: gap of unknown length
2833 4010: contig of 1177 bp in length
4010 4109: gap of unknown length
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Best Local Similarity 100.0%; Pred. NO. 1.8e-07;
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QY 1294 CCTTACCAGTTTGCCTTTGGGCGAGCTGACAA 1327
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DB 170860 CCTTACCAGTTTGCCTTTGGGCGAGCTGACAA 170893

RESULT 24
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AE005865 AE005673
VERSION
AE005865.1 GI:13423361
KEYWORDS
Caulobacter crescentus CB15.
SOURCE
Bacteria; Proteobacteria; alpha subdivision; Caulobacter group; Caulobacter.

REFERENCE
AUTHORS
1 (bases 1 to 12977)
Nierman, W.C., Feldblyum, T.V., Laub, M.T., Paulsen, I.T., Nelson, K.E., Eisen, J.J., Heidelberg, J.F., Alley, M.R., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M.B., Khouri, H., Shetty, J., Berry, K., Uterback, T., Tran, K., Wolf, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Venter, J.C., Shapiro, L. and Fraser, C.M.
Complete genome sequence of Caulobacter crescentus
Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
21173698
11259647

REFERENCE
AUTHORS
2 (bases 1 to 12977)
Nierman, W.C., Feldblyum, T.V., Paulsen, I.T., Nelson, K.E., Eisen, J.J., Heidelberg, J.F., Alley, M.R., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., Laub, M.T., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Shetty, J., Berry, K., Uterback, T., Tran, K., Wolf, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Shapiro, L., Venter, J.C. and Fraser, C.M.
Direct Submission
Submitted (31-JAN-2001) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
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complement(1267. .2109)

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MEDLINE
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AUTHORS
TITLE
JOURNAL
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1. 12977
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repeat_region 10705..10768
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repeat_region complement(11907..12307)
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repeat_region 24374..24439
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repeat_region 25046..25346
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appears that what is one gene in worm are at least two
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Db 19851 GCCAGGGAGTGAGTGTAGAA 19830
|||||
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WPCCOMMENT
Sequence split into 4 fragments LOCUS HSS171M Accession AJ239326
Fragment Name Begin End
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 HSS171M_1 100001 210000
 HSS171M_2 200001 310000
 HSS171M_3 300001 400516
 Continuation (2 of 4) of HSS171M from base 100001 (AJ239326 Homo sapiens chromosome 21)

Query Match 1-2%; Score 22; DB 2; Length 110000;
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QY 605 GGGCTGTGGCGGACACTGTGC 626
 Db 30521 GGGCTGTGGCGGACACTGTGC 30542

RESULT 27
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 LOCUS Homo sapiens chromosome 12 clone RP11-62D5, WORKING DRAFT SEQUENCE, HTG 09-MAY-2002
 DEFINITION 7 unordered pieces.

AC079318
 AC079318.5 GI:20335764
 VERSION HTG: HTGS_PHASE1; HTGS_DRAFT.
 KEYWORDS Homo sapiens.
 SOURCE

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 134151)

REFERENCE

AUTHORS

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amarantunga,H.C., Are,J.R., Ayele,M., Banks,T., Barbara,J., Benton,J., Bimane,K., Blankenburg,K., Bonin,D., Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,K., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Delaney,K.R., Delgado,O., Davy-Carroll,L., Dederich,D.A., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hoques,M., Holloway,C., Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,K., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,G., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokwenkwo,S., Ogih,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonake,T., Sparks,A., Stanley,H., Stone,K., Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,X., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G., and Gibbs,R.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

JOURNAL

COMMENT

Submitted (27-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 134151)
 Worley,K.C.
 Direct Submission
 Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Apr 28, 2002 this sequence version replaced gi:10047601.

Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: HCCN

Center clone name: RP11-62D5

----- Summary Statistics

Sequencing vector: M13;

Chemistry: Dye-primer Bodipy; 91% of reads

Chemistry: Dye-terminator Big Dye; 9% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 129214 bases at least Q40

Consensus quality: 132434 bases at least Q40

Consensus quality: 133922 bases at least Q20

Estimated insert size: 134530; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

consists of 7 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

1 3823: contig of 3823 bp in length

3824 3923: gap of unknown length

3924 8764: contig of 4841 bp in length

8765 8864: gap of unknown length

8865 20193: contig of 11329 bp in length

20194 20293: gap of unknown length

20294 41239: contig of 20946 bp in length

41240 41339: gap of unknown length

41340 59870: contig of 18531 bp in length

59871 59970: gap of unknown length

59971 88914: contig of 28844 bp in length

88915 134151: contig of 45237 bp in length.

88915 134151: contig of 45237 bp in length.

Location/Qualifiers

1. 134151

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="12"

/clone="RP11-62D5"

BASE COUNT 43267 a 24745 c 23175 g 42360 t 604 others

ORIGIN

Query Match 1-2%; Score 22; DB 2; Length 134151;

Best Local Similarity 100.0%; Pred. No. 2;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1779 CTTCTCCACCTGGCCGACGCC 1800

Db 55400 CTTCTCCACCTGGCCGACGCC 55421

RESULT 28

AC125935

LOCUS AC125935

165645 bp DNA linear HTG 18-JUL-2002

Summary Statistics

Chemistry: Vector: Plasmid;
 Assembly program: Phrap; version 0.990329
 Consensus quality: 103558 bases at least Q40
 Consensus quality: 113163 bases at least Q30
 Consensus quality: 118563 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 consists of 67 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1003: contig of 1003 bp in length
 1103: gap of unknown length
 2232: contig of 1129 bp in length
 2332: gap of unknown length
 2333: contig of 1578 bp in length
 3910: contig of 1578 bp in length
 4010: gap of unknown length
 5795: contig of 1785 bp in length
 5895: gap of unknown length
 7135: contig of 1240 bp in length
 7136: gap of unknown length
 7236: contig of 1276 bp in length
 8511: gap of unknown length
 8611: gap of unknown length
 10040: contig of 1429 bp in length
 10140: gap of unknown length
 11309: contig of 1169 bp in length
 11409: gap of unknown length
 12656: contig of 1247 bp in length
 12756: gap of unknown length
 13938: contig of 1182 bp in length
 14038: gap of unknown length
 15250: contig of 1212 bp in length
 15350: gap of unknown length
 16471: contig of 1121 bp in length
 16571: gap of unknown length
 17678: contig of 1107 bp in length
 17778: gap of unknown length
 19347: contig of 1569 bp in length
 19447: gap of unknown length
 20465: contig of 1018 bp in length
 20565: gap of unknown length
 21786: contig of 1221 bp in length
 21886: gap of unknown length
 23005: contig of 1119 bp in length
 23105: gap of unknown length
 24898: contig of 1793 bp in length
 24998: gap of unknown length
 26268: contig of 1270 bp in length
 26368: gap of unknown length
 27368: contig of 1000 bp in length
 27468: gap of unknown length
 28567: contig of 1099 bp in length
 28568: gap of unknown length
 30815: contig of 2148 bp in length
 30915: gap of unknown length
 32809: contig of 1894 bp in length
 32909: gap of unknown length
 35257: contig of 2348 bp in length
 35357: gap of unknown length
 37350: contig of 1993 bp in length
 37450: gap of unknown length
 38233: contig of 1783 bp in length
 39333: gap of unknown length
 41361: contig of 2028 bp in length
 41461: gap of unknown length
 43911: contig of 2450 bp in length

Rattus norvegicus clone CH230-225E7, *** SEQUENCING IN PROGRESS

***, 67 unordered pieces.
 AC125935
 AC125935.1 GI:21671541
 HTG: HTGS_PHASE1.
 Norway rat.
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

1 (bases 1 to 165645)
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amarantunga,H.C., Are,J.R., Ayelle,M., Banks,T.,
 Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
 Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
 Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
 Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
 Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
 Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
 Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
 Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
 Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
 Gorell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
 Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
 Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B.,
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 Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
 Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
 Kratovic,J., Kurech,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
 Li,J., Li,Z., Luchthart,O., Lieu,C., Liu,J., Liu,W., Loulseghe,H.,
 Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
 Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
 Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
 Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
 Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
 Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
 Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
 Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
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 Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,I.,
 Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
 Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H.,
 Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
 Usmani,K., Vasquez,L., Vera,V., Villalobos,D., Vinson,R., Wang,Q.,
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
 Williams,G., Williamson,A., Wleczkyk,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstein,G. and Gibbs,R.

Direct Submission
 Unpublished
 2 (bases 1 to 165645)
 Worley,K.C.
 Direct Submission
 Submitted (02-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 165645)
 Worley,K.C.

Direct Submission
 Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 Project Information
 Center project name: GVR5
 Center clone name: CH230-225E7


```

* 43912 44011: gap of unknown length
* 44012 45450: contig of 1439 bp in length
* 45451 45550: gap of unknown length
* 45551 46963: contig of 1413 bp in length
* 46964 47063: gap of unknown length
* 47064 48971: contig of 1908 bp in length
* 48972 49071: gap of unknown length
* 49072 51156: contig of 2085 bp in length
* 51157 53181: gap of unknown length
* 53182 53281: contig of 1925 bp in length
* 53282 55338: gap of unknown length
* 55339 55438: gap of unknown length
* 55439 56812: contig of 1374 bp in length
* 56813 58505: gap of unknown length
* 58506 58605: gap of unknown length
* 58606 59762: contig of 1157 bp in length
* 59763 59862: gap of unknown length
* 59863 61280: contig of 1418 bp in length
* 61281 63491: contig of 2111 bp in length
* 63492 63591: gap of unknown length
* 63592 65845: contig of 2254 bp in length
* 65846 65945: gap of unknown length
* 65946 67484: contig of 1539 bp in length
* 67485 67585: gap of unknown length
* 67586 70016: contig of 2432 bp in length
* 70017 72211: contig of 2095 bp in length
* 72212 72311: gap of unknown length
* 72312 74548: contig of 2237 bp in length
* 74549 74649: gap of unknown length
* 74650 78391: contig of 3643 bp in length
* 78392 78397: gap of unknown length
* 78398 81897: contig of 3506 bp in length
* 81898 84929: gap of unknown length
* 84930 85029: gap of unknown length
* 85030 88346: contig of 3317 bp in length
* 88347 90378: contig of 1932 bp in length
* 90379 90478: gap of unknown length
* 90479 93152: contig of 2674 bp in length
* 93153 93252: gap of unknown length
* 93253 96475: gap of unknown length
* 96476 96574: gap of unknown length
* 96575 99677: contig of 3103 bp in length
* 99678 102930: gap of unknown length
* 102931 103030: contig of 3153 bp in length
* 103031 106592: gap of unknown length
* 106593 106692: gap of unknown length

```

```

Query Match      1.28; Score 22; DB 2; Length 165645;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1444 GCCAGTTTCCCGAGGACACAT 1465
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Db 56196 GCCAGTTTCCCGAGGACACAT 56217

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```

RESULT 29
AL805954/c
LOCUS      178413 bp DNA linear HTG 29-JUN-2002
DEFINITION Mus musculus chromosome 4 clone RP23-277N22, *** SEQUENCING IN
PROGRESS ***, 11 unordered pieces.
ACCESSION AL805954
VERSION AL805954.2 GI:21615787
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 178413)
Plumb,B.
Direct Submission
Submitted (28-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 26, 2002 this sequence version replaced gi:21614845.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BM277N22
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 175430 bases at least Q40
Consensus quality: 176248 bases at least Q30
Consensus quality: 176809 bases at least Q20
Insert size: 177413; sum-of-contigs
Insert size: 190090; 0.7% error; agarose-fp
Quality coverage: 6.21x in Q20 bases; sum-of-contigs Quality
coverage: 5.87x in Q20 bases; agarose-fp
-----

```

```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

1 9954: contig of 9954 bp in length
9955 10054: gap of 100 bp
10055 14020: contig of 3966 bp in length
14021 14120: gap of 100 bp
14121 25780: contig of 11660 bp in length
25781 25880: gap of 100 bp
25881 48226: contig of 22346 bp in length
48227 48326: gap of 100 bp
48327 65871: contig of 17545 bp in length
65872 65971: gap of 100 bp
65972 74331: contig of 8360 bp in length
74332 74431: gap of 100 bp
74432 84536: contig of 10105 bp in length
84537 84636: gap of 100 bp
84637 94786: contig of 10150 bp in length
94787 94886: gap of 100 bp
94887 100170: contig of 5284 bp in length
100171 100270: gap of 100 bp
100271 104837: contig of 4567 bp in length
104838 104937: gap of 100 bp
104938 178413: contig of 73476 bp in length.

```

```

Location/Qualifiers
1..178413
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosomes="4"
/clone="RP23-277N22"
/clone_lib="RPCI-23"
1 9954
/note="assembly_fragment:01797
fragment_chain:1
clone_end:SP6
vector_side:left"
10055..14020
/note="assembly_fragment:01740
fragment_chain:1"
14121..25780
/note="assembly_fragment:00378

```

misc_feature

misc_feature

misc_feature

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25881..48226
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misc_feature      104938..178413
/note="assembly_fragment:01214
fragment_chain:1"
vector_side:right"
clone_end:T7
BASE COUNT      44698 a 45575 c 45448 g 41618 t 1074 others
ORIGIN

```

```

Query Match      1.2%: Score 22; DB 2; Length 178413;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1635 GGCAGAGAGAGCGAGGAGGCC 1656
|||||
Db 75682 GGCAGAGAGAGCGAGGAGGCC 75661
|||||
RESULT 30
AC079905      189456 bp DNA linear PRI 25-MAY-2002
LOCUS
DEFINITION      Homo sapiens 12 BAC Rpl1-813p10 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
ACCESSION      AC079905
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 189456)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Anarunge,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Bivaga,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowle,S., Brineva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burck,P., Burkett,C., Burrell,K.L., Byrd,N.C., Caron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C., Cleveland,C.D.,
Cox,C., Coyle,M.D., Dethorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
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Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lee,E., Lewis,L.C.,

```

```

Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Loulseged,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Marondel,I., Martin,R.,
Martindale,A., Martinez,E., Massey,E., Mawhney,E., McLeod,M.P.,
Meador,M., Mei,G., Merscher,S., Metzger,M., Miller,A., Miner,G.,
Minor,Z., Mitchell,T., Mohabbat,K., Montgomery,K.T., Morgan,M.,
Morris,S., Moser,M., Neal,D., Nelson,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Ogih,M., Okunolu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Picken,R., Primus,E., Pu,L.L.,
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Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shim,C.,
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Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B.,
Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D.,
Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Williamson,A., Zhou,J.,
Washington,C., Watlington,S., Williams,G., Worley,K., Wu,Y.F.,
Wlarczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., and Gibbs,R.
Zorilla,S., Kuchelapatti,R., Weinstock,G. and Gibbs,R.
Direct Submission
2 (bases 1 to 189456)
Worley,K.C.
Direct Submission
Submitted (17-SEP-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 189456)
Worley,K.C.
Direct Submission
Submitted (01-JUN-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 189456)
Worley,K.C.
Direct Submission
Submitted (05-JUN-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 189456)
Worley,K.C.
Direct Submission
Submitted (07-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
6 (bases 1 to 189456)
Worley,K.C.
Direct Submission
Submitted (02-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
7 (bases 1 to 189456)
Worley,K.C.
Direct Submission
Submitted (25-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jun 1, 2001 this sequence version replaced gi:14010769.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
gc-help@bcm.tmc.edu
CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.
ANNOTATION OF FEATURES:
STS are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.

```

```

----- Distribution of Quality < 40 Bases -----
500|
450|
400|
350|
300|
250|
200|
150|
100|
50|

# bases

*
*
*
*
*
*
*
*
*
*

```

numquery@sanger.ac.uk Cloner requests: clonerrequest@sanger.ac.uk
On Nov 25, 2001 this sequence version replaced gi:17043820.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-36P22 is
from the RP21-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBACE3.6.

FEATURES	source
Location/Qualifiers	
1. .191494	
/organism="Mus musculus"	
/db_xref="taxon:10090"	
/chromosome="2"	
/clone="Rp23-36P22"	
/clone_lib="RPCI-23"	
BASE COUNT	49688 a 46072 c 46038 g 49696 t
ORIGIN	
Query Match	1.2%; Score 22; DB 10; Length 191494;
Best Local Similarity	100.0%; Pred. No. 2;
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1852	ATGAATCAGCTGTAACAAAAA 1873
Db 38657	ATGAATCAGCTGTAACAAAAA 38678
RESULT 32	
AL353591/c	
LOCUS	AL353591 205272 bp DNA linear HTG 13-JUN-2001
DEFINITION	Homo sapiens chromosome 6 clone RP11-366H19, *** SEQUENCING IN
	PROGRESS ***, 18 unordered pieces.
ACCESSION	AL353591
VERSION	AL353591.5 GI:9930866
KEYWORDS	HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1. (bases 1 to 205272)
AUTHORS	Sims, S.
TITLE	Direct Submission
JOURNAL	Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
	CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
	requests: clonerrequest@sanger.ac.uk
	On Aug 27, 2000 this sequence version replaced gi:9863646.
COMMENT	----- Genome Center
	Center: Sanger Centre
	Center code: SC
	Web site: http://www.sanger.ac.uk
	Contact: humquery@sanger.ac.uk
	----- Project Information
	Center project name: BA366H19
	----- Summary Statistics
	Assembly program: XGAP4; version 4.5
	Sequencing vector: plasmid; L08752; 100% of reads
	Chemistry: Dye-terminator Big Dye; 100% of reads
	Consensus quality: 192563 bases at least Q40
	Consensus quality: 197287 bases at least Q30
	Consensus quality: 200442 bases at least Q20
	Insert size: 203572; sum-of-contigs
	Insert size: 183107; 13.0% error; agarose-fp
	Quality coverage: 3.30x in Q20 bases; sum-of-contigs Quality
	coverage: 3.75x in Q20 bases; agarose-fp

	* NOTE: This is a 'working draft' sequence. It currently
	* consists of 18 contigs. The true order of the pieces
	* is not known and their order in this sequence record is
	* arbitrary. Gaps between the contigs are represented as
	* runs of N, but the exact sizes of the gaps are unknown.
	* This record will be updated with the finished sequence
	* as soon as it is available and the accession number will
	* be preserved.

	1 4259: contig of 4259 bp in length
	* 4260 4359: gap of 100 bp
	* 4360 26102: contig of 21743 bp in length
	* 26103 26202: gap of 100 bp
	* 26203 28547: contig of 2345 bp in length
	* 28548 28647: gap of 100 bp
	* 28648 49653: contig of 21006 bp in length
	* 49654 49753: gap of 100 bp

	* 49754 80134: contig of 30381 bp in length
	* 80135 80234: gap of 100 bp
	* 80235 83646: contig of 3412 bp in length
	* 83647 83746: gap of 100 bp
	* 83747 96061: contig of 12315 bp in length
	* 96062 96161: gap of 100 bp
	* 96162 103311: contig of 7150 bp in length
	* 103312 103411: gap of 100 bp
	* 103412 122508: contig of 19097 bp in length
	* 122509 124966: gap of 100 bp
	* 124967 125066: contig of 2358 bp in length
	* 125067 142955: gap of 100 bp
	* 142956 143056: gap of 100 bp
	* 143056 161736: contig of 18681 bp in length
	* 161737 161836: gap of 100 bp
	* 161837 169189: contig of 7353 bp in length
	* 169190 169289: gap of 100 bp
	* 169290 175251: contig of 5962 bp in length
	* 175252 175351: gap of 100 bp
	* 175352 181328: contig of 5977 bp in length
	* 181329 181428: gap of 100 bp
	* 181429 183863: contig of 2435 bp in length
	* 183864 183963: gap of 100 bp
	* 183964 195169: contig of 11206 bp in length
	* 195170 195289: gap of 100 bp
	* 195270 205272: contig of 10003 bp in length.
FEATURES	Location/Qualifiers
source	1. .205272
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="6"
	/clone="RP11-366H19"
	/clone_lib="RPCI-11.2"
misc_feature	1. 4259
	/note="assembly_fragment:00710"
	fragment_chain:1
misc_feature	4360. 26102
	/note="assembly_fragment:00448"
	fragment_chain:1
misc_feature	26203. 28547
	/note="assembly_fragment:01871"
	fragment_chain:1
misc_feature	28648. 49653
	/note="assembly_fragment:01605"
	fragment_chain:1
misc_feature	49754. 80134
	/note="assembly_fragment:01641"
	fragment_chain:1
misc_feature	80235. 83646
	/note="assembly_fragment:01500"
	fragment_chain:1
misc_feature	83747. 96061
	/note="assembly_fragment:01099"
	fragment_chain:1
misc_feature	96162. 103311
	/note="assembly_fragment:00756"
	fragment_chain:2
misc_feature	103412. 122508
	/note="assembly_fragment:01078"
	fragment_chain:2
misc_feature	122609. 124966
	/note="assembly_fragment:01675"
	fragment_chain:2
misc_feature	125067. 142955
	/note="assembly_fragment:01165"
	fragment_chain:3
misc_feature	143056. 161736

misc_feature 169290..175251
/note="assembly_fragment:00119"
misc_feature 175352..181328
/note="assembly_fragment:00401"
misc_feature 181429..183863
/note="assembly_fragment:01812"
misc_feature 183964..195169
/note="assembly_fragment:02127"
misc_feature 195270..205272
/note="assembly_fragment:01692"
clone_end:T7
vector_side:right"

BASE COUNT 53785 a 47341 c 47491 g 54940 t 1715 others
ORIGIN

Query Match 1.2% Score 22; DB 2; Length 205272;
Best Local Similarity 100.0%; Pred. No. 2;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1663 GGCCAGGGAGTGAGTGTAGAA 1684
|||||

Db 95161 GGCCAGGGAGTGAGTGTAGAA 95140

RESULT 33

AC093464

LOCUS

AC093464 208613 bp DNA linear HTG 26-AUG-2001
Mus musculus clone RP23-22511, WORKING DRAFT SEQUENCE, 23 unordered
pieces.

AC093464

AC093464.1 GI:15290910

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE Mus musculus.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 208613)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Mus musculus, clone RP23-22511

Unpublished

2 (bases 1 to 208613)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,W., Graham,L., Grand-Pierre,N.,
Hagos,B., Hearford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., Lacroque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrum,J.,
Menees,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupbach,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talames,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (26-AUG-2001) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

FEATURES

Location/Qualifiers

1..208613
/organism="Mus musculus"
/db_xref="taxon:10090"

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L13278

Center clone name: 225_L1

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 198685 bases at least Q40

Consensus quality: 202938 bases at least Q30

Consensus quality: 204617 bases at least Q20

Insert size: 200000; agarose-fp

Insert size: 206413; sum-of-contigs

Quality coverage: 9.3 in Q20 bases; agarose-fp

Quality coverage: 9.0 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 8002: contig of 8002 bp in length
* 8003 8102: gap of 100 bp
* 8103 8749: contig of 647 bp in length
* 8750 8849: gap of 100 bp
* 8850 9582: contig of 733 bp in length
* 9583 9682: gap of 100 bp
* 9683 10621: contig of 939 bp in length
* 10622 10721: gap of 100 bp
* 10722 11566: contig of 845 bp in length
* 11567 11666: gap of 100 bp
* 11667 12384: contig of 718 bp in length
* 12385 12484: gap of 100 bp
* 12485 13159: contig of 675 bp in length
* 13160 13259: gap of 100 bp
* 13260 13938: contig of 679 bp in length
* 13939 14038: gap of 100 bp
* 14039 15029: contig of 991 bp in length
* 15030 15129: gap of 100 bp
* 15130 17011: contig of 1882 bp in length
* 17012 17111: gap of 100 bp
* 17112 17861: contig of 750 bp in length
* 17862 17961: gap of 100 bp
* 17962 21075: contig of 3114 bp in length
* 21076 21175: gap of 100 bp
* 21176 24751: contig of 3576 bp in length
* 24752 24851: gap of 100 bp
* 24852 31676: contig of 6825 bp in length
* 31677 31776: gap of 100 bp
* 31777 35627: contig of 3851 bp in length
* 35628 35727: gap of 100 bp
* 35728 41367: contig of 5640 bp in length
* 41368 41467: gap of 100 bp
* 41468 47600: contig of 6133 bp in length
* 47601 47700: gap of 100 bp
* 47701 63154: contig of 15454 bp in length
* 63155 63254: gap of 100 bp
* 63255 78870: contig of 15616 bp in length
* 78871 78970: gap of 100 bp
* 78971 89838: contig of 10868 bp in length
* 89839 89938: gap of 100 bp
* 89939 105150: contig of 15212 bp in length
* 105151 105250: gap of 100 bp
* 105251 176270: contig of 71020 bp in length
* 176271 176370: gap of 100 bp
* 176371 208613: contig of 32243 bp in length.

```

/misc_feature /clone="RP23-225L1"
1. .8002 /clone_lib="RPC1-23 Female Mouse BAC"
/clone_end:SP6 /note="assembly_fragment
vector_side:left"
8103. .8749 /note="assembly_fragment"
8850. .9582 /note="assembly_fragment"
9683. 10621 /note="assembly_fragment"
10722. 11566 /note="assembly_fragment"
11667. 12384 /note="assembly_fragment"
12485. 13159 /note="assembly_fragment"
13260. 13938 /note="assembly_fragment"
14039. 15029 /note="assembly_fragment"
15130. 17011 /note="assembly_fragment"
17112. 17861 /note="assembly_fragment"
17962. 21075 /note="assembly_fragment"
21176. 24751 /note="assembly_fragment"
24852. 31676 /note="assembly_fragment"
31777. 35627 /note="assembly_fragment"
35728. 41367 /note="assembly_fragment"
41468. 47600 /note="assembly_fragment"
47701. 63154 /note="assembly_fragment"
63255. 78870 /note="assembly_fragment"
78971. 89838 /note="assembly_fragment"
89939. 105150 /note="assembly_fragment"
105251. 176270 /note="assembly_fragment"
176371. 208613 /note="assembly_fragment
clone_end:T7
vector_side:right"
BASE COUNT 50787 a 53175 c 52217 g 50228 t 2206 others
ORIGIN
Query Match 1.2%; Score 22; DB 2; Length 208613;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1635 GCGAGAGAGCGGAGGAGGCC 1656
|||||
Db 114047 GCGAGAGAGCGGAGGAGGCC 114068

RESULT 34
AC124604
LOCUS AC124604 223898 bp DNA linear HTG 08-AUG-2002
DEFINITION Mus musculus chromosome UNK clone RP23-81K14, WORKING DRAFT
SEQUENCE, 6 unordered pieces.
ACCESSION AC124604
VERSION AC124604.2 GI:22138688
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.

```

```

ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 223898)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 223898)
TITLE Direct Submission
JOURNAL McPherson,J.D. and Waterston,R.H.
AUTHORS 3 (bases 1 to 223898)
TITLE Direct Submission
JOURNAL Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
AUTHORS 3 (bases 1 to 223898)
TITLE Direct Submission
JOURNAL McPherson,J.D. and Waterston,R.H.
AUTHORS Submitted (08-AUG-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
COMMENT On Aug 8, 2002 this sequence version replaced gi:21426746.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BA0081K14
----- Summary Statistics -----
Sequencing vector: M13; 0%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 221926 bases at least Q40
Consensus quality: 22804 bases at least Q30
Consensus quality: 223445 bases at least Q20
Insert size: 224000; agarose-fp
Quality coverage: 13.05 in Q20 bases; agarose-fp
Quality coverage: 10.05 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1021: contig of 1021 bp in length
* 1022 1121: gap of unknown length
* 1122 5763: contig of 4642 bp in length
* 5764 5863: gap of unknown length
* 5864 55986: contig of 50123 bp in length
* 55987 56086: gap of unknown length
* 56087 222815: contig of 166728 bp in length
* 222815 222914: gap of unknown length
* 222915 223359: contig of 445 bp in length
* 223360 223459: gap of unknown length
* 223460 223898: contig of 439 bp in length.
FEATURES
source
location/Qualifiers
1. .223898
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP23-81K14"
misc_feature 1. .1021
/note="assembly_name:Contig13"
misc_feature 1122. .5763
/note="assembly_name:Contig47"
misc_feature 5864. .55986
/note="assembly_name:Contig48"
misc_feature 56087. .222814

```

```

misc_feature      /note="assembly_name:Contig49"
222915. .223359
misc_feature      /note="assembly_name:Contig24"
223460. .223898
/note="assembly_name:Contig29"
BASE COUNT      53864 a 54537 c 55221 g 59764 t      512 others
ORIGIN
Query Match      1.2%   Score 22; DB 2; Length 223898;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 CCTGGCCCTCTTGCACCACC 194
|||||
Db 157107 CCTGGCCCTCTTGCACCACC 157128

RESULT 35
AC090437
LOCUS
DEFINITION      Mus musculus chromosome 6 clone rp23-11f20 strain C57BL/6J, WORKING
DRAFT SEQUENCE, 13 unordered pieces.
AC090437
ACCESSION      AC090437.40 GI:22218506
VERSION
HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE      house mouse.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 264522)
Jiang, X., Song, L. and Roe, B.A.
Mus musculus BAC Clone rp23-11f20
Unpublished
2. (bases 1 to 264522)
Jiang, X., Song, L. and Roe, B.A.
Direct Submission
Submitted (21-FEB-2001) Department of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
3. (bases 1 to 264522)
Jiang, X., Song, L. and Roe, B.A.
Direct Submission
Submitted (14-AUG-2002) Department of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On Aug 14, 2002 this sequence version replaced gi:22165141.
----- Genome Center
Center: Department of Chemistry And Biochemistry
The University of Oklahoma
Center code:UOKNOR
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
2376 contig of 2375 bp in length
2476 gap of unknown length
2476 contig of 2859 bp in length
5335 gap of unknown length
5435 gap of unknown length
8379 contig of 2945 bp in length
8380 gap of unknown length
8479 gap of unknown length
12529 contig of 4050 bp in length
12530 gap of unknown length
12630 contig of 3220 bp in length
15849 gap of unknown length
15950 gap of unknown length
20147 contig of 4198 bp in length
20148 gap of unknown length
20248 contig of 7228 bp in length
27475 contig of 2375 bp in length
27476 gap of unknown length

```

```

* 27576 34464: contig of 6889 bp in length
* 34465 34564: gap of unknown length
* 34565 41578: contig of 7014 bp in length
* 41579 41678: gap of unknown length
* 41679 55200: contig of 13522 bp in length
* 55201 55300: gap of unknown length
* 55301 89659: contig of 34359 bp in length
* 89660 89759: gap of unknown length
* 89760 155919: contig of 66160 bp in length
* 155920 156019: gap of unknown length
* 156020 264522: contig of 108503 bp in length.
FEATURES
Location/Qualifiers
1..264522
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/chromosome="6"
/clone="rp23-11f20"
/clone_lib="RPI-23 Female (C57BL/6J) Mouse BAC Library"
BASE COUNT      69390 a 63608 c 62531 g 67771 t 1222 others
ORIGIN
Query Match      1.2%   Score 22; DB 2; Length 264522;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1852 ATGAATCAGCTGAAAAA 1873
|||||
Db 249233 ATGAATCAGCTGAAAAA 249254

RESULT 36
HS21C102
LOCUS
DEFINITION      Homo sapiens chromosome 21 segment HS21C102.
ACCESSION      AL163302 AP001757 BA000005
VERSION
KEYWORDS
SOURCE      human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 340000)
Hattori, M., Fujiyama, A., Taylor, T.D., Watanabe, H., Yada, T.,
Park, H.S., Toyoda, A., Ishii, K., Totoki, Y., Choi, D.K., Soeda, E.,
Ohki, M., Takagi, T., Sakaki, Y., Taudien, S., Blechschmidt, K.,
Polley, A., Menzel, U., Delabar, J., Kumpf, K., Lehmann, R.,
Patterson, D., Reichwald, K., Rump, A., Schillhabel, M., Schudy, A.,
Zimmermann, W., Rosenthal, A., Kudoh, J., Shibuya, K., Kawasaki, K.,
Asakawa, S., Shintani, A., Sasaki, T., Nagamine, K., Mitsuyma, S.,
Antonarakis, S.E., Minoshima, S., Shimizu, N., Nordsiek, G.,
Hornischer, K., Brandt, P., Scharfe, M., Schoen, O., Desario, A.,
Reichelt, J., Kauer, G., Bloeker, H., Ramser, J., Beck, A., Klages, S.,
Hennig, S., Riesselmann, L., Dagand, E., Wehrmeyer, S., Borzym, K.,
Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and
Yaspo, M.L.
Direct Submission
Submitted (05-MAY-2000) The Chromosome 21 Mapping and Sequencing
Consortium: * RIKEN Genomic Sciences Center, Human Genome Research
Group * Institute of Molecular Biotechnology, Genome Analysis *
Keio University School of Medicine, Dept. of Molecular Biology *
GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular
Genetics (addresses see below)
The Chromosome 21 Mapping and Sequencing Consortium consists of
* RIKEN Genomic Sciences Center, Human Genome Research Group, *
Sagamihara 228-8555, Japan,
* e.mail: sakaki@gsc.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
and
* Institute of Molecular Biotechnology, Genome Analysis, *
Beutenbergstrasse 11, D-07745 Jena, Germany,
* e.mail: gscj-submit@genome.imb-jena.de
* URL: http://genome.imb-jena.de/

```



```

and
* Keio University School of Medicine, Dept. of Molecular Biology, *
  Tokyo 160-8582, Japan,
* e.mail: shimizudmb-med.keio.ac.jp
* URL: http://adenine.dmb.med.keio.ac.jp/
and
* GBF, Dept. of Genome Analysis,
* Mascheroder Weg 1, D-39124 Braunschweig, Germany, * e.mail:
  info.genome@gbf.de
* URL: http://genome.gbf.de/
and
* Max-Planck Institute for Molecular Genetics,
* Ihnestrasse 73, D-14195 Berlin, Germany,
* e.mail: info.chr21molgen.mpg.de
* URL: http://chr21.rz-berlin.mpg.de/.
  Location/Qualifiers
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      /db_xref="taxon:9606"
      /chromosome="21"
      /map="21q22.3"
    <1..56887
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      /map="21q22.3"
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    /clone_lib="LL21NCO2-Q Cosmid library"
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    /clone_lib="RPC11,3-5 PAC library"
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      /db_xref="taxon:9606"
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      /map="21q22.3"
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    /clone_lib="BAC library"
    /note="Accession No. AL133493"
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repeat_region

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3570..3942
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complement(4033..4108)
/note="L1MC4"
/rpt_family="LINE/L1"
/rpt_type=DISPERSED
complement(4146..4440)
/note="AluSx"
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/rpt_type=DISPERSED
complement(4462..4540)
/note="L1MC4"
/rpt_family="LINE/L1"
/rpt_type=DISPERSED
complement(4639..4938)
/note="L1MC4"
/rpt_family="LINE/L1"
/rpt_type=DISPERSED
6323..6499
/note="(CA)n"
/rpt_family="Simple_repeat"
/rpt_type=TANDEM
7939..8070
/note="MT1A1"
/rpt_family="LTR/MaLR"
/rpt_type=DISPERSED
8831..9009
/note="(CA)n"
/rpt_family="Simple_repeat"
/rpt_type=TANDEM
9039..9086
/note="(CA)n"
/rpt_family="Simple_repeat"
/rpt_type=TANDEM
9681..9973
/note="AluSq"
/rpt_family="SINE/Alu"
/rpt_type=DISPERSED
10026..10210
/note="MT2CB"
/rpt_family="LTR/Retroviral"
/rpt_type=DISPERSED
complement(10352..10487)
/note="L1MC1"
/rpt_family="LINE/L1"
/rpt_type=DISPERSED
10513..10547
/note="(CA)n"
/rpt_family="Simple_repeat"
/rpt_type=TANDEM
10615..10676
/note="(TCCA)n"
/rpt_family="Simple_repeat"
/rpt_type=TANDEM
10711..12174
/note="L1MC1"
/rpt_family="LINE/L1"
/rpt_type=DISPERSED
12376..12458
/note="L1p"
/rpt_family="LINE/L1"
/rpt_type=DISPERSED
complement(12547..13571)
/note="L1PA10"
/rpt_family="LINE/L1"
/rpt_type=DISPERSED
13565..15294
/note="L1PA10"
/rpt_family="LINE/L1"
/rpt_type=DISPERSED
complement(15672..15818)

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/rpt_type=DISPERSED
complement(16149..16241)
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/rpt_family="DNA/MER1_type"
/rpt_type=DISPERSED
19408..19479
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/rpt_family="DNA/MER1_type"

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Query Match 1.2% Score 22; DB 9; Length 340000;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 605 GGGCTGTGGCGGCACCTGTGC 626
|||||
Db 2240 GGGCTGTGGCGGCACCTGTGC 2261

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RESULT 37

LOCUS BC033766

DEFINITION Homo sapiens, clone MGC:45023 IMAGE:4177041, mRNA, complete cds.

ACCESSION BC033766

VERSION BC033766.1 GI:21707448

KEYWORDS MGC.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Strausberg,R.

Direct Submission

Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs@mail.nih.gov

Tissue Procurement: David N. Louis, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc.mgc@nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 68 Row: b Column: 21
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10835086.

FEATURES

source

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1..1050
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/db_xref="taxon:9606"
/clone="MGC:45023 IMAGE:4177041"
/tissue_type="Brain, anaplastic oligodendroglioma with

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1p/19q loss"
/clone_lib="NCI_CGAP_Brn67"
/lab_host="DHI08"
/note="Vector: pCMV-SPORT6"
25..351
/codon_start=1
/product="Unknown (protein for MGC:45023)"
/protein_id="AAH33766.1"
/db_xref="GI:21707449"
/translation="MAAPCLLRGRGAGALKTMLOEAQVFRGLASTVLSAASGKSEKG
QFQNSKKQSPKPKPAPVPAEPFDNTYKNLQHDYSTVTFDLNLELSKFRMPQSSG
RESPRH"

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CDS

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BASE COUNT 292 a 270 c 225 g 263 t
ORIGIN

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Query Match 1.1% Score 21; DB 9; Length 1050;
 Best Local Similarity 100.0%; Pred. No. 7.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1856 ATCAGCTGAAAAAATAAAAA 1876
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Db 986 ATCAGCTGAAAAAATAAAAA 1006

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RESULT 38

LOCUS RLE431175

DEFINITION Rhizobium leguminosarum bv. viciae plasmid pRL6JI fixA,B,C, & W genes, deltanifH gene and ORFs 71,79 & 5.

ACCESSION AJ431175

VERSION AJ431175.1 GI:18857702

KEYWORDS deltanifH gene; fixA gene; fixB gene; fixC gene; fixW gene; ORF5; ORF71; ORF79.

SOURCE Rhizobium leguminosarum bv. viciae.

ORGANISM Rhizobium leguminosarum bv. viciae

Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.

REFERENCE 1

AUTHORS Martinez,M.

TITLE Regulacion simbiotica de la expresion del sistema hidrogenasa por NifA en R. leguminosarum bv. viciae

JOURNAL Thesis (2000) Department of Biotechnologia, Universidad Politecnica

REFERENCE 2

AUTHORS Martinez,M., Palacios,J.M., Imperial,J. and Ruiz-Argueso,T.

TITLE Autoregulacion of nifA in symbiosis of Rhizobium leguminosarum bv. viciae UPW791

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 5061)

AUTHORS Martinez,M.

TITLE Direct Submission

JOURNAL Submitted (14-FEB-2002) Martinez M., Biotechnologia, ETSI Agronomos

Uni. Politecnica Madrid, Ciudad Universitaria s/n, Madrid, SPAIN

FEATURES

source

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/organism="Rhizobium leguminosarum bv. viciae"
/specific_host="Poa"
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/plasmid="pRL6JI"
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/gene="deltanifH"
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/codon_start=1
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/protein_id="CAD24014.1"
/db_xref="GI:18857703"
/translation="MAALRQIAFYKGKIGKSTTSQNTLAALVDHVPVPIIRIGG
YAQ"

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complement(223..312)

gene="deltanifH"

complement(223..227)

RBS

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/note="RpoN-binding consensus site"
complement(399..401)
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complement(411..413)
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959..961
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972..974
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1039..1054
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ORF71"
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1107..1292
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/db_xref="GI:18857705"
/translations="MASCICIRPHLPVTVTITLSEIRINVTTHPQKPFQKTRSP
AFVQPMERAPLFEIGNATRADTWPEGLIPRARS"
1418..1433
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fixw"
1512..1514
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1515..2072
/gene="fixw"
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1527..2072
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/protein_id="CAD24017.1"
/db_xref="GI:18857706"
/translation="MASSLSGSPAPSIKALDWLURGEPLSYFQLDKIYVVFSTTCG
YLGPEISDLAKLHKFSDTGVFEFGIAASEKAATADARAGVDASITKSLPTNIRMG
FDRSGEMDEWLKASLSFHPVKTFFVDRDGSIAFIGDLVMLQDVLPKVLDGTRASAE
AKNAEKERIAEGETYAAQIVS"
2003..2007
/gene="fixw"
/note="ORF5"
2014..2217
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/codon_start=1
/transl_table=11
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/protein_id="CAD24018.1"
/db_xref="GI:18857707"

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2234..2237
/gene="fixA"
2249..3100
/gene="fixA"
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/transl_table=11
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/protein_id="CAD24019.1"
/db_xref="GI:18857708"
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ALQVRNYGGEVTVLTGMPMAEQALRRALKHAGRAVLLTRHRFAGSDTLATSYALS
QAVAKIGESYGADIVFTGQTIIDGTAQVGGIAKRLNLQQLTYTVTKIVSIDTSHRE
LMVERHAESGTQMLKSTLPCLITVLEGVNAIRGSLDDAFRAARSPVLKWAADAGIG
ELTKCGLRGSPTVVKRVFAPGPRAEKAMQMDINDKTLAEVAADTAAAIIFAREPVLERK
LTSHGNE"
3223..4254
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/transl_table=11
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/db_xref="GI:18857709"
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PAIEEFAYGADIAVLVPSPLLYNVRNEPFTKALDTLVTTHKPEILLGATTLGRDLA
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ATPQREBKPIGRVIOHELTWVEEAIVTKVLAFLCNDGSEQSDLSNDIVVGGIGLGA
AGNLOYLRNLATTIGGVCGRPVVKGMPADRCQFQSGSHQITRPKLYIAAGISGAVQ
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4231..4235
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4241..5061
/gene="fixC"
4241..>5061
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/codon_start=1
/transl_table=11
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/protein_id="CAD24021.1"
/db_xref="GI:18857710"
/translation="MTKSKFDAIVIGAGMSGNAAAYSMARRGLKVLQLERGEHSGSKN
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YTTITRAQDKNFESSKVRAGGTVLCETATKLRDRSGSVIGYTDREGGVILLADV
LAEGVNLGTRAGRDMPKPNVLAVERHMPPEVTAERFGLTGEGSCVIEAGGT
ISRGMAGLGFLYTNKESISVGICLVSLAESMENPYRLLDAPKQHSIRPLLAGS"
BASE COUNT 1150 a 1398 c 1463 g 1050 t
ORIGIN

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Query Match 1.1%; Score 21; DB 1; Length 5061;
 Best Local Similarity 100.0%; Pred. No. 7.4;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1756 GCCAGTGGTCCAAAAGGCTG 1776
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Db 3942 GCCAGTGGTCCAAAAGGCTG 3962

RESULT 39

HSU22027/c

LOCUS

DEFINITION

ACCESSION

7215 bp DNA linear PRI 01-JAN-1997
 Human cytochrome P450 (CYP2A6V2) gene, complete cds.

```

VERSION      U22027.1  GI:1008461
KEYWORDS     Homo sapiens.
SOURCE       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM     Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 7215)
AUTHORS      Fernandez-Salguero, P., Hoffman, S.M., Cholerton, S., Mohrenweiser, H.,
              Raunio, H., Rautio, A., Pelkonen, O., Huang, J.D., Evans, W.E.,
              Idle, J.R., et al.
TITLE        A genetic polymorphism in coumarin 7-hydroxylation: sequence of the
              human CYP2A6 genes and identification of variant CYP2A6 alleles
JOURNAL      Am. J. Hum. Genet. 57 (3), 651-660 (1995)
MEDLINE      95397851
PUBMED       7668294
REFERENCE    2 (bases 1 to 7215)
AUTHORS      Fernandez-Salguero, P.
TITLE        Direct Submission
JOURNAL      Submitted (01-MAR-1995) Pedro Fernandez-Salguero, National
              Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20894, USA
FEATURES     Location/Qualifiers
              source
                1..7215
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                /db_xref="taxon:9606"
                782..790
                791..6489
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                4257..4398,4873..5060,5577..5718,6308..6489)
                /gene="CYP2A6V2"
                /codon_start=1
                /product="cytochrome p450"
                /protein_id="AAB40518.1"
                /db_xref="GI:1008462"
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                EQATPDWFKGVGVFVSGNCRAKQLLRPAITLRFQGVKGRGIEREESGFLIEAI
                RSTHGANTDPTFFLSTVSNVSIIVFGDRFDYKKEFLSLMLMIGIFQFTSTGTQ
                LYEMFSSVMKHLPGQQAQFLLQLEDFIARKVEHNTQDLPNSPRDFIDSLRMQ
                EEKNPTEFLKLMMSITNLFIAGTETVSTLHYGELLMKHPEVEAKVHEIDRV
                IGKRPQFEDRKNMYPMEAVTHEIQRFCDVIPMSLARVKDTRDFFLPKGIEVF
                PMLGSVLDRLEFFSNRDNFPQHELKGQKRDFAEVPFSIRKNCIEGELARMELF
                LFTTVMONFLKSSQSPKIDVSPKHVGFATIPRNYTMSFLPR"
                791..970
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                /number=1
                1237..1399
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                /gene="CYP2A6V2"
                /number=3
                2499..2659
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                /number=4
                3207..3383
                /gene="CYP2A6V2"
                /number=5
                4257..4398
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                /number=6
                4873..5060
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                6308..6489
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                /number=9
                6490..6744
                1646 a 2196 c 1746 g 1627 t
              3'UTR
              BASE COUNT
              ORIGIN

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Query Match      1.1%; Score 21; DB 9; Length 7215;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1634 GGGCAGAGAGAGCGGAGG 1654
      |||||
Db 1605 GGGCAGAGAGAGCGGAGG 1585

RESULT 40
A47885/c A47885 7216 bp DNA linear PAT 07-MAR-1997
LOCUS     Sequence 3 from Patent WO9534679.
ACCESSION A47885
VERSION   A47885.1 GI:2301752
KEYWORDS  .
SOURCE    unidentified.
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 7216)
AUTHORS   Gonzalez, F.J. and Idle, J.R.
TITLE     DEFECTS IN DRUG METABOLISM
JOURNAL   Patent: WO 9534679-A 3 21-DEC-1995;
          US HEALTH (US)
COMMENT   Other publication AU 2860295 960105.
FEATURES  Location/Qualifiers
            1..7216
            /organism="unidentified"
            /db_xref="taxon:32644"
            1646 a 2196 c 1746 g 1627 t
            1 others
          BASE COUNT
          ORIGIN

Query Match      1.1%; Score 21; DB 6; Length 7216;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1634 GGGCAGAGAGAGCGGAGG 1654
      |||||
Db 1605 GGGCAGAGAGAGCGGAGG 1585

RESULT 41
AR069321/c AR069321 7216 bp DNA linear PAT 18-FEB-2000
LOCUS     Sequence 3 from patent US 5891633.
ACCESSION AR069321
VERSION   AR069321.1 GI:7220209
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 7216)
AUTHORS   Gonzalez, F.J. and Idle, J.R.
TITLE     Defects in drug metabolism
JOURNAL   Patent: US 5891633-A 3 06-APR-1999;
          Location/Qualifiers
            1..7216
            /organism="unknown"
            1646 a 2196 c 1746 g 1627 t
            1 others
          BASE COUNT
          ORIGIN

Query Match      1.1%; Score 21; DB 6; Length 7216;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1634 GGGCAGAGAGAGCGGAGG 1654
      |||||
Db 1605 GGGCAGAGAGAGCGGAGG 1585

RESULT 42
HSU22028/c

```

Mon Dec 30 09:16:06 2002

us-09-944-896-49.oli10.rge

```

LOCUS       HSU22028               8778 bp    DNA        linear        PRI 01-JAN-1997
DEFINITION   Human cytochrome P450 (CYP2A13) gene, complete cds.
ACCESSION    U22028
VERSION      U22028.1  GI:1777436
KEYWORDS     Homo sapiens.
SOURCE       Homo sapiens.
ORGANISM     Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 8778)
AUTHORS      Fernandez-Salguero,P., Hoffman,S.M., Cholerton,S., Mohrenweiser,H.,
Raunio,H., Rautio,A., Pelkonen,O., Huang,J.D., Evans,W.E.,
Idle,J.R. et al.
TITLE        A genetic polymorphism in coumarin 7-hydroxylation: sequence of the
human CYP2A genes and identification of variant CYP2A6 alleles
JOURNAL      Am. J. Hum. Genet. 57 (3), 651-660 (1995)
MEDLINE      95397851
PUBMED       7668294
REFERENCE    2 (bases 1 to 8778)
AUTHORS      Fernandez-Salguero,P.
TITLE        Direct Submission
JOURNAL      Submitted (01-MAR-1995) Pedro Fernandez-Salguero, National
Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20894, USA
COMMENT      On Jan 14, 1997 this sequence version replaced gi:1008463.
FEATURES             Location/Qualifiers
     source          1..8778
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     652..660
                     661..8137
                     /gene="CYP2A13"
                     join(661..840,1117..1279,2232..2381,2590..2750,3917..4093,
                     5813..5954,6440..6627,7155..7296,7956..8137)
                     /gene="CYP2A13"
                     /codon_start=1
                     /product="cytochrome P450"
                     /protein_id="BAB40519.1"
                     /db_xref="GI:1777437"
     translation     "MLASGLLLVILLACLTVMVLMVNRKSRGKLPDPPPLPFI
NYLQNTQNTNMLKISERYGPVFTIHLPFRVVLGHDVAKALVDQAEFSRG
EQATDMFKGYFAFSNGERAKQLRRESIATLRFVGKRGIERIEEAGFLDAL
RGTHGANDTFYFLSRTVSNVISIVGDFRDEKFEFLSLRMLGRFPQGTSTGQ
LYEMSSVMKHLPGPOQAQKLEQLEDFIAKVEHQNRTLDPNSPRDFIDSLIRMQ
BEENKPTVEFLKLVMTLNLFFAGTETVSTLRYGLLLMKHPVEAKVHEEDRV
TKNRQPFEDRAKMPYTEAVTHEIQEGDMLPMGLAHVKNKDTKFRDFLPKGTVEF
PMLGSLRDPFRFSSNPQDCSQHFELDEKQPKSDAFVFPFSIGKRYCFEGELARMELF
LFTTIMQNFRTKSPQSKPDIDVSPKHVGFATIPRNYTMSFLPR"
     exons           661..840
                     /gene="CYP2A13"
                     /number=1
                     1117..1279
                     /gene="CYP2A13"
                     /number=2
                     2232..2381
                     /gene="CYP2A13"
                     /number=3
                     2590..2750
                     /gene="CYP2A13"
                     /number=4
                     3917..4093
                     /gene="CYP2A13"
                     /number=5
                     5813..5954
                     /gene="CYP2A13"
                     /number=6
                     6440..6627
                     /gene="CYP2A13"
                     /number=7
                     7155..7296
                     /gene="CYP2A13"
                     /number=8
                     7956..8137
                     /gene="CYP2A13"

3'UTR       /number=9
            8138..8390
BASE COUNT   2030 a 2663 c 2014 g 2071 t
ORIGIN
Query Match      1.1%; Score 21; DB 9; Length 8778;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1634 GGGCAGAGAGGCGAGGAGG 1654
    |||
Db 1492 GGGCAGAGAGGCGAGGAGG 1472

RESULT 43
LOCUS         A47886/c              8779 bp    DNA        linear        PAT 07-MAR-1997
DEFINITION    Sequence 4 from Patent WO9534679.
ACCESSION     A47886
VERSION       A47886.1  GI:2301753
KEYWORDS      unidentified.
SOURCE        unidentified.
ORGANISM      unidentified.
REFERENCE     1 (bases 1 to 8779)
AUTHORS       Gonzalez,F.J. and Idle,J.R.
TITLE         DEFECTS IN DRUG METABOLISM
JOURNAL       Patent: WO 9534679-A 4 21-DEC-1995;
              US HEALTH (US)
COMMENT       Other publication AU 2860295 960105.
FEATURES             Location/Qualifiers
     source          1..8779
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT   2030 a 2663 c 2015 g 2071 t
ORIGIN
Query Match      1.1%; Score 21; DB 6; Length 8779;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1634 GGGCAGAGAGGCGAGGAGG 1654
    |||
Db 1493 GGGCAGAGAGGCGAGGAGG 1473

RESULT 44
LOCUS         AR069322/c           8779 bp    DNA        linear        PAT 18-FEB-2000
DEFINITION    Sequence 4 from patent US 5891633.
ACCESSION     AR069322
VERSION       AR069322.1  GI:7220210
KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 8779)
AUTHORS       Gonzalez,F.J. and Idle,J.R.
TITLE         Defects in drug metabolism
JOURNAL       Patent: US 5891633-A 4 06-APR-1999;
              Location/Qualifiers
FEATURES             Location/Qualifiers
     source          1..8779
                     /organism="unknown"
BASE COUNT   2030 a 2663 c 2015 g 2071 t
ORIGIN
Query Match      1.1%; Score 21; DB 6; Length 8779;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1634 GGGCAGAGAGGCGAGGAGG 1654
    |||
Db 1493 GGGCAGAGAGGCGAGGAGG 1473

```

```

RESULT 45
AL807743
LOCUS
DEFINITION
    Human DNA sequence from clone RP11-1047H1 on chromosome X, complete
    sequence.
ACCESSION
    AL807743
VERSION
    AL807743.6
KEYWORDS
    HTG.
SOURCE
    Homo sapiens.
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 30826)
AUTHORS
    Chapman, J.
TITLE
    Direct Submission
JOURNAL
    Submitted (18-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
    Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clonerequest@sanger.ac.uk
    humquery@sanger.ac.uk
COMMENT
    On Jul 19, 2002 this sequence version replaced gi:21694492.
    ----- Genome Center
    Center: Wellcome Trust Sanger Institute
    Center code: SC
    Web site: http://www.sanger.ac.uk
    Contact: humquery@sanger.ac.uk
    -----
    During sequence assembly data is compared from overlapping clones.
    Where differences are found these are annotated as variations
    together with a note of the overlapping clone name. Note that the
    variation annotation may not be found in the sequence submission
    corresponding to the overlapping clone, as we submit sequences with
    only a small overlap as described above.
    This sequence was finished as follows unless otherwise noted: all
    regions were either double-stranded or sequenced with an alternate
    chemistry or covered by high quality data (i.e., phred quality >=
    30); an attempt was made to resolve all sequencing problems, such
    as compressions and repeats; all regions were covered by at least
    one plasmid subclone or more than one M13 subclone; and the
    assembly was confirmed by restriction digest. The following
    abbreviations are used to associate primary accession numbers given
    in the feature table with their source databases: Em, EMBL; Sw,
    SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP
    database can be found at
    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
    was generated from part of bacterial clone contigs of human
    chromosome X, constructed by the Sanger Centre Chromosome X Mapping
    Group. Further information can be found at
    http://www.sanger.ac.uk/HGP/ChrX
    RP11-1047H1 is from the library RPCI-11.4 constructed by the group
    of Pieter de Jong. For further details see
    http://www.chori.org/bacpac/home.htm
    VECTOR: pBAC3.6.
    Location/Qualifiers
        source
            1..30826
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /chromosome="X"
                /clone="RP11-1047H1"
                /clone_lib="RPCI-11.4"
BASE COUNT
    9154 a 6286 c 6465 g 8921 t
ORIGIN
    Query Match 1.1%; Score 21; DB 9; Length 30826;
    Best Local Similarity 100.0%; Pred. No. 7.6;
    Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1842 GTATTAAATTATGATCAGCT 1862
    |||||
    Db 8393 GTATTAAATTATGATCAGCT 8413
    |||||
    RESULT 46
HSDJ127L3/c
LOCUS
DEFINITION
    Human DNA sequence from clone RP1-127L3 on chromosome 11p13
    Contains GSSs and STSs, complete sequence.
ACCESSION
    AL096793
VERSION
    AL096793.20
KEYWORDS
    HTG.
SOURCE
    human.
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 73198)
AUTHORS
    Direct Submission
TITLE
    Submitted (29-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
    CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
    requests: clonerequest@sanger.ac.uk
COMMENT
    On Sep 29, 2000 this sequence version replaced gi:10178889.
    During sequence assembly data is compared from overlapping clones.
    Where differences are found these are annotated as variations
    together with a note of the overlapping clone name. Note that the
    variation annotation may not be found in the sequence submission
    corresponding to the overlapping clone, as we submit sequences with
    only a small overlap as described above.
    The following abbreviations are used to associate primary accession
    numbers given in the feature table with their source databases:
    Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
    on the WORMPEP database can be found at
    http://www.sanger.ac.uk/Projects/C_elegans/wormpep IMPORTANT: This
    sequence is not the entire insert of clone RP1-127L3 it may be
    shorter because we sequence overlapping sections only once, except
    for a 100 base overlap.
    The true left end of clone RP1-69B10 is at 73099 in this sequence.
    The true right end of clone RP1-181J22 is at 100 in this sequence.
    This sequence has been finished according to sequence map criteria
    as follows. An attempt is made to resolve all sequencing problems,
    such as compressions and repeats, but not necessarily within known
    annotated repeat sequence elements. Where the sequence is
    ambiguous, there is an annotation using the 'unsure' feature key.
    This sequence was generated by the Sanger Centre from a human
    chromosome 11 bacterial clone contig constructed by Niederfuhr A.
    Hummerich H, Gavin B, Boyle S, Little PF, Gessler M. Genomics 1998
    Oct 15;53(2):155-63
    RP1-127L3 is from the library RPCI-1 constructed by the group of
    Pieter de Jong. For further details see
    http://www.chori.org/bacpac/home.htm
    VECTOR: pCIPAC2.
    Location/Qualifiers
        source
            1..73198
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /chromosome="11"
                /map="p13"
                /clone="RP1-127L3"
                /clone_lib="RPCI-1"
repeat_region
    1..700
        /note="LIMA3 repeat: matches 5524..6214 of consensus"
repeat_region
    701..1001
        /note="AluSc repeat: matches 1..296 of consensus"
repeat_region
    1002..1081
        /note="LIMA3 repeat: matches 6214..6294 of consensus"
repeat_region
    1210..1334
        /note="FLAM_A repeat: matches 1..100 of consensus"
repeat_region
    1335..1386
        /note="26 copies 2 mer ta 86% conserved"
repeat_region
    1391..1380
        /note="LIPA3 repeat: matches 3636..5925 of consensus"
repeat_region
    3681..3909
        /note="SVA repeat: matches 3..231 of consensus"
repeat_region
    3910..7547
        /note="LIPA3 repeat: matches 1..3637 of consensus"
repeat_region
    7625..7933
        /note="LIM2 repeat: matches 1555..1830 of consensus"

```

```
repeat_region /note=.8595 repeat: matches 5852. .6481 of consensus"
repeat_region 8596. .9316 /note="L1PA10 repeat: matches 5439. .6159 of consensus"
repeat_region 9317. .9330 /note="L1MC4 repeat: matches 6481. .6493 of consensus"
repeat_region 9331. .9639 /note="AluX repeat: matches 1. .309 of consensus"
repeat_region 9640. .10077 /note="L1MC4 repeat: matches 6493. .6911 of consensus"
repeat_region 10078. .10385 /note="AluJo repeat: matches 1. .289 of consensus"
repeat_region 10386. .10465 /note="L1MC4 repeat: matches 6911. .7005 of consensus"
repeat_region 10466. .10762 /note="AluSg1 repeat: matches 1. .297 of consensus"
repeat_region 10763. .10873 /note="L1MC4 repeat: matches 7005. .7234 of consensus"
repeat_region 10916. .11374 /note="L1MC3 repeat: matches 7078. .7523 of consensus"
repeat_region 11373. .11811 /note="L1M4 repeat: matches 2572. .3021 of consensus"
repeat_region 11798. .12026 /note="L1MD repeat: matches 1239. .1464 of consensus"
repeat_region 12863. .13196 /note="MER44A repeat: matches 2. .332 of consensus"
repeat_region 13197. .13723 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 13723. .15327 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 15327. .15562 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 15562. .16738 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 16738. .17316 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 17316. .17563 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 17563. .18592 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 18592. .19079 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 19079. .19658 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 19658. .19912 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 19912. .20139 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 20139. .20634 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 20634. .21772 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 21772. .22112 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 22112. .22843 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 22843. .23577 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 23577. .25711 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 25711. .26172 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 26172. .27088 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 27088. .27514 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 27514. .28739 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 28739. .29040 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 29040. .30391 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 30391. .32607 /note="L1MC3 repeat: matches 2. .332 of consensus"
repeat_region 32607. .34340 /note="L1MC3 repeat: matches 2. .332 of consensus"
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repeat_region /note="MER52A repeat: matches 1. .1755 of consensus"
repeat_region 34341. .34437 /note="HAL1 repeat: matches 1500. .1583 of consensus"
repeat_region 34437. .35236 /note="AluSg repeat: matches 1. .286 of consensus"
repeat_region 35236. .36916 /note="AluJo repeat: matches 1. .304 of consensus"
repeat_region 36916. .37309 /note="FLAM_A repeat: matches 2. .130 of consensus"
repeat_region 37309. .37880 /note="MIR repeat: matches 1. .143 of consensus"
repeat_region 37880. .38434 /note="L1 copies 2 mer ta 100% conserved"
repeat_region 38434. .38855 /note="L1PA5 repeat: matches 5738. .6137 of consensus"
repeat_region 38855. .39347 /note="L1 repeat: matches 2550. .2687 of consensus"
repeat_region 39347. .39674 /note="L2 repeat: matches 2608. .2746 of consensus"
repeat_region 39674. .40011 /note="L1MC4 repeat: matches 7228. .7508 of consensus"
repeat_region 40011. .40322 /note="AluY repeat: matches 1. .311 of consensus"
repeat_region 40322. .40525 /note="L1PA15 repeat: matches 5958. .6157 of consensus"
repeat_region 40525. .40595 /note="L1MC4 repeat: matches 7516. .7587 of consensus"
repeat_region 40595. .40860 /note="AluSx repeat: matches 44. .309 of consensus"
repeat_region 40860. .41191 /note="L1MC4 repeat: matches 7587. .7888 of consensus"
repeat_region 41191. .41455 /note="AluJo repeat: matches 1. .250 of consensus"
repeat_region 41455. .41898 /note="AluSg repeat: matches 1. .288 of consensus"
repeat_region 41898. .42516 /note="L1 copies 2 mer aa 92% conserved"
repeat_region 42516. .42734 /note="match: STS: Em:G06939"
repeat_region 42734. .43246 /note="AluSx repeat: matches 3. .297 of consensus"
repeat_region 43246. .43878 /note="L1PA6 repeat: matches 6004. .6141 of consensus"
repeat_region 43878. .44795 /note="L1P repeat: matches 3614. .4523 of consensus"
repeat_region 44795. .45290 /note="match: GSS: Em:A0812912"
repeat_region 45290. .45237 /note="match: GSS: Em:AQ237862"
repeat_region 45237. .45296 /note="match: STS: Em:G06966"
repeat_region 45296. .45293 /note="match: GSS: Em:A0821283"
repeat_region 45293. .45216 /note="match: GSS: Em:AQ436325"
repeat_region 45216. .45216 /note="match: GSS: Em:AQ436325"
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Query Match 1.1%; Score 21; DB 9; Length 73198;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1856 ATCAGCTGAAAAA 1876
Db 32330 ATCAGCTGAAAAA 32310

RESULT 47
AC078903

LOCUS AC078903 95359 bp DNA linear PRI 17-JUL-2002
DEFINITION Homo sapiens chromosome 17, clone RP11-1084K4, complete sequence.
ACCESSION AC078903
VERSION AC078903.11 GI:21886885
KEYWORDS HTG.
SOURCE human.

repeat_region 10889..10967
/rpt_family="(TG)n"
repeat_region 11419..11495
/rpt_family="MIR"
repeat_region 12567..12629
/rpt_family="Cr-rich"
repeat_region 13649..13694
/rpt_family="(CCCC)n"
unsure 15951..15956
/note="<30 qual SNGL region"
repeat_region 16009..16108
/rpt_family="(CA)n"
repeat_region complement(16298..16402)
/rpt_family="L3"
repeat_region 16403..16705
/rpt_family="AluSb"
repeat_region 16705..17002
/rpt_family="AluSx"
repeat_region complement(17003..17086)
/rpt_family="L3"
repeat_region complement(17603..17767)
/rpt_family="AluJb"
repeat_region 18379..18568
/rpt_family="MIR3"
repeat_region complement(18996..19107)
/rpt_family="Charlie8"
repeat_region 19358..19430
/rpt_family="MIR"
repeat_region 19823..20000
/rpt_family="MIR"
repeat_region complement(22396..22505)
/rpt_family="MIR"
repeat_region 23219..23293
/rpt_family="MIR"
repeat_region 23868..23907
/rpt_family="(CA)n"
repeat_region 23983..24034
/rpt_family="(CA)n"
repeat_region 24608..24677
/rpt_family="MIR3"
repeat_region 24698..24863
/rpt_family="MIR3"
repeat_region 25028..25226
/rpt_family="LIME4A"
repeat_region 27634..27665
/rpt_family="(A)n"
repeat_region 27815..27837
/rpt_family="GC-rich"

Query Match 1.1%; Score 21; DB 9; Length 95359;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAGGCGAGGAGGCGAGTGAGG 1663
|||||
Db 66420 GAGGCGAGGAGGCGAGTGAGG 66440

RESULT 48
AC010494 105448 bp DNA linear PRI 18-APR-2000
LOCUS Homo sapiens chromosome 16 clone CTD-2349B8, complete sequence.
DEFINITION
AC010494
VERSION AC010494.4 GI:7109400
KEYWORDS HTG.

SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 105448)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Unpublished

REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 105448)
DOE Joint Genome Institute.
Direct Submission

Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

3 (bases 1 to 105448)
DOE Joint Genome Institute and Stanford Human Genome Center.

REFERENCE
AUTHORS
TITLE
JOURNAL

Direct Submission
Submitted (29-FEB-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA

REFERENCE
AUTHORS
TITLE
JOURNAL

4 (bases 1 to 105448)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission

Submitted (18-APR-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA

On Feb 29, 2000 this sequence version replaced gi:6938856.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.shgc.stanford.edu

Quality: Phrap Quality >=40 99.7% of Sequence;

Estimated Total Number of Errors is 0.3.

STS Content:

SHGC-52956 G36733.

FEATURES
source

Location/Qualifiers
1..105448
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/clone="CTD-2349B8"

BASE COUNT 28900 a 25016 c 24114 g 27418 t
ORIGIN

Query Match 1.1%; Score 21; DB 9; Length 105448;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAGGCGAGGAGGCGAGTGAGG 1663
|||||

Db 54552 GAGGCGAGGAGGCGAGTGAGG 54572
|||||

RESULT 49
AL773521

LOCUS Sus scrofa clone XX-339A5, *** SEQUENCING IN PROGRESS ***, 4
DEFINITION
AL773521
VERSION
AL773521.7 GI:22316197
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE pig.

ORGANISM

Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 119707)
Sehra, H.
Direct Submission

Submitted (14-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Aug 19, 2002 this sequence version replaced gi:21911701.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: humquerry@sanger.ac.uk

----- Project Information

Center project name: bs339A5

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator; 11% of reads

Chemistry: Dye-terminator Big Dye; 88% of reads

Consensus quality: 118859 bases at least Q40
Consensus quality: 119194 bases at least Q30
Consensus quality: 119351 bases at least Q20
Insert size: 119407; sum-of-contigs
Insert size: 117704; 8.6% error; agarose-fp
Quality coverage: 9.65x in Q20 bases; sum-of-contigs Quality
coverage: 10.29x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 2906: contig of 2906 bp in length
* 2907 3006: gap of 100 bp
* 3007 24103: contig of 21097 bp in length
* 24104 24203: gap of 100 bp
* 24204 73965: contig of 49762 bp in length
* 73966 74065: gap of 100 bp
* 74066 119707: contig of 45642 bp in length.

FEATURES

source
1. .119707
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="SBAB"
1. .2906
/note="assembly_fragment:01782"
3007. .24103
/note="assembly_fragment:01878"
24204. .73965
/note="assembly_fragment:01931"
74066. .119707
/note="assembly_fragment:02763"
BASE COUNT 32568 a 27491 c 27653 g 31695 t 300 others
ORIGIN

Query Match 1.1%; Score 21; DB 2; Length 119707;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 872 CTGTCCCTGGCTACACGGG 892
|||||
Db 21637 CTGTCCCTGGCTACACGGG 21657

RESULT 50
AL773562/c

LOCUS AL773562 126895 bp DNA linear HTG 16-AUG-2002
DEFINITION Sus scrofa clone XX-649D6, *** SEQUENCING IN PROGRESS ***, 2
unordered pieces.

ACCESSION AL773562
VERSION AL773562.10 GI:22316199
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE pig.

ORGANISM

Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Sehra, H.

Direct Submission
Submitted (14-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 19, 2002 this sequence version replaced gi:21955693.

COMMENT

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk

----- Project Information
Center project name: BS649D6
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator; 13% of reads
Chemistry: Dye-terminator Big Dye; 86% of reads
Consensus quality: 126617 bases at least Q40
Consensus quality: 126617 bases at least Q30
Consensus quality: 126713 bases at least Q20
Insert size: 126795; sum-of-contigs
Insert size: 126270; 8.2% error; agarose-fp
Quality coverage: 9.62x in Q20 bases; sum-of-contigs Quality
coverage: 10.33x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 53711: contig of 53711 bp in length
* 53712 53811: gap of 100 bp
* 53812 126895: contig of 73084 bp in length.

FEATURES

source
1. .126895
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="SBAB"
1. .53711
/note="assembly_fragment:00021"
fragment_chain:1
clone_end:SP6
vector_side:left
53812. .126895
/note="assembly_fragment:03452"
fragment_chain:1
misc_feature 1. .53711
misc_feature 53812. .126895

BASE COUNT 29013 a 31647 c 34436 g 31698 t 101 others
ORIGIN

Query Match 1.1%; Score 21; DB 2; Length 126895;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 872 CTGTCCCTGGCTACACGGG 892
|||||
Db 77606 CTGTCCCTGGCTACACGGG 77586

Search completed: December 29, 2002, 01:55:42
Job time : 9886 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 16:45:43 ; Search time 1771.2 Seconds
(without alignments)
12124.644 Million cell updates/sec

Title: US-09-944-896-49_COPY_123_1448

Perfect score: 1326

Sequence: 1 atgtgtcatccagagacctc.....gaaacggttacatctgcccag 1326

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	754	56.9	836	13	BI764403
2	752.2	56.7	1034	14	BM924615
3	723.4	54.6	928	13	BI517774
4	684.6	51.6	1076	13	BM547887
5	676	51.0	710	13	BI760121
6	632.2	47.7	939	13	BI757380

622.2 46.9 645 14 BM695392
579.8 43.7 704 9 AL040183
516.2 38.9 709 13 BI759120
489.8 36.9 916 13 BI759353
470.2 35.5 852 13 BI762690
335.4 25.3 463 9 AI792411
313.4 23.6 429 12 BF198258
293.4 22.6 500 13 BI761101
293.2 22.1 521 13 BI340175
271.6 20.5 339 12 EG608968
213.8 16.1 299 13 BI775946
199.2 15.0 392 10 AW437073
176.2 13.3 634 10 BB602462
168 12.7 321 13 BI359591
168 12.7 411 14 W79362
158 11.9 617 9 AI307814
156.8 11.8 523 10 AW786132
153.2 11.6 612 12 BF057185
152.8 11.5 611 10 AW299257
149 11.2 744 14 BQ006636
141 10.6 612 14 BQ446805
136.6 10.3 457 13 BI759735
118 8.9 263 13 BM481198
114.6 8.6 483 12 BF078053
114 8.6 756 12 BF527554
110.8 8.4 351 10 AW314352
110.6 8.3 650 10 BB496358
100.6 7.6 629 13 BI134777
90 6.8 578 14 BQ720124
83.4 6.3 659 17 BH327544
81 6.1 459 10 AW465507
80.6 6.1 260 13 BI976862
80 6.0 405 14 BM708158
80 6.0 495 9 AI989724
78 5.9 509 9 AI627475
77.4 5.8 494 9 AI433291
73.4 5.5 336 10 AW436875
73 5.5 490 10 AW001740
68.2 5.1 606 17 BH040326

ALIGNMENTS

RESULT 1
BI764403
LOCUS 603046141F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5186219 5',
DEFINITION BI764403 mRNA linear EST 25-SEP-2001
ACCESSION BI764403.1 GI:15755981
VERSION BI764403
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 836)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M11465 row: b column: 12
High quality sequence stop: 761.
Location/Qualifiers 1. .836

FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5186219"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT 157 a 255 c 271 g 153 t
ORIGIN
Query Match 56.9%; Score 754; DB 13; Length 836;
Best Local Similarity 97.7%; Pred. No. 1.9e-159;
Matches 807; Conservative 0; Mismatches 15; Indels 4; Gaps 4;
QY 102 GGAGGAGCTCCGATGCCGGAGCCCTGAACAGAGAGAGATTCTTCCTCTCCCT 161
|||||
DB 1 GGAGCAGGCTCCGATGCCGGAGCCCTGAACAGAGAGAGATTCTTCCTCTCCCT 60
QY 162 GCACAAACCGCTCGGAGCTGGGTCCAGCCGCCCTGCGGCTGCATCGGAGGCTGGACTG 221
|||||
DB 61 GCACACCGCTCGGAGCTGGGTCCAGCCGCCCTGCGGCTGCATCGGAGGCTGGACTG 120
QY 222 GAGTGACAGCTGGCCCACTGGCTCAAGCGAGGCGCCCTCTGTGGAATCCCAACCCC 281
DB 121 GAGTGACAGCTGGCCCACTGGCTCAAGCGAGGCGCCCTCTGTGGAATCCCAACCCC 180
QY 282 GAGCTGGCATCGGCTGTGGCGCACCTCCAGTGGGCTGGACATGCAGCTGCTGCC 341
DB 181 GAGCTGGCATCGGCTGTGGCGCACCTCCAGTGGGCTGGACATGCAGCTGCTGCC 240
QY 342 CGCGGCTTGGCTCTCTTTGTAAGTGGTTCAGCTATGTTTTCAGAGGGGCGACGGTA 401
DB 241 CGCGGCTTGGCTCTCTTTGTAAGTGGTTCAGCTATGTTTTCAGAGGGGCGACGGTA 300
QY 402 CAGCCACGGCGAGGAGAGTGTGTCGACAGCCACCTGTCACCCACTACAGCAGCTCGT 461
DB 301 CAGCCACGGCGAGGAGTGTGTCGACAGCCACCTGTCACCCACTACAGCAGCTCGT 360
QY 462 GTGGGCACTCAAGCCAGCTGGGCTGTGGCGCACCTGTGCTCTGAGGCCACACAGC 521
DB 361 GTGGGCACTCAAGCCAGCTGGGCTGTGGCGCACCTGTGCTCTGAGGCCACACAGC 420
QY 522 GATAGAAGCTTTGTCTGTGCTCTACTCCCGGAGGCAACTGGGAGGTCAACGGGAAGAC 581
DB 421 GATAGAAGCTTTGTCTGTGCTCTACTCCCGGAGGCAACTGGGAGGTCAACGGGAAGAC 480
QY 582 AATCATCCCTATAGAAGGGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTG 641
DB 481 AATCGTCCCTATAGAAGGGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTG 540
QY 642 CTTCAGGCTGGACCATCAGGGGGGCTGTGTGAGTTCCTCCAGGATCTTGTTCGAT 701
DB 541 CTTCAGGCTGGACCATCAGGGGGGCTGTGTGAGTTCCTCCAGGATCTTGTTCGAT 599
QY 702 GAGCTGCCAGAACCATGGAGCTCTCAACATCAGCACCTGCCACTGCCACTGTCCCTCGG 761
DB 600 GAGCTGCCAGAACCATGGAGCTCTCAACATCAGCACCTGCCACTGCCACTGTCCCTCGG 659
QY 762 CTACAGGGCAGATATGCAAGTGAAGTGCAGCTGCAGTGTGTGACGGCCGGTTCGG 821
DB 660 CTACAGGGCAGATATGCAAGTGAAGTGCAGTGTGTGACGGCCGGTTCGG 719
QY 822 GGAGGAGGAGTGTCTGTG-CGTCTGT-GACATCGGCTACGGGGGAGCCAGTGTGCCACC 879
|||||

Db 720 GGAGGAGAGTGCTCGTGACGCTCTGTGACATCGGTAGCGGGGAGACAGTGTGCCACC 779
QY 880 AA-CGTGCAATTTCCCTCCACACCTGTGACCTGAGGATCGACGGA 924
|||||
Db 780 AAGGTGCAATTTCCCTCCACACCTGTGACCTGAGGATCGACGGA 825
RESULT 2
LOCUS BM924615 1034 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6767842 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5761001
5', mRNA sequence.
ACCESSION BM924615
VERSION BM924615.1 GI:19374994
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1034)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12808 row: o column: 18
High quality sequence stop: 685.
FEATURES
source
1..1034
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5761001"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT 186 a 336 c 321 g 189 t 2 Others
ORIGIN
Query Match 56.7%; Score 752.2; DB 14; Length 1034;
Best Local Similarity 93.4%; Pred. No. 5.4e-159;
Matches 840; Conservative 0; Mismatches 50; Indels 9; Gaps 5;
QY 1 ATGCTGATCCAGAGACCTCCCTGGCGGGGCGCATCTCCTGGCTGTCTTGGCCCTC 60
|||||
DB 120 ATGCTGATCCAGAGACCTCCCTGGCGGGGCGCATCTCCTGGCTGTCTTGGCCCTC 179
QY 61 CTTGGCACCACTGGCGAGAGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCC 120
|||||
DB 180 CTTGGCACCACTGGCGAGAGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCC 239
QY 121 GGAGCCCTGAACAGAGAGAGATTCTTCCTCTCTCCCTGCACAAACCCGCTCGCAGC 180
|||||
DB 240 GGAGCCCTGAACAGAGAGAGATTCTTCCTCTCTCCCTGCACAAACCCGCTCGCAGC 299
QY 181 TGGTTCACGCCCTTCGGCTGACATGGCGGAGGCTGGAGTGCACAGCTTGGCCCAA 240
|||||

Db 300 TGGTCCAGCCCCCTGGCGCTGACATGCGGAGGCTGGAGTGACAGCCTGCGCCAG 359
QY 241 CTGGCTCAAGCCAGGCGACCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGCGCTG 300
Db 360 CTGGCTCAAGCCAGGCGACCCCTCTGTGGAACCCCAACCCGAGCCTGGCTGCGGCCG 419
QY 301 TGGCGCACCCCTGCAAGTGGGTGGAAACATGACAGCTGCTGCCCGCGGCTTGGCGTCTTT 360
Db 420 TGGCGCACCCCTGCAAGTGGGTGGAAACATGACAGCTGCTACCCTGCGGCTTGGTCTCTT 479
QY 361 GTTCAAGTGGTCAAGCTATGTTTGCAGAGGGGAGCGGTACAGCCAGCGCGCAGAGAG 420
Db 480 GTCAAGTGGTCAAGCTATGTTTGCAGAGGGGAGCGGTACAGCCAGCGCGCAGAGAG 539
QY 421 TGTGCTGCAACGACCCCTGCAAGCTACAGCGAGCTGCTGGGCGACCTCAAGCCAG 480
Db 540 TGTGCTGCAACGACCCCTGCAAGCTACAGCGAGCTGCTGGGCGACCTCAAGCCAG 599
QY 481 CTGGGCTGTGGGCGGACCTGTGCTCTGCAGGCGGACGAGGATAGAGCCCTTGTCTGT 540
Db 600 CTGGGCTGTGGGCGGACCTGTGCTCTGCAGGCGGAGCGAGGATAGAGCCCTTGTCTGT 659
QY 541 GCCTACTCCCCCGGAGGCACTGGAGGTC-AACGGGAGAGCAATCATCCCTATAGAAG 599
Db 660 GCCTACTCCCCCGGAGGCACTGGAGGTC-AACGGGAGAGCAATCATCCCTATAGAAG 719
QY 600 GGCTGCTGTGTGCTGCTGACAGGCGAGTCTGCTGAGGCTGCTCAAGAGCCTGGGACCA 659
Db 720 GGCTGCTGTGTGCTGCTGACAGGCGAGTCTGCTGAGGCTGCTCAAGAGCCTGGGACCA 779
QY 660 TGCA-GGGGGGCTCTGTGAGTTCGCCAGGATCTTGTGCGATGAGTCCCAAGCCATG 718
Db 780 TGCAAGGGGGGCTCTGTGAGTTCGCCAGGATCTTGTGCGATGAGTCCCAAGCCATG 838
QY 719 GAGCTCTCAACATCAGCAGCTGCGACTGCGACTGTCGCCCTGGCTACAGGCGCAGATCT 778
Db 839 GAGCTCTCAACATCAGCAGCTGCGACTGCGACTGTCGCCCTGGCTACAGGCGCAGATCT 898
QY 779 GCCAAGTGAAGTGCAG-CCTGAGTGTGTGACGCGGCTTCCGGG-AGGAGGAGT 832
Db 899 GCCAAGTGAAGTGCAGCCTGCANTGTGTCACGCGGTTTCCGGGAGAGATGCTT 958
QY 833 GCTCGTGGCTGTGACATCGGCTACGGGGGAGCCAGTGTGCCACCAAGAGTGCATTTT 891
Db 959 CTGCGCTCTTAACATCGGCTAGGGGGGGAACCCAGGTCGCCCGCCAGGGGCGCATTT 1017

RESULT 3
BI517774
LOCUS 603042018f1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5182397 5',
DEFINITION mRNA sequence.
ACCESSION BI517774
VERSION BI517774.1 GI:15342566
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 928)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cchapts-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1455 row: c column: 06

High quality sequence stop: 860.

FEATURES
Source

1. .928
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5182397"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"

/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

BASE COUNT 169 a 293 c 307 g 159 t
ORIGIN

Query Match 54.6%; Score 723.4; DB 13; Length 928;
Best Local Similarity 94.9%; Pred. No. 1.6e-152;
Matches 823; Conservative 0; Mismatches 36; Indels 8; Gaps 7;

QY 2 TGCTGTCATCCAGAGACCTCCCTGGCGGGGACATCTCTGGCTGTGCTGCGCCCTCC 61

Db 63 TGCTGTCATCCAGAGACCTCCCTGGCGGGGACATCTCTGGCTGTGCTGCGCCCTCC 122

QY 62 TTGGCACCACTGGGCGAGAGGTGGCCACCCAGCTGCAGGAGGCTCCGATGGCGG 121

Db 123 TTGGCACCGCTGGGCGAGAGGTGGCCACCCAGCTGCAGGAGGCTCCGATGGCGG 182

QY 122 GAGCCCTGACAGAGAGAGAGTTTCTGCTCTCTCCCTGCACACCCGCTGCGCAGCT 181

Db 183 GAGCCCTGACAGAGAGAGAGTTTCTGCTCTCTCCCTGCACACCCGCTGCGCAGCT 242

QY 182 GGGTCCAGCCCTGGCGCTGACATGGGAGGCTGGAGTGGAGTGGAGTGGAGTGGAGT 241

Db 243 GGGTCCAGCCCTGGCGCTGACATGGGAGGCTGGAGTGGAGTGGAGTGGAGTGGAGT 302

QY 242 TGGCTCAAGCCAGGCGACCCCTCTGTGGAATCCCAACCCAGCCTGGCATCCGCGCTGT 301

Db 303 TGGCTCAAGCCA-GGCAGCCCTCTGTGGAACCCCAACCCAGCCTGGCGTCCGCGCTGT 361

QY 302 GGGCGACCCCTGCAAGTGGGCTGGAACATGACAGTGTCTGCCCGGGGCTTGGCGTCTTTG 361

Db 362 GGGCGACCCCTGCAAGTGGGCTGGAACATGACAGTGTCTGCCCGGGGCTTGGCGTCTTTG 421

QY 362 TTGAAGTGGTCAAGCTATGGTTTCAGAGGGGCGCGGTACAGCCAGCGGCGAGAGT 421

Db 422 TCGAAGTGGTCAAGCTATGGTTTCAGAGGGGCGCGGTACAGCCAGCGGCGAGAGT 481

QY 422 GTGCTCGCAAGCCAGCTGCACCCACTACAGCAGCTCGTGTGGGCCACTCAAGCCAGC 481

Db 482 GTGCTCGCAAGCCAGCTGCACCCACTACAGCAGCTCGTGTGGGCCACTCAAGCCAGC 541

QY 482 TGGGCTGTGGGCGGACCTGTGCTTGCAGGCCAGACAGCATAGAGCCTTTGCTGTG 541

Db 542 TGGGCTGTGGGCGGACCTGTGCTTGCAGGCCAGACAGCATAGAGCCTTTGCTGTG 601

QY 542 CCTACTCCCCGGGAGGCACTGGGAGGTCAACGGGAAACATCATCCCTATAGAAGG 601

Db 602 CCTACTCCCCGGGAGGCACTGGGAGGTCAACGGGAAACATCATCCCTATAGAAGG 661

QY 602 GTGCTGTGTTTCTGCTGACAGCAGCTGTCTCAGGCTGTCTCAAGCCTGGGACCATG 661

Db 662 GTGCTGTGTTTCTGCTGACAGCAGCTGTCTCAGGCTGTCTCAAGCCTGGGACCATG 721

QY 662 CAGGGGGGCTGTGTGAGGTCCCCAGGATCCTT-GTCGATGAGTGGCAG-AAACATGG 719

Db 722 CAGGGGGGCTGTGTGAGGTCCCCAGGATCCTTGTGTCGATGAGTGGCAGAAACCATGG 781


```

QY 720 ACCTCTCAACATCAGACACCTGCGCCACTGTCCTCCCTGCGGTACACGGCGCAGATACT- 778
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 782 ACCTCTCAACATCAG-ACCTGGCAGCTGGCAGTCTCCCTCTGTGTAACACGGCGCAGATCTG 840
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 779 GCGAAGTGAGGTGACGCTGCACTG-TGTGACAGCGCGGTTCGCGGA--GGAGGAGTGT 835
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 841 GCGAAGTGATGTGACGCTGCACTGTTGTCGCGCGCGGTTCGCGGAAGGAGGATGCC 900
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 836 CGTGGCTCTGTGACATCGGCTACGGGG 862
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 901 CAGGGGCTCGGACATCGGAACGGGG 927
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
LOCUS BM547887 1076 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_5531767 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5732633
5', mRNA sequence.
ACCESSION BM547887
VERSION BM547887.1 GI:18782034
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1076)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12735 row: a column: 18
High quality sequence start: 9
High quality sequence stop: 677.

FEATURES
source
location
1..1076
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5732633"
/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
(destroyed); Site_2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."
BASE COUNT 192 a 358 c 338 g 182 t 6 others
ORIGIN
Query Match 51.6%; Score 684.6; DB 13; Length 1076;
Best Local Similarity 93.1%; Pred. No. 9.2e-144;
Matches 737; Conservative 0; Mismatches 52; Indels 3; Gaps 2;

QY 1 ATGCTGCATCCAGAGACCTCCCTGGCGGGGATCTCCTGGCTGTCTCTGGCCCTC 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 256 ATGCTGCATCCAGAGACCTCCCTGGCGGGGATCTCCTGGCTGTCTCTGGCCCTC 315
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 CTGGCACCACCTGGGACAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGCC 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 316 CTGGCACCACCTGGGACAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGCC 375
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY 121 GGAGCCCTGAACAGAGGAGAGTTTCTTGCTCTCTCCCTGCACAAACCGCCTGCGCAGC 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 376 GGAGCCCTGAACAGAGGAGAGTTTCTTGCTCTCTCCCTGCACAAACCGCCTGCGCAGC 435
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TGGGTCCAGCCCTGCGGCTGACATGGGAGGCTGGAGTGGAGTGACAGCCTGGGCCAA 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 436 TGGGTCCAGCCCTGCGGCTGACATGGGAGGCTGGAGTGGAGTGACAGCCTGGGCCAA 495
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 CTGGCTCAAGCCAGGCGGACGCCCTCTGTGGAATCCCAACCCGAGCCTGGCCTCGGCCG 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 496 CTGGCTCAAGCCAGGCGGACGCCCTCTGTGGAATCCCAACCCGAGCCTGGCCTCGGCCG 555
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 TGGCGCACCCCTGCAAGTGGGCTGGAACATGCACTGCTGCCCGCGGCTTGGCGTCTCTT 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 556 TGGCGCACCCCTGCAAGTGGGCTGGAACATGCACTGCTGCCCGCGGCTTGGCGTCTCTT 615
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 GTTGAAGTGGTCAAGCCTATGTTTCAGAGGGGACGGGTACAGCCGCGGAGAGAG 420
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 616 GTTGAAGTGGTCAAGCCTATGTTTCAGAGGGGACGGGTACAGCCGCGGAGAGAG 675
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 421 TGTGCTCGCAACGCCACCTGCACCCACTACACGCACTGCTGTGGGCCACCTCAAGCCAG 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 676 TGTGCTCGCAACGCCACCTGCACCCACTACACGCACTGCTGTGGGCCACCTCAAGCCAG 735
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 481 CTGGGCTGTGGGCGGCGCACTGTGCTCTCAGGCGCCAGACAGCAGATAGAAGCTTTGTCTGT 540
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Db 736 CTGGGCTGTGGGCGGCGCACTGTGCTCTCAGGCGCCAGACAGCAGATAGAAGCTTTGTCTGT 795
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 541 GCCTACTCCCGCGGAGCAACTGGGAGGTCACGGGAGCAACAATCAT-CCCCTATAAGAA 599
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 796 GCCTACTCCCGCGGAGCAACTGGGAGGTCACGGGAGCAACAATCATCCCCTATAAGAA 855
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 600 GGGTGCCTGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAGCCCTGGGACCA 659
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 856 GGGTGCCTGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAGCCCTGGGACCA 915
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 660 TGCAGGGGGG--CTCTGTGAGGTGCCAGGAATCTTTCGATGAGTGCAGAGAACCAT 717
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 916 TGCAGGGGGGCGCTCTTGGGAGGTCCCGCAGGAATCTCTGCGATGACCTGCCANAAACCA 975
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 718 GGAGGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCTGGCTACAGGCGCAGATAC 777
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 976 TGGAGGTCTCACATCAGCACCTGCCACTGCCACTGTCCCTGGCTACCGCGCAAAACT 1035
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QY 778 TGCCAAAGTGAGG 789
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1036 TGCCAGGAGGGG 1047
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RESULT 5
BI760121
LOCUS BI760121 710 bp mRNA linear EST 25-SEP-2001
DEFINITION 60304615F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5184962 5',
mRNA sequence.
ACCESSION BI760121
VERSION BI760121.1 GI:15751699
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 710)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

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http://image.llnl.gov
Plate: LLAM11461 row: n column: 03
High quality sequence stop: 704.

FEATURES

source
1. 710
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:5184962"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pcmv-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

BASE COUNT 131 a 228 c 226 g 125 t
ORIGIN
Query Match 51.0%; Score 676; DB 13; Length 710;
Best Local Similarity 98.4%; Pred. No. 6.7e-142;
Matches 693; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
QY 87 GCACCCAGCTGAGAGAGGCTCCGATGGCGGAGCCCTGACAGAGAGAGTTT 146
Db 6 GGCACCCAGCTGAGAGAGGCTCCGATGGCGGAGCCCTGACAGAGAGAGTTT 65
QY 147 CTTGCTCTCTCCCTGCACACCCGCTCGCAGCTGGCTCCAGCCCTCGGCTGACAT 206
Db 66 CTTGCTCTCTCTCCCTGCACACCCGCTCGCAGCTGGCTCCAGCCCTCGGCTGACAT 125
QY 207 GCGGAGGCTGGAGTGGAGTACAGCTGGCCCACTGGCTCAAGCCAGGCGACCCCTCTG 266
Db 126 GCGGAGGCTGGAGTGGAGTACAGCTGGCCCACTGGCTCAAGCCAGGCGACCCCTCTG 185
QY 267 TGGATCCCAACCCGAGCCTGGATCCGGCTGTGGCGCACCCCTGCAAGTGGCTGGAA 326
Db 186 TGGATCCCAACCCGAGCCTGGATCCGGCTGTGGCGCACCCCTGCAAGTGGCTGGAA 245
QY 327 CATCAGCTGCTGCCGGGCTTGGCTCTCTTCTTGAAGTGGTCAAGCTATGTTTC 386
Db 246 CATCAGCTGCTGCCGGGCTTGGCTCTCTTCTTGAAGTGGTCAAGCTATGTTTC 305
QY 387 AGAGGGGACGGTACAGCCAGCGGCGAGAGAGTGTCTGCAACGCCACCTGCACCCA 446
Db 306 AGAGGGGACGGTACAGCCAGCGGCGAGAGAGTGTCTGCAACGCCACCTGCACCCA 365
QY 447 CTACAGGAGCTGTGTGGGCACCTCAAGCCAGCTGGGCTGTGGGCGCACCTGTGCTC 506
Db 366 CTACAGGAGCTGTGTGGGCACCTCAAGCCAGCTGGGCTGTGGGCGCACCTGTGCTC 425
QY 507 TGCAGGCGACAGAGATAGAGCTTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 566
Db 426 TGCAGGCGACAGAGATAGAGCTTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 485
QY 567 GGTCAGGGGAGAACATCATCCCCCTATAGAAGGCTGCTGTGTCTCTCTCTCTCTCTCT 626
Db 486 GGTCAGGGGAGAACATCATCCCCCTATAGAAGGCTGCTGTGTCTCTCTCTCTCTCTCT 545
QY 627 CAGTGTCTCAGCTGCTTCAAGCCTGGGACCATCGAGGGGGCTCTGTGAGGTCCCCAG 686
Db 546 CAGTGTCTCAGCTGCTTCAAGCCTGGGACCATCGAGGGGGCTCTGTGAGGTCCCCAG 605
QY 687 GAATCCTTGTGCGATGAGCTGCCAAGCATGGAGCTCTCAACATCAGCACCTGCGACTG 746
Db 606 GAATCCTTGTGCGATGAGCTGCCAAGCATGGAGCTCTCAACATCAGCACCTGCGACTG 665
QY 747 CCACTGTCCCCCTGGCTACAC-GGGCAGATACTGCCAAGTGGAG 789

Db 666 CCAGTGTCCCTGGCTACAGGGCGAGATACTCCCAAGTGAGG 709

RESULT 6

BI757380

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Bi757380

603029310F1 NIH_MGC_114 Homo sapiens cdna clone IMAGE:5199674 5',

mrna sequence.

939 bp mrna linear EST 25-SEP-2001

GI:15748958

Human

Human sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 939)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs@email.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11500 row: c column: 03

High quality sequence stop: 778.

FEATURES

Location/Qualifiers

1..939

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="IMAGE:5199674"

/clone_lib="NIH_MGC_114"

/lab_host="DH10B"

/note="Organ: brain; Vector: pcmv-SPORT6; Site_1: NotI;

Site_2: EcoRV (destroyed); RNA source anonymous pool of 6

male brains, age range 23-27 yo. Library is oligo-dT

primed and directionally cloned (EcoRV site is destroyed

upon cloning). Average insert size 1.5 kb, insert size

range 1-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 019. Note:

this is a NIH_MGC Library."

BASE COUNT 168 a 286 c 320 g 165 t

ORIGIN

Query Match 47.7%; Score 632.2; DB 13; Length 939;

Best Local Similarity 96.1%; Pred. No. 5.5e-132;

Matches 670; Conservative 0; Mismatches 23; Indels 4; Gaps 2;

QY 1 ATGCTGATCCAGAGACCTCCCTGGCGGGGGATCTCTCTGGCTGTGCTCTGGCCCTC 60

Db 50 ATGCTGATCCAGAGACCTCCCTGGCGGGGGATCTCTCTGGCTGTGCTCTGGCCCTC 109

QY 61 CTTGGCCACCACTGGGAGAGGTGTGGCCACCCAGCTGTCAGGAGAGGCTCCGATGGCC 120

Db 110 CTTGGCCACCACTGGGAGAGGTGTGGCCACCCAGCTGTCAGGAGAGGCTCCGATGGCC 169

QY 121 GGAGCCCTGAACAGAGAGAGTTCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180

Db 170 GGAGCCCTGAACAGAGAGAGTTCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 229

QY 181 TGGTCCAGCCCTCCCTGGGCTGACATGGGAGGCTGGAGTGGAGTGGAGCTGGCCCAA 240

Db 230 TGGTCCAGCCCTCCCTGGGCTGACATGGGAGGCTGGAGTGGAGTGGAGCTGGCCCAA 289

QY 241 CTGCTCAAGCAGGAGGAGCCCTCTGTGGAATCCCAACCCAGGCTGGCATCCGCGCTG 300

Db 290 CTGCTCAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 348

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QY 301 TGGCGACCCCTGCAAGTGGGCTGGAACATGCAGCTGTGCCCGGGCTTGGGCTCCTTT 360
Db 349 TGGCGACCCCTGCAAGTGGGCTGGAACATGCAGCTGTGCCCGGGCTTGGGCTCCTTT 408
QY 361 GTTGAAGTGGTCAAGCTATGTTTTCAGAGGGGCGAGGGTACAGCCACGCGGAGGAGAG 420
Db 409 GTTGAAGTGGTCAAGCTATGTTTTCAGAGGGGCGAGGGTACAGCCACGCGGAGGAGAG 468
QY 421 TGTGCTCGCAAGCCACCTGCACCCACTACACGACGCTCGTGTGGGCCACCTCAAGCCAG 480
Db 469 TGTGCTCGCAAGCCACCTGCACCCACTACATGACGCTGTGTGGGCCACCTCAAGCCAG 528
QY 481 CTGGGCTGTGGGCGCACCTGTGCTCTGCAGGCGCAGACGAGATAGAACGCTTGTGCTGT 540
Db 529 CTGGGCTGTGGGCGCACCTGTGCTCTGCAGGCGCAGGACGAGATAGAACGCTTGTGCTGT 588
QY 541 GCCTACTCCCCGGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCTTAAAGAG 600
Db 589 GCCTACTCCCCAGAGGCAACTGGGAGGTCAACGGGAAGACAATCTGCTTAAAGAG 648
QY 601 GTGCTGTGTTGCTGCTGTCGTCGACAGCCAGTGTCTCAGGCTGTCTCAAGGCTGGGACCA - 659
Db 649 GTGCTGTGTTGCTGCTGTCGTCGACAGCCAGTGTCTCAGGCTGTCTCAAGGCTGGGACCA 708
QY 660 --TGCAGGGGGGCTTCTGTGAGGTGCCAGGAATCCTT 694
Db 709 TGCAGGGGGGCTTCTGTGAGGTGCCAGGAATCCTT 745

RESULT 7
BM695392
LOCUS
DEFINITION
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  UI-E-COI-aev-n-19-0-UI-r1 UI-E-COI Homo sapiens cDNA clone
  UI-E-COI-aev-n-19-0-UI 5', mRNA sequence.
ACCESSION
  BM695392
VERSION
  BM695392.1 GI:19008650
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 645)
AUTHORS
  Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE
  Normalization and subtraction: two approaches to facilitate gene
  discovery
JOURNAL
  Genome Res. 6 (9), 791-806 (1996)
MEDLINE
  9704477
COMMENT
  Contact: Soares, MB
  Program for Rat Gene Discovery and Mapping
  University of Iowa
  451 Eckstein Medical Research Building Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: msoares@blue.weeg.uiowa.edu
  CDNA Library prepared by: Dr. Gregg Hageman
  Tissue Procurement: Dr. M. Bento Soares, University of Iowa
  CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Researchers may obtain clones from Research
  Genetics (www.resgen.com).
  Seq primer: M13 Reverse.
  Location/Qualifiers
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      /db_xref="taxon:9606"
      /clone="UI-E-COI-aev-n-19-0-UI"
      /clone_lib="UI-E-COI"
      /tissue_type="optic nerve"
      /dev_stage="adult"
      /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
      /note="Organ: eye; Vector: pT73-pac (Pharmacia) with a
        modified polylinker; Site_1: EcoR I; Site_2: Not I;

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UI-E-COI is a normalized cDNA library containing the following tissue(s): optic nerve. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCATTAAGTG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 136 a 187 c 196 g 126 t
ORIGIN

Query Match 46.9%; Score 622.2; DB 14; Length 645;
Best Local Similarity 99.5%; Pred. No. 8.5e-130;
Matches 624; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 590 CCTATAAGAAAGGGTCCCTGGTTCGCTTCGACAGCCAGTGTCTCAGGCTGTTCAAAG 649
Db 1 CCTATAAGAAAGGGTCCCTGGTTCGCTTCGACAGCCAGTGTCTCAGGCTGTTCAAAG 60
QY 650 CCTGGGACCATGTCAGGGGGGCTCTGTGAGTCCCCAGGAATCCTTGTCCCATCAGCTGCC 709
Db 61 CCTGGGACCATGTCAGGGGGGCTCTGTGAGTCCCCAGGAATCCTTGTCCCATCAGCTGCC 120
QY 710 AGAACCATGAGCGTCTCAACATCAGCACCTGCCACTGTCCCTGCTGGCTACACGG 769
Db 121 AGAACCATGAGCGTCTCAACATCAGCACCTGCCACTGTCCCTGCTGGCTACACGG 180
QY 770 GCATATCTGCAAGTGTGAGTGTGACCCCTGCAGTGTGTCACGGCGGTTCCGGGAGGAG 829
Db 181 GCATATCTGCAAGTGTGAGTGTGACCCCTGCAGTGTGTCACGGCGGTTCCGGGAGGAG 240
QY 830 AGTGTCTGTGCTGTGTGACATCGGCTACGGGGGAGCGCCAGTGTGCCACCAAGTGCATT 889
Db 241 AGTGTCTGTGCTGTGTGACATCGGCTACGGGGGAGCGCCAGTGTGCCACCAAGTGCATT 300
QY 890 TTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGAGTGTTCATGTGTCTTCAGAGG 949
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QY 950 CAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGCGGGGTGCTGGCCCCAGA 1009
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QY 1010 TCAAGAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGCGCGCTGGAGACCACCA 1069
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QY 1070 ACGAGGTGACTGACAGTGAATTCGAGACCAAGGAATCTTGGATCGGGCTTCACCTACAAGA 1129
Db 481 ACGAGGTGATTGACAGTGAATTCGAGACCAAGGAATCTTGGATCGGGCTTCACCTACAAGA 540
QY 1130 CCGCCAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCTTCACCAAGTTTGCCT 1189
Db 541 CCGCCAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCTTCACCAAGTTTGCCT 600
QY 1190 TTGGGCAGCCTTGACAAACCCAGCGGCTGG 1216
Db 601 TTGGGCAGCCTTGACAAACCCAGCGGTTTG 627

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RESULT 8

AL040183

LOCUS

DEFINITION

ACCESSION

VERSION

AL040183.1

GI:5409148

AL040183

DEFINITION

ACCESSION

VERSION

AL040183.1

GI:5409148

AL040183

DEFINITION

ACCESSION

VERSION

AL040183.1

GI:5409148

AL040183

DEFINITION

ACCESSION

VERSION

AL040183.1

GI:5409148

AL040183

DEFINITION

ACCESSION

VERSION

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AL040183

DEFINITION

ACCESSION

VERSION

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GI:5409148

AL040183

DEFINITION

ACCESSION

VERSION

AL040183.1

GI:5409148

AL040183

DEFINITION

ACCESSION

VERSION

AL040183.1

GI:5409148

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL 1 (bases 1 to 704)
COMMENT Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehrer, et al.)
Unpublished (1999)
Contact: Koehrer K
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
s1 sequence also available.
This clone (DKFZp434F2413) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
source
1. 704
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp434F2413"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/note="vector; pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 150 a 207 c 207 g 139 t 1 others
ORIGIN
Query Match 43.7%; Score 579.8; DB 9; Length 704;
Best Local Similarity 97.1%; Pred. No. 3.1e-120;
Matches 664; Conservative 0; Mismatches 13; Indels 7; Gaps 7;
QY 535 GTCTGTGCTACTCCCGGAGGCACTGGAGGTCAACGGGAAGCAATCATCCCTAT 594
Db 1 GTCTGTGCTACTCCCGGAGGCACTGGAGGTCAACGGGAAGCAATCATCCCTAT 60
QY 595 AAGAGGGTGTGCTGTCTGCACAGCCAGTGTCTCAGGCTGCTCAAGGCTGG 654
Db 61 AAGAGGGTGTGCTGTCTGCACAGCCAGTGTCTCAGGCTGCTCAAGGCTGG 120
QY 655 GACCATGAGGGGGCTGTGAGGTCCCGAGGAATCTTGTGCGCATGAGTCCGAGAAC 714
Db 121 GACCATGAGGGGGCTGTGAGGTCCCGAGGAATCTTGTGCGCATGAGTCCGAGAAC 180
QY 715 CATGAGCTCTCAACATCAGCAGCTGCCACTGCCACTGCCCTGCCCTGACGGGCAGA 774
Db 181 CACGAGCTCTCAACATCAGCAGCTGCCACTGCCACTGCCCTGCCCTGACGGGCAGA 240
QY 775 TACTGCCAAGTGAAGTGAAGTGTGTGTCAGCGCGGTTCGCGGAGGAGGAGTGC 834
Db 241 TACTGCCAAGTGAAGTGAAGTGTGTGTCAGCGCGGTTCGCGGAGGAGGAGTGC 300
QY 835 TCGTCCGTGTGACATCGGCTACGGGGGAGCCCACTGTGCCACCAAGGTGCAATTTCCC 894
Db 301 TCGTCCGTGTGACATCGGCTACGGGGGAGCCCACTGTGCCACCAAGGTGCAATTTCCC 359
QY 895 TTCCACACTGTGACCTGAGGATCGACGAGAGCTGCTCATGTGTCTTC-AGAGCAGA 953
Db 360 TTCCACACTGTGACCTGAGGATCGACGAGAGCTGCTCATGTGTCTTC-CAAGAGCAGA 419
QY 954 CACCTATTACAGAGCAGGATGAAATGTCAGAGGAAGGGGGTGTGTCGCCAGATCAA 1013
Db 420 CACCTATTACAGAGCAGA-CATGAAATGTCAGAGGAHA-GGGGGTGTGTCGCCAGATCAA 477
QY 1014 GAGCAGAAAGTGC-AGGACATGCTCTGCCTTCATCTGGGCCGCCCTGAGACCAACG 1072
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Db 478 GAGCCACAAAGTGCAANGACATCTCCCTTCTATCTTGGCCGCTGGAGACCACCAACG 537
QY 1073 AGGTGACTGACACTGACTTCGAGACCAAGAACTTCTGATCGGCTCACCTACAGACCG 1132
Db 538 AGGTGATTGACACTGACTTCTAGACCA-GAATCTCTGATCGGCTCACCTACAGACCG 596
QY 1133 CAAGGACTCTCTCCGCTGGGCCACAGGAGGAGCACCAGGCTTCCACAGTTTGGCTTTG 1192
Db 597 CC-AGGACTCTCTCCGCTGGGCCACAGGAGCACCAGGCTTCCACAGTTTGGCTTTG 655
QY 1193 GGCAGCTGACACACACCGGGCTGG 1216
Db 656 GGCAGCTGACACACCGGGCTGG 679
RESULT 9
BI759120 709 bp mrna linear EST 25-SEP-2001
LOCUS 603042530F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5182999 5',
DEFINITION mRNA sequence.
ACCESSION BI759120
VERSION BI759120.1 GI:15750698
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 709)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution by: Incyte Genomics, Inc.
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1456 Row: 1 column: 08
High quality sequence stop: 709.
Location/Qualifiers
source
1. 709
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5182999"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pcMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT 124 a 240 c 220 g 125 t
ORIGIN
Query Match 38.9%; Score 516.2; DB 13; Length 709;
Best Local Similarity 98.3%; Pred. No. 6.7e-106;
Matches 532; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
QY 1 ATGTGTCATCCAGACACCTCCCTGCGGGGGGAGTCTCTGCTGCTGCTGCTGCTGCTC 60
Db 170 ATGTGTCATCCAGACACCTCCCTGCGGGGGGAGTCTCTGCTGCTGCTGCTGCTGCTC 229
QY 61 CTGGCACCACCTGGGCGAGAGGTGTGGCCACCCAGCTCAGGAGCAGCTCGGATGGCC 120
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Db 230 CTGTGACCCGCTGGCGAGAGTGTGGCCACCCAGCTGACGAGCAGGCTCCGATGGCC 289

Qy 121 GGAGCCCTGAACAGGAGAGTGTGTGCTCCTCCCTGCACAAACCGCTGCCACG 180

Db 290 GGAGCCCTGAACAGGAGAGTGTGTGCTCCTCCCTGCACAAACCGCTGGCGAGC 349

Qy 181 TGGGTTCAGCCCTGGCGCTGACATCGGAGGCTGGAGTGACAGCCCTGGCCCA 240

Db 350 TGGGTTCAGCCCTGGCGCTGACATCGGAGGCTGGAGTGACAGCCCTGGCCCA 409

Qy 241 CTGGCTCAAGCGAGGAGCCCTGTGTGGATCCCAACCCCGAGCTGGCATCGGCTG 300

Db 410 CTGGCTCAAGCGA-GGCGAGCCCTGTGTGGATCCCAACCCCGAGCTGGCGTGG 468

Qy 301 TGGCGCACCCCTGCAAGTGGGTGGAACATGACAGCTGCTGCCCGGGCTTGGCGTCTT 360

Db 469 TGGCGCACCCCTGCAAGTGGGTGGAACATGACAGCTGCTGCCCGGGCTTGGCGTCTT 528

Qy 361 GTTGAAGTGTGACCCCTATGTTTGCAGAGGGGAGCGGTACAGCCAGCGGCGAGAG 420

Db 529 GTGGAAGTGTGACCCCTATGTTTGCAGAGGGGAGCGGTACAGCCAGCGGCGAGAG 588

Qy 421 TGTGCTCGCAAGCGACCTGACCCACCTACACGAGCTGCTGGCGCACCTCAAGCCAG 480

Db 589 TGTGCTCGCAAGCGACCTGACCCACCTACACGAGCTGCTGGCGCACCTCAAGCCAG 648

Qy 481 CTGGGCTGTGGGGGCGACCTGTGCTCTGCAGCCAGACAGCGATAGAAGCCCTTGTCTGT 540

Db 649 CTGGGCTGTGGGGGCGACCTGTGCTCTGCAGCCAGGCGAGATAGAAGCCCTTGTCTGT 708

Qy 541 G 541

Db 709 G 709

RESULT 10

BI759353

LOCUS 603043013F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183330 5',

DEFINITION mRNA sequence.

ACCESSION BI759353

VERSION BI759353.1 GI:15750931

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999).

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLAM11457 row: j column: 03
High quality sequence stop: 723.

FEATURES

Location/Qualifiers

1..916

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5183330"

/clone_lib="NIH_MGC_116"

/lab_host="DH10B"

/note="organ: pooled colon, kidney, stomach; Vector: PCMV-SPO16; Site:1; Noti: Site_2; Ecorv (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2

stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (Ecorv site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library.

BASE COUNT 153 a 306 c 278 g 178 t 1 others

Query Match 36.9%; Score 489.8; DB 13; Length 916;
Best Local Similarity 90.5%; Pred. No. 6.5e-100;
Matches 701; Conservative 0; Mismatches 57; Indels 17; Gaps 16;

Qy 1 ATGCTGCATCCAGAGACCTCCCTGGCCGGGGGATCTCTG- GCTGTGCTCTGGCCCT 59

Db 143 ATGCTGCATCCAGAGACCTCCCTGGCCGGGGGATCTCTGAGCTGTGCTCTGGCCCT 202

Qy 60 CCTTG-GCACCACTGGGCAGAGTGTGGCCACC-CCAGCTGCA-GGAGCAGGCTCCGAT 116

Db 203 CCTTGTGCACCACTGGGCAGAGTGTGGCCACCACCAGCTGCAATGGAGGCTCCGAT 262

Qy 117 GGCCGGAGCCCTGAACAGAGGAGAGTTCCTTGTGCTCTCTCCCTGCACAAACCGCTG-C 175

Db 263 GGCCGGAGCCCTGAACAGAGGAGAGTTCCTTGTGCTCTCTCCCTGCACAAACCGCTGTC 322

Qy 176 GCAGCTGGGTTCAGCCCTCCCTGGCG-CTGACATGGGAGGCTGGAGTGGAGTGA- GCCT 233

Db 323 GCAGCTGGGTTCAGCCCTCCCTGGCGCTGTGACATGGGAGGCTGGAGTGGAGTGA- GCCT 382

Qy 234 GGCCCAACTGGCTCAAGCCAGGCGACCCCTCTGTGGAAATCCCAACCCCGAGCTGGCATC 293

Db 383 GGCCCAACTGGCTCAAGCCAGGCGACCCCTCTGTGGAAATCCCAACCCCGAGCTGGCATC 442

Qy 294 CGGCTGTGGCGACCCCTGCAAGTGGGCTGGAAACA-TGCAGCTGCTGCCCGGGCTGG 352

Db 443 CGGCTGTGGCGACCCCTGCAAGTGGGCTGGAAATTCGAGCTGCTGCCCGGGCTGG 502

Qy 353 CGTCTCTTCTTGAAGTGGTCAAGCTATGTTTGCAGAGGGG--CAGCGGTACAGCCAGC 410

Db 503 CGTCTCTTCTTGAAGTGGTCAAGCTATGTTTGCAGAGGGGCGATGCGGTACAGCCAGC 562

Qy 411 GCAGGAGA-GTGTGCTGC-AACGCCACCTGCACCACTACACGAGCTGCTGTGGGCC 468

Db 563 GCAGGAGATGTGTGCTCAAAAGCCAGCTGACCCACTACACGAGCTGCTGTGGGCC 622

Qy 469 ACCTCAAGCCAGCTGGGCTGTGGGGGCGACC-TGTGCTGTGAGGCCAGACAGCGATAGA 527

Db 623 A-CTCAAGCCAGCTGGGCTGTGGGGGCGACCCTGTGCTCTGACAGGCCAGACAGCGATAGA 681

Qy 528 AGCCTTTGCTGTGCTACTCTCCCGGAGGCAACTGGAGGTCAACGGGAAGACAATCAT 587

Db 682 AGCCTTTGCTGTGCTACTCTCCCGGAGGCACTGGAGGTACCGGGAAGACAATCAT 741

Qy 588 CCCCTAAGAAGGCTGTGTGCTGCTC-TGCACAGCCAGTGTCTCAGGCTGTCTTCA 646

Db 742 CCCCTAAGAAGGCTGTGTGCTGCTCTTGCACAGCCAGTGTCTCAGGCTGTCTTCA 800

Qy 647 AAGCCTGGGACCATCAGGGGGGCTGTGTGAGTGTCCCAAGGAATCTTGTGCGATGAGCT 706

Db 801 AAGCCTGGGACCATCAGGGGGGCTGTGTGAGTGTCCCAAGGAATCTTGTGCGATGAGCT 860

Qy 707 GCCAGACCA-TGGAGCTCTCAACATCAGCACTGCCACTGCCACTGTCCCTGTG 760

Db 861 GCCAGACCA-TGGAGCTCTCAACATCAGCACTGCCACTGCCACTGTCCCTGTG 915

RESULT 11

BI762690

LOCUS 603048444F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188643 5',

DEFINITION mRNA sequence.

ACCESSION BI762690

BI762690 852 bp mRNA linear EST 25-SEP-2001

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VERSION      BU762690.1  GI:15754256
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1 (bases 1 to 852)
JOURNAL      NIH-MGC http://mgi.nci.nih.gov/.
COMMENT      National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgaps-r@mail.nih.gov
              Tissue Procurement: Life Technologies, Inc.
              CDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
              Clone Distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM1471 row: g column: 12
              High quality sequence stop: 849.
FEATURES     1..852
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              /clone="IMAGE:5188643"
              /clone_lib="NIH_MGC_116"
              /lab_host="DH10B"
              /note="Organ: pooled colon, kidney, stomach; Vector:
              pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
              source anonymous pool of 3 colons, age 26 yo male, 49 yo
              female, 71 yo male colon; 46 yo male kidney, and pool of 2
              stomachs, 62 yo male and 70 yo female. Library is
              oligo-dT primed and directionally cloned (EcoRV site is
              destroyed upon cloning). Average insert size 1.4 kb,
              insert size range 1-3 kb. Library is normalized and
              enriched for full-length clones and was constructed by C.
              Gruber (Invitrogen). Research Genetics tracking code
              023. Note: this is a NIH_MGC Library."
BASE COUNT   146 a 283 c 269 g 154 t
ORIGIN
Query Match      35.5%; Score 470.2; DB 13; Length 852;
Best Local Similarity 95.6%; Pred. No. 1.6e-95;
Matches 559; Conservative 0; Mismatches 18; Indels 8; Gaps 7;

QY 1 ATGCTGATCCAGAGACCTCCCTGGCCGGGGGCAFTCTCTGCTGTGTCTCTGGCCCTC 60
Db 258 ATGCTGATCCAGAGACCTCCCTGGCCGGGGGCAFTCTCTGCTGTGTCTCTGGCCCTC 60
QY 61 CTTGGCACCACCTGGGCAGAGTGTGGCCACCACCCAGCTGCAGAGAGCGTCCGATGGCC 120
Db 318 CTTGGCACCACCTGGGCAGAGTGTGGCCACCACCCAGCTGCAGAGAGCGTCCGATGGCC 120
QY 121 GGAGCCCTGAACAGGAAGAGAGTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Db 378 GGAGCCCTGAACAGGAAGAGAGTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
QY 181 TGGGTCCAGCCCTGGCGCTGACATGGGAGGCTGGAGTGGAGTACAGCCCTGGCCCAA 240
Db 438 TGGGTCCAGCCCTGGCGCTGACATGGGAGGCTGGAGTGGAGTACAGCCCTGGCCCAA 240
QY 241 CTGGCTCAAGCAGGCGACCTCTGTGGAAATCCCAACCCAGAGCTGCATCCGCGCTG 300
Db 497 CTGGCTCAAGCAGGCGACCTCTGTGGAAATCCCAACCCAGAGCTGCATCCGCGCTG 300
QY 301 TGGGCGACCTTCAGAGTGGGTGGAAATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 359
Db 556 TGGGCGACCTTCAGAGTGGGTGGAAATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 359
QY 360 TGTGGAAGT-GGTGAGCTATGGTTTTCAGAGGGGCGAGCGGTACAGCCAGCGG-CAGGA 417
Db 616 GGTGGAAGTGGGTGAGCTATGGTTTTCAGAGGGGCGAGCGGTACAGCCAGCGGCGGCA 417

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QY 418 GAGTGTGCTCGACACGCCACCTGCACCCACTACA-CGACAGTCGTGTGGCCACCTCAAG 476
Db 676 GAGTGTGCTCGACACGCCACCTGCACCCACTACA-CGACAGTCGTGTGGCCACCTCAAG 476
QY 477 CCAGCTGGGCTGTGGGGGGGACCT--GTGCTCTGACGCCAGACGATAGAGCCCTTT 534
Db 736 CCAGCTGGGCTGTGGGGGGGACCTGTGCTCTGACGCCAGGAGCGGATAGAGCCCTTT 534
QY 535 GTCTGTGCTTACTCCCGGGAGGCAACTGGGAGGTCAACGGGAAG 579
Db 796 GTCTGTGCTTACTCCCGGGAGGCAACTGGGAGGTCAACGGGAAG 579

RESULT 12
AI792411
LOCUS   AI792411
DEFINITION
an34b09.y5 Gessler Wilms tumor Homo sapiens cDNA clone
IMAGE:1700537 5' similar to TR:043692 O43692 25 KDA TRYPSIN
INHIBITOR. ; mRNA sequence.
ACCESSION AI792411 GI:5340127
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 463)
AUTHORS   NCI/NIH-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute / National Institute of Dental Research,
          Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
          Unpublished (1997)
JOURNAL   Contact: Robert Strausberg, Ph.D.
          Email: cgaps-r@mail.nih.gov
COMMENT   This clone is available royalty-free through LLNL; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          This read is a RESEQUENCE of a previously sequenced human clone
          Original clone citation: see original entry for original citation
          information
          This 5' resequenced clone has no previous 5' data to verify this
          new read against
          Seq primer: -40RP from Gibco
          High quality sequence stop: 429.
FEATURES  Location/Qualifiers
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          /db_xref="taxon:9606"
          /clone="IMAGE:1700537"
          /clone_lib="Gessler Wilms tumor"
          /sex="pooled (6)"
          /lab_host="DH10B"
          /note="Vector: pSPORT1; Site:1: SalI; Site:2: NotI; RNA
          was prepared from a pool of 6 anonymous Wilms' tumor RNAs.
          RNA was prepared by acid-phenol, followed by one round of
          oligo dT selection. cDNA library preparation was with
          the BRL/Life Tech. Superscript Plasmid system. An
          oligo-dT NotI primer for first strand synthesis generated
          gcggccccc(t)n at the 3' end of the clones. A 5' SalI
          adaptor was used with sequence 5'-gtcgaccacgctcg-3'.
          Resulting cDNAs were size selected (average size 2 kb),
          NotI digested, and ligated into NotI/SalI-cut pSPORT1.
          Library was constructed by Dr. Manfred Gessler."
BASE COUNT 80 a 163 c 143 g 77 t
ORIGIN
Query Match      25.3%; Score 335.4; DB 9; Length 463;
Best Local Similarity 99.7%; Pred. No. 3e-65;
Matches 336; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 127 ATGCTGATCCAGAGACCTCCCTGGCGGGGGGCAATCTCTGCTGTGCTGCTGCTGCTGCT 60
Db 127 ATGCTGATCCAGAGACCTCCCTGGCGGGGGGCAATCTCTGCTGTGCTGCTGCTGCTGCTGCT 60

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61	CTTGGCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGACGAGCTCCGATGCC	120
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121	GGAGCCCTGAACAGGAAGGAGAGTTCTTGTGCTCTCTCCCTGCCACAACCGCTGGCGCAGC	180
247	GGAGCCCTGAACAGGAAGGAGAGTTCTTGTGCTCTCTCCCTGTCACAACCGCTGGCGCAGC	306
181	TGGGTCCAGCCCTTCGCGCTGCATCGCGAGGTGGAGCTGGAGTGCACAGCTGGCCCAA	240
307	TGGGTCCAGCCCTTCGCGCTGCATCGCGAGGTGGAGCTGGAGTGCACAGCTGGCCCAA	366
241	CTGGCTCAAGCCAGGCGAGCCCTCTGTGTAATCCCAACCCGAGCGCTGCATCCGSCCTG	300
367	CTGGCTCAAGCCAGGCGAGCCCTCTGTGTAATCCCAACCCGAGCGCTGGGTCCGSCCTG	426
301	TGGGCACCCCTGCAAGTGGGTGGAACTGCAGCTGC	460
427	TGGGCACCCCTGCAAGTGGGTGGAACTGCAGCTGC	463
RESULT 13		
BBF198258		
LOCUS		
DEFINITION		
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
Sus scrofa		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
1 (bases 1 to 429)		
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,		
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.		
and Keele,J.W.		
Design and use of two pooled tissue normalized cDNA libraries for		
EST discovery in swine		
Unpublished (2000)		
Contact: Smith Tpl		
USDA, ARS, US Meat Animal Research Center		
PO Box 166, Clay Center, NE 68933-0166, USA		
Tel: 402 762 4366		
Fax: 402 762 4390		
Email: smith@email.marc.usda.gov		
Single pass sequencing. Bases called and alt.trimmed with phred		
v0.980904.e. Vector identified by cross_match with the -mnscore 18		
and -mismatch 12 options.		
PCR Primers		
FORWARD: AGGAACACAGCTATGACCAT		
BACKWARD: GTTTCCCGATCAGCAGC		
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Location/Qualifiers		
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/clone_lib="MARC 2P1G"		
/tissue_type="pooled"		
/lab_host="DH10B"		
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;		
Library made from pooled tissue from testis, ovary,		
endometrium, hypothalamus, pituitary, and placenta."		
BASE COUNT		
97 a 125 c 122 g 85 t		
ORIGIN		
Query Match 23.68; Score 313.4; DB 12; Length 429;		
Best Local Similarity 84.88; Pred. No. 2.6e-60;		
Matches 386; Conservative 0; Mismatches 41; Indels 28; Gaps 2;		
Qy	838	TGCGTCTGTGCATCGGCTACGGGGAGCCAGGTGTGCCACAAGGTGCATTTCCCTTC 897
ph	2	TGCTTGTGTATGCTTGTATGGGGAGCCAGGTGTGCCACAAGGTGCATTTCCCTTC 61

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 15:41:47 ; Search time 3382.86 Seconds
(without alignments)
11407.612 Million cell updates/sec

Title: US-09-944-896-49_COPY_123_1448

Perfect score: 1326

Sequence: 1 atgtcgtcatccagagacctc.....gaaaccgttacatctgcccag 1326

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_ov:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_vl:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_mu:*

21: em_mu:*

22: em_mu:*

23: em_mu:*

24: em_mu:*

25: em_mu:*

26: em_mu:*

27: em_mu:*

28: em_mu:*

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34: em_mu:*

35: em_mu:*

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37: em_mu:*

38: em_mu:*

39: em_mu:*

40: em_mu:*

41: em_mu:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1254	94.6	1341	6	AX191493	Sequence
2	1254	94.6	1775	6	AX191503	Sequence
3	862.8	65.1	3293	9	HS0804652	Sequence
4	672.8	50.7	690	6	AX366554	Sequence
5	647.8	48.9	2900	9	AB060195	Macaca fa
6	240.4	18.1	180596	9	AC009060	Homo sapi
7	240.4	18.1	205044	2	AC009125	Homo sapi
8	238.8	18.0	163427	9	AC009053	Homo sapi
9	238.8	18.0	177479	9	AC009153	Homo sapi
10	238.8	18.0	197460	2	AC126771	Homo sapi
11	237.4	17.9	200409	2	AC097331	Pan trogl
12	237.2	17.9	204182	2	AC097271	Pan trogl
13	234	17.6	191108	2	AC097265	Pan trogl
14	232.2	17.5	179675	9	AC026468	Homo sapi
15	232.2	17.5	190595	9	AC009022	Homo sapi
16	192.6	14.5	79023	2	AC021951	Homo sapi
17	145.8	11.0	1328	9	BC008616	Homo sapi
18	145.6	11.0	179237	2	AC111287	Rattus no
19	145.6	11.0	197326	2	AC098076	Rattus no
20	139.4	10.5	200755	2	AC093451	Mus muscu
21	133.8	10.1	79023	2	AC021951	Homo sapi
22	124	9.4	200409	2	AC097331	Pan trogl
23	122.4	9.2	205044	2	AC009125	Homo sapi
24	95.8	7.2	2340	9	AK096051	Homo sapi
25	75	5.7	125020	9	AF429315	Homo sapi
26	68.2	5.1	179237	2	AC111287	Rattus no
27	60.6	4.6	125020	9	AF429315	Homo sapi
28	55.2	4.2	1491	6	AX101173	Sequence
29	55.2	4.2	1669	6	AX235371	Sequence
30	55.2	4.2	1690	9	AK027395	Sequence
31	55.2	4.2	1824	6	AX358802	Sequence
32	55.2	4.2	1824	6	AX362295	Sequence
33	55.2	4.2	2272	6	AX101175	Sequence
34	55.2	4.2	4574	6	AX086850	Sequence
35	55.2	4.2	4574	9	HS0801829	Sequence
36	55.2	4.2	4877	6	AX285067	Sequence
37	55.2	4.2	4877	6	AX285068	Sequence
38	55.2	4.2	4877	6	AX285079	Sequence
39	55	4.1	2403	6	AX235373	Sequence
40	53.6	4.0	2400	6	AX235369	Sequence
41	53.2	4.0	3052	10	AF109674	Sequence
42	48.8	3.7	166126	2	AP003686	Oryza sat
43	48.4	3.7	2664	9	HSHEPEGF	H.sapiens D
44	48.4	3.7	2668	9	HSTNX12	X1923 H.sapiens X
45	48.4	3.7	100267	9	HS080336A	Homo sapien

ALIGNMENTS

RESULT 1	AX191493	1341 bp	DNA	linear	PAT 15-AUG-2001
LOCUS	Sequence	15 from Patent WO0149728.			
DEFINITION	AX191493				
ACCESSION	AX191493.1	GI:15209675			
VERSION					
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1341)				
AUTHORS	Kato, S. and Kimura, T.				
TITLE	Human proteins having hydrophobic domains and dnas encoding these proteins				

[illegible]

QY	1	ATGCTGGATCCAGAGACCTCCCTTGCCCGGGGGCATCTCTGGCTGTGCTCCTGGCCCTC	60
Db	62	ATGCTGCATCCAGAGACCTCCCTTGCCCGGGGGCATCTCTGGCTGTGCTCCTGGCCCTC	121
QY	61	CTTGGCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGACGAGCTCCGATGGCC	122
Db	122	CTTGGCACCCTTGCGCAGAGGTGTGGCCACCCAGCTGCAGGACGAGCTCCGATGGCC	181
QY	121	GGAGCCCTGAACAGGAAGAGAGTTCTTGTGCTCTCCCTGCACACCCGCTGCGCAGC	180
Db	182	GGAGCCCTGAACAGGAAGAGAGTTCTTGTCTCTCCCTGCACACCCGCTGCGCAGC	241
QY	181	TGGGTCCAGCCCTCGGCTGCATGCGGAGGTGAGTGGATGACAGCCTGGCCAA	301
Db	242	TGGGTCCAGCCCTCGGCTGCATGCGGAGGTGAGTGGATGACAGCCTGGCCAA	361
QY	241	CTGGTCTAAGCAGGCGACCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCGGCGCTG	300
Db	302	CTGGTCTAAGCAGGCGACCCCTCTGTGGAATCCCAACCCGAGCCTGGCGCTG	361
QY	301	TGGCCACCCCTGCAGTGGCTGTGAACATGCTGCTGCCCGGGCTTGGCGTCTCTTT	360
Db	362	TGGCCACCCCTGCAGTGGCTGTGAACATGCTGCTGCCCGGGCTTGGCGTCTCTTT	421
QY	361	GTGTAAGTGGTCAGCCTATGTTTTCAGAGGGGAGCGGTACAGCCACCGGCTTGGCGTCTCTTT	420
Db	422	GTGTAAGTGGTCAGCCTATGTTTTCAGAGGGGAGCGGTACAGCCACCGGCTTGGCGTCTCTTT	481
QY	421	TGTGCTGCCAAGCCACCTGCAACCATACACGAGCTCGTGTGGGCCACCTCAAGCCAG	480
Db	482	TGTGCTGCCAAGCCACCTGCAACCATACACGAGCTCGTGTGGGCCACCTCAAGCCAG	541
QY	481	CTGGCTGTGGCGGGCACCTGTGCTGTGACAGCCACAGACCGATAGAAGCTTTGTCTGT	540
Db	542	CTGGCTGTGGCGGGCACCTGTGCTGTGACAGCCACAGACCGATAGAAGCTTTGTCTGT	601
QY	541	GCCTACTCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATATCCCTCATAGAAG	600
Db	602	GCCTACTCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATATCCCTCATAGAAG	661
QY	601	GGTGCCTTGGTTCGCTCTGCACAGCCAGTGTCTAGGCTGCTTCAAAGCTTGGACCAT	660
Db	662	GGTGCCTTGGTTCGCTCTGCACAGCCAGTGTCTAGGCTGCTTCAAAGCTTGGACCAT	721
QY	661	GCAGGGGGCTGTGTGAGTTCGCCAGGAATCTTCTCGCATGAGCTGCCAGAACCATGGA	720
Db	722	GCAGGGGGCTGTGTGAGTTCGCCAGGAATCTTCTCGCATGAGCTGCCAGAACCATGGA	781
QY	721	CGTCTCAACATCAGCACCTTGCCACTGCCACTGTCCCTTGGCTACACGGGAGACTGTC	780
Db	782	CGTCTCAACATCAGCACCTTGCCACTGCCACTGTCCCTTGGCTACACGGGAGACTGTC	841
QY	781	CAAGTGAGTGCAGCTGCAAGTGTGTGACGGCCCGTTCGGGAGGAGGAGTGTCTGTGC	840
Db	842	CAAGTGAGTGCAGCTGCAAGTGTGTGACGGCCCGTTCGGGAGGAGGAGTGTCTGTGC	901
QY	841	GTCTGTGACATCGGCTACGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCAC	900
Db	902	GTCTGTGACATCGGCTACGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCAC	961
QY	901	ACCTGTGACCTGAGGATCGAGGAGACTGCTCATGTGTGCTTTCAGAGGAGCAGACCTAT	960
Db	962	ACCTGTGACCTGAGGATCGAGGAGACTGCTCATGTGTGCTTTCAGAGGAGCAGACCTAT	1021
QY	961	TACAGAGCCAGATCAATGTTCAGAGAAAGCGGGGTGCTGGCCCAAGATCAAGAGCCAG	1020
Db	1022	TACAGAGCCAGATCAATGTTCAGAGAAAGCGGGGTGCTGGCCCAAGATCAAGAGCCAG	1081
QY	1021	AAAGTGCAGGACATCCTCGCCTTCTATCTGGGCGCCTGGAGACCACAGAGGTGACT	1080
Db	1082	AAAGTGCAGGACATCCTCGCCTTCTATCTGGGCGCCTGGAGACCACAGAGGTGACT	1141

Qy	1081	GACAGTGACTTCGAGACCAGGAACCTTCTGGATCGGGCTCACCTACAAGACCGCCCAAGGAC	1140
Db	1142	GACAGTGACTTCGAGACCAGGAACCTTGTGATCGGGCTCACCTACAAGACCGCCCAAGGAC	1201
Qy	1141	TGCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCCACAGTTTTCCTTTGGGCAGCCT	1200
Db	1202	TGCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCCACAGTTTTCCTTTGGGCAGCCT	1261
Qy	1201	GACAAACCACGGGTGTGTGGCTGAGTGCTGCCATGGGTTTGCAACTGGCGTGGAGCTG	1260
Db	1262	GACAAACCAC-----GGTTTGGCAAAGTTCGCTGGAGCTG	1294
Qy	1261	CAGGCTTCAGCTGCCTTCAACTGGACGACGACGCGTGTGAAAACCGGTAACATC	1320
Db	1295	CAGGCTTCAGCTGCCTTCAACTGGAAACACGACGCGTGTGAAAACCGGTAACATC	1354
Qy	1321	TGCCAG 1326	
Db	1355	TGCCAG 1360	
RESULT 3			
HSM804652			
LOCUS			
DEFINITION Homo sapiens mRNA; cDNA DKFzp686E1934 (from clone DKFz686E1934). PRI 10-JUL-2002			
ACCESSION AL833339			
VERSION AL833339.1 GI:21733974			
KEYWORDS			
SOURCE human.			
ORGANISM Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE 1 (bases 1 to 3293)			
AUTHORS Ottenwälder,B., Obermaier,B., Mewes,H.W., Weil,B., Amid,C. and Wiemann,S.			
TITLE Direct Submission			
JOURNAL	Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY		
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix (Martinsried/Germany) within the cdna sequencing consortium of the German Genome Project. This clone (DKFzp686E1934) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cdna/. Location/Qualifiers		
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/db_xref="taxon:9606"			
/clone="DKFz686E1934"			
/tissue_type="cdna-collection"			
/clone_lib="686 (synonym: hlcc3)". Vector pSportL_Sfi; host			
/DI08; sites SfIIA + SfiIB			
/dev_stage="adult"			
polya_signal 3171..3176			
polya_site 3190			
BASE COUNT 783 a 946 c * 967 g 597 t			
ORIGIN			
Query Match 65.1%; Score 862.8; DB 9; Length 3293;			
Best Local Similarity 98.6%; Pred. No. 9e-169;			
Matches 870; Conservative 0; Mismatches 12; Indels 0; Gaps 0;			
Qy	1	ATGCTGCATCCAGAGACCTCCCTTGGCCGGGGGCATCTCTTGCTGTGCCTCTGCGCCTC	60
Db	194	ATGCTGCATCCAGAGACCTCCCTTGGCCGGGGGCATCTCTTGCTGTGCCTCTGCGCCTC	253
Qy	61	CTTGCCACCATCTGGGCAGAGGTGGCCACCCACCTGCAGGAGGAGGCTCCGATGGCC	120
Db	254	CTTGCCACCGCTGGGCAGAGGTGGCCACCCACCTGCAGGAGGAGGCTCCGATGGCC	313
Qy	121	GGAGCCCTGACAGAAGAGAGTTCTTTGTCTCTCTCTCTGACACACCGCTGCGCAGC	180

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Db	314	GGAGCCCTGAACAGGAGAGAGATTCTTCTCCTCCCTGACACACCGCTGGCAGC	373	
Qy	181	TGGGTCCAGCCCTGCGGCTGACATGCGGAGGCTGAGCTGGAGTGACAGCCTGGGCCAA	240	
Db	374	TGGGTCCAGCCCTGCGGCTGACATGCGGAGGCTGAGCTGGAGTGACAGCCTGGGCCAA	433	
Qy	241	CTGGCTCAAGCAGGAGCGCTCTCTGGAATCCCAACCCCGAGCCTGGCATCCGGCTG	300	
Db	434	CTGGCTCAAGCAGGAGCGCTCTCTGGAATCCCAACCCCGAGCCTGGCATCCGGCTG	493	
Qy	301	TGGCGCACCTTGAAGTGGGCTGGAACATGCTGCTGCCCGGGCTTGGCTGCTTT	360	
Db	494	TGGCGCACCTTGAAGTGGGCTGGAACATGCTGCTGCCCGGGCTTGGCTGCTTT	553	
Qy	361	GTTGAAGTGGTACGCTATGTTTGCAGAGGGGAGCGGTACAGCCGCGGAGGAG	420	
Db	554	GTCGAAGTGGTACGCTATGTTTGCAGAGGGGAGCGGTACAGCCGCGGAGGAG	613	
Qy	421	TGTGCTCGCAACGCCACTGCACCCACTACAGCAGCTGCTGGTGGGCCACCTCAAGCCAG	480	
Db	614	TGTGCTCGCAACGCCACTGCACCCACTACAGCAGCTGCTGGTGGGCCACCTCAAGCCAG	673	
Qy	481	CTGGGCTGGGGGACCTGTGCTCTGCAGGCGGAGGAGGATAGAGGCTTGTCTGT	540	
Db	674	CTGGGCTGGGGGACCTGTGCTCTGCAGGCGGAGGAGGATAGAGGCTTGTCTGT	733	
Qy	541	GCCTACTCCCGGAGGCAACTGGGAGTCAACGGGAGGAGGATATCCCTTATAGAG	600	
Db	734	GCCTACTCCCGGAGGCAACTGGGAGTCAACGGGAGGAGGATATCCCTTATAGAG	793	
Qy	601	GGTGCCTGGTGTGCTGTGCAGCAGGCTGTCTCAGGCTGTTCAAGCCTGGGACCAT	660	
Db	794	GGTGCCTGGTGTGCTGTGCAGCAGGCTGTCTCAGGCTGTTCAAGCCTGGGACCAT	853	
Qy	661	CGAGGGGCTGTGAGGTGCTCCAGGATCCTTGTGCGATGAGTGGCAGAACCATGGA	720	
Db	854	CGAGGGGCTGTGAGGTGCTCCAGGATCCTTGTGCGATGAGTGGCAGAACCATGGA	913	
Qy	721	CGTCTCAACATCAGACCTGCGCAGTGCACACTGTCCTGCTGCTGCTGCTGCTGCTG	780	
Db	914	CGTCTCAACATCAGACCTGCGCAGTGCACACTGTCCTGCTGCTGCTGCTGCTGCTG	973	
Qy	781	CAAGTGAGTGAGCTGAGCTGCTGAGTGTGACGCGGCTTCCGGGAGGAGGAGTCTGCTG	840	
Db	974	CAAGTGAGTGAGCTGAGCTGCTGAGTGTGACGCGGCTTCCGGGAGGAGGAGTCTGCTG	1033	
Qy	841	GTCCTGACATCGCTACGGGGAGCCCGAGTGTGCCACCAAG	882	
Db	1034	GTCCTGACATCGCTACGGGGAGCCCGAGTGTGCCACCAAG	1075	
RESULT 4				
LOCUS	AX366554	Sequence 321 from Patent WO0206317.	690 bp	DNA
ACCESSION	AX366554			linear
VERSION	AX366554.1	GI:18697979		
KEYWORDS	human.			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1			
AUTHORS	Mitcham, J.L., King, G.E., Algate, P.A., Fling, S.P., Retter, M.W., Fanger, G.R., Reed, S.G., Vedvick, T.S., Carter, D., Hill, P. and Albone, E.			
TITLE	Compositions and methods for the therapy and diagnosis of ovarian cancer			
JOURNAL	Patent: WO 0206317-A 321 24-JAN-2002;			
FEATURES	CORIXA CORPORATION (US)			
source	Location/Qualifiers			
	1..690			
RESULT 5				
LOCUS	AB060195	Macaca fascicularis brain cDNA clone:QcCE-21387, full insert	2900 bp	mRNA
ACCESSION	AB060195			linear
VERSION	AB060195.1	GI:13676426		
KEYWORDS	oilgo capping; fis (full insert sequence);			
SOURCE	Macaca fascicularis adult male cerebellum cortex cDNA to mRNA, clone_lib:macaque brain cDNA library QcCE clone:QcCE-21387.			
ORGANISM	Macaca fascicularis			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; Cercopitheciniae; Macaca.			
REFERENCE	1 (sites)			
BASE COUNT				
ORIGIN	148 a	197 c	212 g	131 t
Query Match				
Best Local Similarity 50.7%; Score 672.8; DB 6; Length 690;				
Matches 685; Conservative 0; Mismatches 4; Indels 1; Gaps 1;				
Qy	482	TGGGCTGTGGGGGCGGACCTGCTCTGCGAGCCAGACAGCGATAGAGCCTTTGTCTGTG	541	
Db	1	TGGGCTGTGGGGGCGGACCTGCTCTGCGAGCCAGACAGCGATAGAGCCTTTGTCTGTG	60	
Qy	542	CCTACTCCCGGAGGCAACTGGGAGGTCAACGGGAGGACATCATCCCTATAAGAGG	601	
Db	61	CCTACTCCCGGAGGCAACTGGGAGGTCAACGGGAGGACATCATCCCTATAAGAGG	120	
Qy	602	GTGCTGTGGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAGCCTGGGACCATG	661	
Db	121	GTGCTGTGGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAGCCTGGGACCATG	180	
Qy	662	CAGGGGGCTGTGAGGTCCCGAGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGAC	721	
Db	181	CAGGGGGCTGTGAGGTCCCGAGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGAC	240	
Qy	722	GTCTCAACATCAGCAGCTGCCACTGTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG	781	
Db	241	GTCTCAACATCAGCAGCTGCCACTGTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG	300	
Qy	782	AAAGTGGTGCAGCCCTGCTGAGTGTGTCACGCGCGGTTCCGGGAGGAGGAGTCTGCTG	841	
Db	301	AAAGTGGTGCAGCCCTGCTGAGTGTGTCACGCGCGGTTCCGGGAGGAGGAGTCTGCTG	360	
Qy	842	TCGTGACATCGGCTACGGGGAGCCAGTGTGCCACCAAGTGTGCTTCCCTTCCACA	901	
Db	361	TCGTGACATCGGCTACGGGGAGCCAGTGTGCCACCAAGTGTGCTTCCCTTCCACA	420	
Qy	902	CCTGTGACCTGAGGATCGACGGAGACTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG	961	
Db	421	CCTGTGACCTGAGGATCGACGGAGACTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG	480	
Qy	962	ACAG - AGCCAGGATGAATGTGAGAGGAAGCGGGGTGCTGGGCCAGATCAAGAGCCAG	1020	
Db	481	ACAGAGCCAGGATGAATGTGAGAGGAAGCGGGGTGCTGGGCCAGATCAAGAGCCAG	540	
Qy	1021	AAAGTGGAGGATCTCGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1080	
Db	541	AAAGTGGAGGATCTCGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600	
Qy	1081	GACAGTGAATTCGAGACAGGAACTTCTGGATCGGGCTCACCTACAAGACCCGCAAGGAC	1140	
Db	601	GACAGTGAATTCGAGACAGGAACTTCTGGATCGGGCTCACCTACAAGACCCGCAAGGAC	660	
Qy	1141	TCCTTCCGCTGGGCCACAGGGGAGCACCAG	1170	
Db	661	TCCTTCCGCTGGGCCACAGGGGAGCACCAG	690	
RESULT 5				
LOCUS	AB060195	Macaca fascicularis brain cDNA clone:QcCE-21387, full insert	2900 bp	mRNA
ACCESSION	AB060195			linear
VERSION	AB060195.1	GI:13676426		
KEYWORDS	oilgo capping; fis (full insert sequence);			
SOURCE	Macaca fascicularis adult male cerebellum cortex cDNA to mRNA, clone_lib:macaque brain cDNA library QcCE clone:QcCE-21387.			
ORGANISM	Macaca fascicularis			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; Cercopitheciniae; Macaca.			
REFERENCE	1 (sites)			

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REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 205044)
DOE Joint Genome Institute.
Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jun 21, 2000 this sequence version replaced gi:7689944.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 595469
Center clone name: RPCI-11_492H8

Summary Statistics
Consensus quality: 156671 bases at least Q40
Consensus quality: 183548 bases at least Q30
Consensus quality: 189961 bases at least Q20
Estimated insert size: 189500; agarose-fp estimation
Quality coverage: 3.4 in Q20 bases; sum-of-contigs estimation
Quality coverage: 3.23 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 60 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES
source

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/db_xref="taxon:9606"
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/clone="RP11-296110"
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BASE COUNT
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Query Match
Best Local Similarity 89.4%; Pred. No. 5.9e-40;
Matches 270; Conservative 0; Mismatches 31; Indels 1; Gaps 1;
Qy 214 CTGGACTGAGTACAGCTGCCCAACTGGCTCAAGCCAGGCGACCCCTCTCTGGAATC 273
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Qy 274 CCAACCCGAGGCTGGCACTCCGGCTGTGGCGCACCCCTGCAAGTGGGCTGGAAATGCGAG 333
Db 78575 CCAACCCGAGGCTGGCACTCCGGCTGTGGCGCACCCCTGCAAGTGGGCTGGAAATGCGAG 78634
Qy 334 CTGCTGCCCGGGCTGGCGCTCTTTTGAAGTGGTCAAGCTATGTTGCGAGAGGGG 393
Db 78635 CTGCTGCCCGGGCTGGCGCTCTTTTGAAGTGGTCAAGCTATGTTGCGAGAGGGG 78694
Qy 394 CAGCGTACAGCCAGCCGCGGAGAGAGTGTGCTCGCAACGCCACCTGCACCCACTACACG 453
Db 78695 CAGCGTACAGCCAGCCGCGGAGAGAGTGTGCTCGCAACGCCACCTGCACCCACTACACG 78754
Qy 454 CAGCT-CGTGTGGCCACCTCAAGCCAGCTGGGCTGTGGGGGGACCTGTGCTCTGCAGG 512
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RESULT 7
AC009125/c

LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

AC009125
LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

AC009125
LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

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SEQUENCE, 60 unordered pieces.
AC009125
VERSION
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KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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VERSION
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KEYWORDS
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SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

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DEFINITION
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KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

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DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

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LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

AC009125
LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

AC009125
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VERSION
AC009125.5 GI:8575963
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HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

AC009125
LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

AC009125
LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

AC009125
LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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DEFINITION
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VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

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LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

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LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

AC009125
LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

AC009125
LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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AC009125
LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 205044)

AC009125
LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
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DEFINITION
SEQUENCE, 60 unordered pieces.
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AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

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LOCUS
DEFINITION
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AC009125
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KEYWORDS
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REFERENCE
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LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
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ORGANISM
Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

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LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

AC009125
LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

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DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
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AC009125
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DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
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HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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AC009125
LOCUS
DEFINITION
SEQUENCE, 60 unordered pieces.
AC009125
VERSION
AC009125.5 GI:8575963
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 205044)

* 25922 26021: gap of unknown length
 * 26022 27292: contig of 1271 bp in length
 * 27293 27392: gap of unknown length
 * 27393 28954: contig of 1562 bp in length
 * 28955 29054: gap of unknown length
 * 29055 30763: contig of 1709 bp in length
 * 30764 30863: gap of unknown length
 * 30864 32893: contig of 2030 bp in length
 * 32894 32993: gap of unknown length
 * 32994 34228: contig of 1235 bp in length
 * 34229 34329: gap of unknown length
 * 34330 36129: contig of 1801 bp in length
 * 36130 36229: gap of unknown length
 * 36230 38136: contig of 1907 bp in length
 * 38137 38236: gap of unknown length
 * 38237 39974: contig of 1738 bp in length
 * 39975 40074: gap of unknown length
 * 40075 41564: contig of 1490 bp in length
 * 41565 41664: gap of unknown length
 * 41666 43566: contig of 1902 bp in length
 * 43567 43666: gap of unknown length
 * 43668 45289: contig of 1623 bp in length
 * 45290 45389: gap of unknown length
 * 45390 47644: contig of 2255 bp in length
 * 47645 47744: gap of unknown length
 * 47746 50582: contig of 2838 bp in length
 * 50583 50682: gap of unknown length
 * 50684 53054: contig of 2372 bp in length
 * 53055 53154: gap of unknown length
 * 53155 54755: contig of 1601 bp in length
 * 54756 54855: gap of unknown length
 * 54856 57553: contig of 2708 bp in length
 * 57554 57664: gap of unknown length
 * 57665 59770: contig of 2106 bp in length
 * 59771 59869: gap of unknown length
 * 59870 61958: contig of 2088 bp in length
 * 61959 62057: gap of unknown length
 * 62060 65392: contig of 3335 bp in length
 * 65393 65492: gap of unknown length
 * 65493 68420: contig of 2928 bp in length
 * 68421 68520: gap of unknown length
 * 68521 71229: contig of 2709 bp in length
 * 71230 71329: gap of unknown length
 * 71330 73628: contig of 2299 bp in length
 * 73629 73728: gap of unknown length
 * 73729 77868: contig of 4140 bp in length
 * 77869 77969: gap of unknown length
 * 77970 81037: contig of 3068 bp in length
 * 81038 81136: gap of unknown length
 * 81137 83328: contig of 2192 bp in length
 * 83329 83428: gap of unknown length
 * 83429 86409: contig of 2981 bp in length
 * 86410 86509: gap of unknown length
 * 86510 90134: contig of 3625 bp in length
 * 90135 90234: gap of unknown length
 * 90235 93916: contig of 3682 bp in length
 * 93917 94016: gap of unknown length
 * 94017 97718: contig of 3702 bp in length
 * 97719 97818: gap of unknown length
 * 97819 100965: contig of 3147 bp in length
 * 100966 101065: gap of unknown length
 * 101066 105157: contig of 4091 bp in length
 * 105157 105257: gap of unknown length
 * 105257 110076: contig of 4820 bp in length
 * 110076 110176: gap of unknown length
 * 110177 114320: contig of 4144 bp in length
 * 114321 114420: gap of unknown length
 * 114421 120993: contig of 6573 bp in length
 * 120994 121093: gap of unknown length
 * 121094 127991: contig of 6898 bp in length
 * 127992 128091: gap of unknown length
 * 128092 136414: contig of 8323 bp in length
 * 136415 136514: gap of unknown length

* 136515 150305: contig of 13791 bp in length
 * 150306 150405: gap of unknown length
 * 150406 163992: contig of 13587 bp in length
 * 163993 164092: gap of unknown length
 * 164093 186975: contig of 22883 bp in length
 * 186976 187075: gap of unknown length
 * 187076 205044: contig of 17969 bp in length.
 FEATURES Location/Qualifiers
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/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="16"
 /clone_lib="RP11-492H8"
 /clone="RP11-492H8"

BASE COUNT 54631 a 45103 c 45331 g 53992 t 5987 others
 ORIGIN

Query Match 18.1%; Score 240.4; DB 2; Length 205044;
 Best Local Similarity 89.4%; Pred. No. 5.9e-40;
 Matches 270; Conservative 0; Mismatches 31; Indels 1; Gaps 1;

QY 214 CTGGACTGGAGTACACGCTGGCCCACTGCTCAAGCCAGGCGAGCCCTCTGTGGAATC 273
 Db 96235 CAGGACTGGAGTACACGCTGGCCCACTGCTCAAGCCAGGCGAGCCCTCTGTGGAATC 273
 QY 274 CCAACCCCGAGCCTGGGCTCCGCGCTGTGGCGCACCTGCAAGTGGGCTGGAACATGCAG 333
 Db 96175 CCAACCCCGAGCCTGGGCTCCGCGCTGTGGCGCACCTGCAAGTGGGCTGGAACATGCAG 333
 QY 334 CTGCTCCCGCGGCTGGGCTCTTTGTTGAAGTGTGAGCTGAGCTGATGTTTGCAGAGGGG 393
 Db 96115 CTGCTCCCGCGGCTGGGCTCTTTGTTGAAGTGTGAGCTGAGCTGATGTTTGCAGAGGGG 393
 QY 394 CAGCGGTACAGCCACGCGGCGAGGAGTGTGCTCGCAACGCCACCTGCACCCACTACACG 453
 Db 96055 CAGCGGTACAGCCACGCGGCGAGGAGTGTGCTCGCAACGCCACCTGCACCCACTACACG 453
 QY 454 CAGCT-CGTGTGGGCGACCTCAAGCCAGCTGGGCTGTGGCGGCGACCTGTGCTCTGCAGG 512
 Db 95995 CAGGTGAGTGTGCTGCAGGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 512
 QY 513 CC 514
 Db 95935 TC 95934

RESULT 8
 AC009053
 LOCUS AC009053 163427 bp DNA linear PRI 27-JUL-2001
 DEFINITION Homo sapiens chromosome 16 clone RP11-252A24, complete sequence.
 ACCESSION AC009053
 VERSION AC009053.7 GI:15022678
 KEYWORDS HIG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 163427)
 DOE Joint Genome Institute and Stanford Human Genome Center.
 Direct Submission
 Unpublished
 JOURNAL
 AUTHORS
 TITLE
 REFERENCE 2 (bases 1 to 163427)
 DOE Joint Genome Institute.
 Direct Submission
 Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 3 (bases 1 to 163427)
 DOE Joint Genome Institute and Stanford Human Genome Center.
 Direct Submission
 Submitted (27-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
 On Jul 27, 2001 this sequence version replaced gi:9256116.
 Draft Sequence Produced by DOE Joint Genome Institute


```

COMMENT
Baylor Plaza, Houston, TX 77030, USA
On Jun 21, 2002 this sequence version replaced gi:21450389.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: ZUAQ
Center clone name: RP43-53A2
----- Summary Statistics
Sequencing vector: Plasmid; M7789
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 187810 bases at least Q40
Consensus quality: 190821 bases at least Q30
Consensus quality: 193098 bases at least Q20
Estimated insert size: 212811; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-gel estimation
Quality coverage: 0x in Q70 bases; sum-of-contigs estimation

```

```

* -----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
*
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* As soon as it is available and the accession number will
* be preserved.
*

```

[illegible]

FEATURES	source
Location/Qualifiers	
1..200409	
/organism="pan troglodytes"	
/db_xref="taxon:9598"	
/col_xref="pan43-53a2"	

BASE COUNT 55207 a 46732 c 45615 g 51554 t 1301 others

ORIGIN

Query Match 17.9%; Score 237.4; DB 2; Length 200409;

Best Local Similarity 87.9%; Pred. NO. 2.5e-39;

Accession 0. Mismatches 36; Indels 1; Gaps 1;

[illegible]

QY	269	GAATCCAAACCCGAGAGCTTGCATCCGGCCTGTGCGCACCCCTGCAAGTGGGCTGGAACA	328
Db	177535	GAACCCAAACCCGAGAGCTTGCATCCGGCCTGTGCGCACCCCTGCAAGTGGGCTGGAACA	177476
QY	329	TGCAGAGCTGCTGCCCGGGGCTTGGCGTCTTTGTTGAAGTGTGACCCCTATGTTTGCAG	388
Db	177475	TGCAGAGCTGCTGCCCGGGGCTTGGCGTCTTTGTCGAACTGTGTCAGCCCTATGTTTGCAG	177416
QY	389	AGGGGCAGCGGTACAGCCACGCGGAGAGAGTGTGCTCGCACGCCACCTGCACCCACT	448
Db	177415	AGGGGCAGCGGTACAGCCACGCGGAGAGAGTGTGCTCGCAACGCCACCTGCACCCACT	177356
QY	449	ACAGCGAGCT-CGTGCTGGCGCCACCTCAAGCCAGCTGGGCTGTGGGGGCGCACCTGTGTGCTCT	507
Db	177355	ACAGCGAGGTGAGTGTGCTGAGGTGAGCCAGGTGCCAGCTCCCAAGATACAGACTTCC	177296
QY	508	GCAGGCC	514
Db	177295	ACTGGGC	177289

RESULT	12
AC097271	
LOCUS	204182 bp DNA linear HTG 20-OCT-2001
DEFINITION	Pan troglodytes clone RP43-35B16, WORKING DRAFT SEQUENCE, 8
ACCESSION	AC097271
VERSION	AC097271.1 GI:16117534
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE	Pan troglodytes.

Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 204182)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amarutunga,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burcher,P., Burkett,C., Burrell,K.J., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gundaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,B.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Jarlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
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Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M.,
Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
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Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.B.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N.,
Sisson,I., Sodergren,E., Sonalke,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K.F., Wu,Y., Xia,Y., Zhou,T., Zorrillas,S., Nelson,D.,

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Weinstock,G. and Gibbs,R.
 Direct Submission
 Unpublished
 2 (bases 1 to 204182)
 Worley,K.C.
 Direct Submission
 Submitted (13-OCT-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: ZUAY
 Center clone name: RP43-35B16
 ----- Summary Statistics
 Sequencing vector: Plasmid; M7789
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 202604 bases at least Q40
 Consensus quality: 204032 bases at least Q30
 Consensus quality: 205164 bases at least Q20
 Estimated insert size: 200244; sum-of-contigs estimation
 Quality coverage: 0x in Q20 bases; agarose-fp estimation
 Quality coverage: 9.4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 8 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of 'N', but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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48993	49092:	gap of unknown length	
49093	90443:	contig of 41350 bp in	length
90443	90542:	gap of unknown length	
90543	124888:	contig of 34346 bp in	length
124888	124988:	gap of unknown length	
124989	145269:	contig of 20281 bp in	length
145270	145369:	gap of unknown length	
145370	173261:	contig of 27892 bp in	length
173262	173361:	gap of unknown length	
173362	186532:	contig of 13171 bp in	length
186533	186632:	gap of unknown length	
186633	201672:	contig of 15040 bp in	length
201673	201772:	gap of unknown length	
201773	204182:	contig of 2410 bp in	length.

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Location/Qualifiers
1. .204182
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-35B16"
52711 a 50970 c 50521 g 49254 t 726 others

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Similarity	17.9%;	Score 237.2;	DB 2;	Length 204182;
	88.7%;	Pred. No. 2.7e-39;		

[illegible]

Qy	334	CTGTGCCCCGGGGCTTGGCGTCCTTTGTTGAAGTGGTCAGCCTATGTTTGCAGAGGG	393
Db	8113	CTGTGCCCCGGGGCTTGGCGTCCTTTGTTGAAGTGGTCAGCCTATGTTTGCAGAGGG	8172
Qy	394	CAGCGGTACACCCACGCGGGCAGGAGAGTGTCTCGCAACGCCACCTGCACCCACTACACG	453
Db	8173	CAGCGGTACACCCACGCGGGCAGGAGAGTGTCTCGCAACGCCACCTGCACCCACTACACG	8232
Qy	454	CAGCT-CGTGTGGGCCACCTCAAGCCAGCTGGGTGGGGCGCACCTGTGCTCTGCAGG	512
Db	8233	CAGGTGAGTGTGTGTCAGGTTGAGGCCAGCGTGCCAGCTCCACAGATACAGACTTCCAC	8292
Qy	513	CC 514	
Db	8293	GC 8294	
RESULT	13		
LOCUS	AC097265/c		
DEFINITION	191108 bp	DNA	linear
	Pan troglodytes clone RP43-119N13,	WORKING DRAFT SEQUENCE,	4
	unordered pieces.		
ACCESSION	AC097265		
VERSION	AC097265.3	GI:16328241	
KEYWORDS	HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.		
SOURCE	Pan troglodytes.		
ORGANISM	Pan troglodytes		

ORGANISM	pan troglodytes
REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
AUTHORS	1 (bases 1 to 191108) Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F. R., Allen, C., Allbrooks, S. L., Amarutunge, H. C., Are, J. R., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N. P., Buhay, C., Burch, P., Burkett, C., Burrell, K. L., Byrd, N. C., Carron, T. F., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C. D., Cox, C., Coyle, M. D., Dathorne, S. R., David, R., Davila, M. L., Davis, C., Davy-Carroll, L., Dederich, D. A., Delaney, K. R., Delgado, O., Denn, A. L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J., Earhart, C., Edgar, D., Edwards, C. C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hoques, M., Holloway, C., Hollins, B., Homs, J. F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L., Li, J., Li, Z., Lichtharge, O., Lieu, C., Liu, J., Liu, W., Loulseghe, H., Lozada, M., Mapa, P., Martin, R., Lucier, R., Lucindale, A., Ma, J., Maheshwari, M., Mapua, P., Metcalf, M. P., Meador, M., Martinez, E., Massey, E., Mahwiney, E., McClend, M. P., Mohabbat, K., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Newton, N., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okunolu, G., Oragunye, N., Peters, L., Pickens, R., Pace, A., Payton, B., Peery, J., Perez, L., Rivers, M., Rojas, A., Rojubokan, I., Rolfe, L., Ruiz, S., Saverly, G., Scherer, S., Scott, G., Shen, H., Shoohtari, N., Sisson, I., Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Taber, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalob, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, F., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
	Direct Submission
	Unpublished
	2 (bases 1 to 191108)
	Worley, K. C.
TITLE	JOURNAL
REFERENCE	
AUTHORS	

TITLE
JOURNAL
REFERENCE
AUTHORS

Mon Dec 30 09:16:14 2002

TITLE Direct Submission
JOURNAL Submitted (13-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Oct 23, 2001 this sequence version replaced gi:16258969.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: ZUAR
Center clone name: RP43-119N13
----- Summary Statistics
Sequencing vector: Plasmid; M77789
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 191814 bases at least Q40
Consensus quality: 193054 bases at least Q30
Consensus quality: 194113 bases at least Q20
Estimated insert size: 193275; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 9.3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will be preserved.

* 1 121806: contig of 121806 bp in length
* 121807 121906: gap of unknown length
* 121907 172531: contig of 50625 bp in length
* 172532 172631: gap of unknown length
* 172632 180970: contig of 8339 bp in length
* 180971 181070: gap of unknown length
* 181071 191108: contig of 10038 bp in length.

FEATURES
source
1. .191108
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-119N13"
BASE COUNT 49835 a 45817 c 45055 g 50100 t 301 others
ORIGIN
Query Match 17.6%; Score 234; DB 2; Length 191108;
Best Local Similarity 88.1%; Pred. No. 1.3e-38;
Matches 266; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY 214 CTGGACTGGAGTGACAGCGCTGGCCCAACTGGCTCAAGCCAGGCGAGCCCTCTGTGAATC 273
DB 63506 CAGGACTGGAGTGACAGCGCTGGCCCAACTGGCTCAAGCCAGGCGAGCCCTCTGTGAATC 63447
QY 274 CCAACCCGAGCGCTGGCATTGGCGCTGGCGACCTGCAAGTGGCTGGAACATGCAG 333
DB 63446 CCAACCCGAGCGCTGGCATTGGCGCTGGCGACCTGCAAGTGGCTGGAACATGCAG 63387
QY 334 CTGCTGCCCGCGGCTTGGCGTCTTTGTTGAAGTGGCTGACCTATGTTTGCAGAGGG 393
DB 63386 CTGCTGCCCGCGGCTTGGCGTCTTTGTTGAAGTGGCTGACCTATGTTTGCAGAGGG 63327
QY 394 CAGCGGTACAGCCAGCGGACGAGAGTGTCTGCGAACGCCACTGCAACCACTACACG 453
DB 63326 CAGCGGTACAGCCAGCGGACGAGAGTGTCTGCGAACGCCACTGCAACCACTACACG 63267
QY 454 CAGCT-CGTGTGGCGCCACCTCAAGCCAGCTGGGCTGTGGCGGACCTGTGCTGTGCAGG 512
DB 63266 CAGGTGAGTGTGCTGCAGGTTGAGCGGCTGCCAGCTGCCAGATACAGACTTCCACTGG 63207

QY 513 CC 514
DB 63206 GC 63205
RESULT 14
AC026468/c
LOCUS AC026468
DEFINITION Homo sapiens chromosome 16 clone RP11-419C5, complete sequence.
ACCESSION AC026468
VERSION AC026468.6
KEYWORDS GI:16596532
SOURCE HTG.
ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 179675)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 179675)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 179675)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Nov 2, 2001 this sequence version replaced gi:14589452.
Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

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/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-419C5"
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ORIGIN
Query Match 17.5%; Score 232.2; DB 9; Length 179675;
Best Local Similarity 96.7%; Pred. No. 3e-38;
Matches 237; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 214 CTGGACTGGAGTGACAGCGCTGGCCCAACTGGCTCAAGCCAGGCGAGCCCTCTGTGAATC 273
DB 46561 CAGGACTGGAGTGACAGCGCTGGCCCAACTGGCTCAAGCCAGGCGAGCCCTCTGTGAATC 46502
QY 274 CCAACCCGAGCGCTGGCATTGGCGCTGGCGACCTGCAAGTGGCTGGAACATGCAG 333
DB 46501 CCAACCCGAGCGCTGGCATTGGCGCTGGCGACCTGCAAGTGGCTGGAACATGCAG 46442
QY 334 CTGCTGCCCGCGGCTTGGCGTCTTTGTTGAAGTGGCTGACCTATGTTTGCAGAGGG 393


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Db 46441 CTGCTACCCGCGGCTTGGTGTCTTGTGGAAGTGTCTAGCCTATGTTGCAGAGGG 46382
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QY 454 CAGCT 458
Db 46321 CAGGT 46317

RESULT 15
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LOCUS 190595 bp DNA linear PRI 07-FEB-2002
DEFINITION Homo sapiens chromosome 16 clone RP11-106J23, complete sequence.
AC009022
VERSION AC009022.9 GI:18581696
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 190595)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 190595)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 190595)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Feb 7, 2002 this sequence version replaced gi:16924076.
Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
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Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
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BASE COUNT 51435 a 43243 c 43697 g 52220 t
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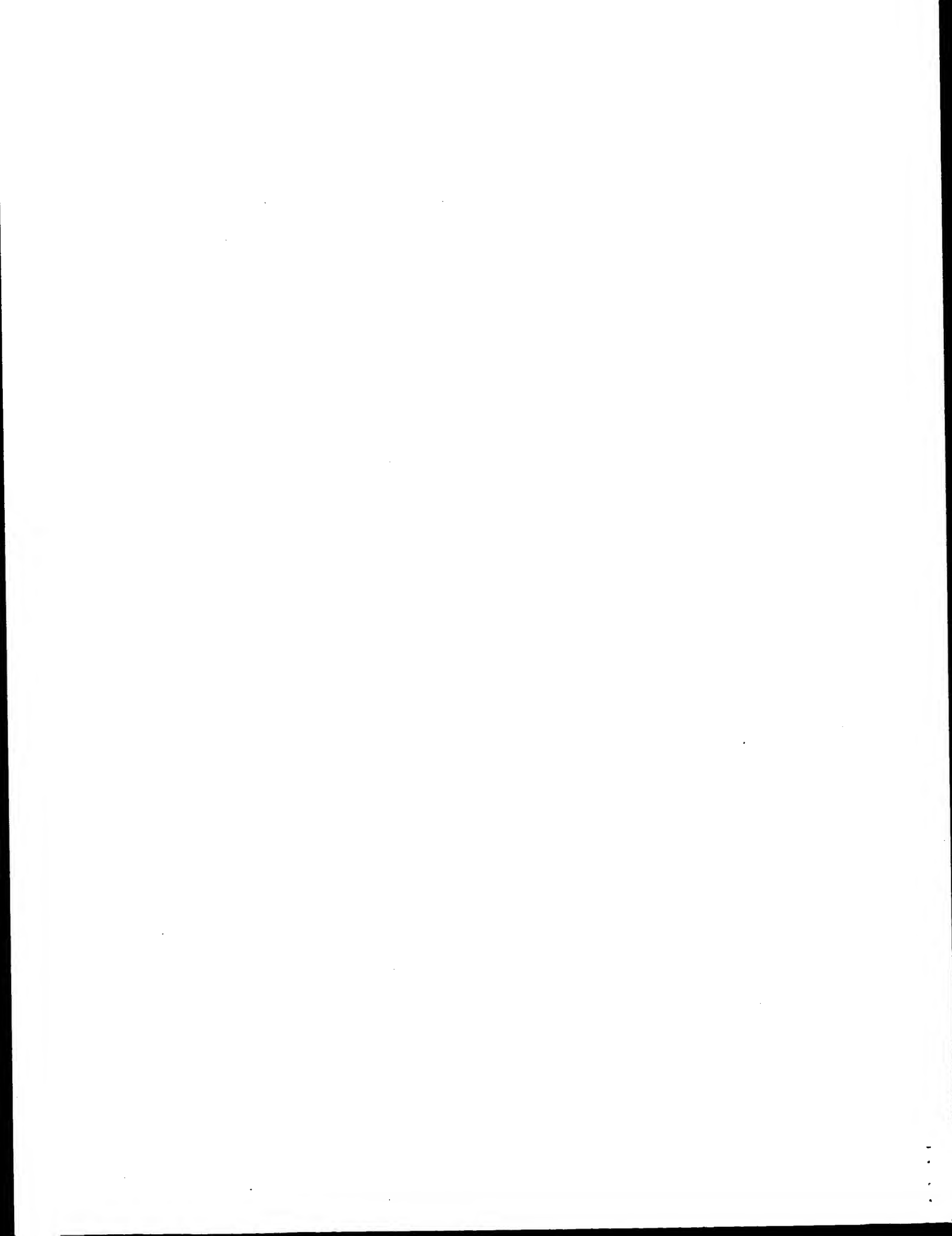
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Db 188865 CCAACCCCGAGGCTGGCATCCCGCCTGTGGCCGACCCCTGCAAGTGGGCTGGAACATGCAG 188806
QY 334 CTGCTGCCCGCGGGCTTGGCGTCCCTTTGTTGAAGTGGTCAGCCTATGTTGTCAGAGGGG 393
Db 188805 CTGCTACCCGCGGGCTTGGTGTCTTGTGGAAGTGGTCAGCCTATGTTGTCAGAGGGG 188746
QY 394 CAGCGGTACAGCCAGCGCGGAGGAGTGTCTCGAAGCCACCTGCACCCACTACAG 453
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QY 454 CAGCT 458
Db 188685 CAGCT 188681

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Search completed: December 28, 2002, 20:14:24
Job time : 4575.86 secs

Query Match 17.5%; Score 232.2; DB 9; Length 190595;
Best Local Similarity 96.7%; Pred. No. 3e-38;
Matches 237; Conservative 0; Mismatches 8; Indels 0; Gaps 0;



Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1876	100.0		1876	9	US-09-944-413-49	Sequence 49, Appl
2	1876	100.0		1876	9	US-09-944-403-49	Sequence 49, Appl
3	1876	100.0		1876	9	US-09-944-896-49	Sequence 49, Appl
4	1876	100.0		1876	9	US-09-944-944-49	Sequence 49, Appl
5	1876	100.0		1876	10	US-09-866-028-49	Sequence 49, Appl
6	1876	100.0		1876	10	US-09-944-449-49	Sequence 49, Appl
7	1876	100.0		1876	10	US-09-944-457-49	Sequence 49, Appl
8	1876	100.0		1876	10	US-09-945-587-49	Sequence 49, Appl
9	1876	100.0		1876	10	US-09-945-085-49	Sequence 49, Appl
10	1876	100.0		1876	10	US-09-944-396-49	Sequence 49, Appl
11	1876	100.0		1876	10	US-09-944-097-49	Sequence 49, Appl
12	1876	100.0		1876	10	US-09-944-432-49	Sequence 49, Appl
13	1876	100.0		1876	10	US-09-943-762-49	Sequence 49, Appl
14	1876	100.0		1876	10	US-09-944-654-49	Sequence 49, Appl
15	1876	100.0		1876	10	US-09-943-851A-49	Sequence 49, Appl
16	1776.2	94.7		1923	9	US-10-042-141-12	Sequence 12, Appl
17	1776.2	94.7		1923	10	US-09-726-643-12	Sequence 12, Appl
18	1751	93.3		1856	10	US-09-790-264-1	Sequence 1, Appl
19	1293	68.9		1338	10	US-09-790-264-3	Sequence 3, Appl

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QY 1441 TCTGCCAGTTTCCAGGAGCAGCATCTCCCGTGGGCGCCAGGCTCTGAGGCGCTGACCA 1500
Db 1441 TCTGCCAGTTTCCAGGAGCAGCATCTCCCGTGGGCGCCAGGCTCTGAGGCGCTGACCA 1500
QY 1501 CATGGCTCCCTCGCTGGGCGCACCGGCTCTGCTTACCTGTGTGCTGCCACCTGTCT 1560
Db 1501 CATGGCTCCCTCGCTGGGCGCACCGGCTCTGCTTACCTGTGTGCTGCCACCTGTCT 1560
QY 1561 GGAACAAGGCGCAGGTTAAGACACATGCTCATGTCCAAAGAGGTTCTACAGCTTGCAC 1620
Db 1561 GGAACAAGGCGCAGGTTAAGACACATGCTCATGTCCAAAGAGGTTCTACAGCTTGCAC 1620
QY 1621 AATGCCAGAAGTTGGGCGAGAGAGGAGGAGGCGGCGGCTGAGGCGGAGGAGTGAGTGT 1680
Db 1621 AATGCCAGAAGTTGGGCGAGAGAGGAGGAGGCGGCGGCTGAGGCGGAGGAGTGAGTGT 1680
QY 1681 AGAAGAAGCTGGGCGCTTGGGCGTCTTTTGTGATGGAAGATGGGCTTCAATTAGATGC 1740
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QY 1741 GAAGAGAGGAGACACCGCAGTGTCCAAAGGCTCTCTTCCACCTGGGCGGAGACCC 1800
Db 1741 GAAGAGAGGAGACACCGCAGTGTCCAAAGGCTCTCTTCCACCTGGGCGGAGACCC 1800
QY 1801 TGTGGGCGAGGAGCTTCCCTGTGGCATGAACCCCGGCTATTAATATGAATCAG 1860
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QY 1861 CTGAAAAA 1876
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RESULT 2

US-09-944-403-49

; Sequence 49, Application US/09944403

; Patent No. US20020165143A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Flivaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kijavin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

APPLICANT: Tamas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548PIC1
CURRENT APPLICATION NUMBER: US/09/944,403
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: NO. US20020165143A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: NO. US20020165143A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000

;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 49
;; LENGTH: 1876
;; TYPE: DNA
;; ORGANISM: Homo Sapien
;; US-09-944-403-49

Query Match 100.0%; Score 1876; DB 9; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTCCTTTTCCACAGCCAGCCGCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTG 60

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DB 61 AGAAACAAGCCGGTGGCTGAGCCAGGCTGTGCACGAGCACCTGACGGGCCCAACAGAC 120

QY 121 COATGCTGCATCCAGAGACCTCCCTGGCCGGGGGATCTCTGGCTGTGTCTCTGGCC 180
DB 121 COATGCTGCATCCAGAGACCTCCCTGGCCGGGGGATCTCTGGCTGTGTCTCTGGCC 180

QY 181 TCCTTGGACACACCTGGGAGAGGTGTGCCACCCAGCTGCAGGAGCAGCTCCGATGG 240
DB 181 TCCTTGGACACACCTGGGAGAGGTGTGCCACCCAGCTGCAGGAGCAGCTCCGATGG 240

QY 241 CCGGAGCCCTGAACAGAGAGAGTTCCTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB 241 CCGGAGCCCTGAACAGAGAGAGTTCCTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300

QY 301 GTGGGTCCAGCCCTCGGGCTGACATGCGGAGGTGGAGCTGAGTGACAGCTGGCC 360
DB 301 GTGGGTCCAGCCCTCGGGCTGACATGCGGAGGTGGAGCTGAGTGACAGCTGGCC 360

QY 361 AACTGCTCAAGCCAGGAGCCCTCTGTGAAATCCCAACCCGAGCTGGCATCCGCC 420
DB 361 AACTGCTCAAGCCAGGAGCCCTCTGTGAAATCCCAACCCGAGCTGGCATCCGCC 420

QY 421 TGTGGCGCACCTTGCAAGTGGGCTGGAACATGCAAGCTGCTGCCCGGGCTTGGCTCT 480
DB 421 TGTGGCGCACCTTGCAAGTGGGCTGGAACATGCAAGCTGCTGCCCGGGCTTGGCTCT 480

QY 481 TTGTTGAAGTGGTCAAGCTATGTTTTCAGAGGGGAGCGGTACAGCCAGCGGAGAG 540
DB 481 TTGTTGAAGTGGTCAAGCTATGTTTTCAGAGGGGAGCGGTACAGCCAGCGGAGAG 540

QY 541 AGTGTGCTCGCAAGCCACCTGCACCCACATACAGCAGCTCGTGTGGGCCACCTCAAGCC 600
DB 541 AGTGTGCTCGCAAGCCACCTGCACCCACATACAGCAGCTCGTGTGGGCCACCTCAAGCC 600

QY 601 AGCTGGGCTGTGGCGGACCTGTGCTCTGAGGCCAGACGCGATAGAAGCCTTGTCT 660
DB 601 AGCTGGGCTGTGGCGGACCTGTGCTCTGAGGCCAGACGCGATAGAAGCCTTGTCT 660

QY 661 GTGCCCTACTCCCGGAGGCAACTGGGAGGTCAAGGGAGACATCATCCCTATAAGA 720
DB 661 GTGCCCTACTCCCGGAGGCAACTGGGAGGTCAAGGGAGACATCATCCCTATAAGA 720

QY 721 AGGTGCTGCTGTGCTCTGACAGCAGCTGTCTCAGGCTGCTCAAGGCTTGGGACC 780
DB 721 AGGTGCTGCTGTGCTCTGACAGCAGCTGTCTCAGGCTGCTCAAGGCTTGGGACC 780

QY 781 ATGCAGGGGGGCTCTGTGAGGTCCCGAGGAATCCTTCTCGCATGAGCTGCCAGACCATG 840
DB 781 ATGCAGGGGGGCTCTGTGAGGTCCCGAGGAATCCTTCTCGCATGAGCTGCCAGACCATG 840

QY 841 GACGTCTCAACATCAGCACTGCCACTGCTCCCTGGCTACACGGGCAGATACT 900
DB 841 GACGTCTCAACATCAGCACTGCCACTGCTCCCTGGCTACACGGGCAGATACT 900

QY 901 GCCAAGTGAAGTGCAGCCTGCAGTGTGCACGGCCGGTTCGGGAGGAGGAGTGTCTGT 960
DB 901 GCCAAGTGAAGTGCAGCCTGCAGTGTGCACGGCCGGTTCGGGAGGAGGAGTGTCTGT 960

QY 961 GCCTCTGTGACATFCGGCTACGGGGAGCCAGTGTGCCACCAAGTGTCTTCCCTTCC 1020
DB 961 GCCTCTGTGACATFCGGCTACGGGGAGCCAGTGTGCCACCAAGTGTCTTCCCTTCC 1020

QY 1021 ACACCTGTACCTGAGGATCGAGGAGCTCTTCTATGCTGTCTTTCAGAGGAGACACCT 1080
DB 1021 ACACCTGTACCTGAGGATCGAGGAGCTCTTCTATGCTGTCTTTCAGAGGAGACACCT 1080

QY 1081 ATTACAGAGCCAGGATGAAATGTGCAGAGGAAAGCGGGGTGCTGGCCAGATCAAGAGCC 1140
DB 1081 ATTACAGAGCCAGGATGAAATGTGCAGAGGAAAGCGGGGTGCTGGCCAGATCAAGAGCC 1140

QY 1141 AGAAAGTGCAGGAGATCTCCCTTCTATCTGGCCGGCTGGAGACCAACAGAGGTGA 1200
DB 1141 AGAAAGTGCAGGAGATCTCCCTTCTATCTGGCCGGCTGGAGACCAACAGAGGTGA 1200

QY 1201 CTGACAGTGAATTCGAGACCAAGGAATCTTCTGATCGGGCTCACCTTACAGACCGCAAG 1260
DB 1201 CTGACAGTGAATTCGAGACCAAGGAATCTTCTGATCGGGCTCACCTTACAGACCGCAAG 1260

QY 1261 ACTCCTTCCGCTGGGCCACAGGGGAGCACAGGCTTCCACAGTTCCTTGGCCAGC 1320
DB 1261 ACTCCTTCCGCTGGGCCACAGGGGAGCACAGGCTTCCACAGTTCCTTGGCCAGC 1320

QY 1321 CTGACACCAAGCCGCTGGTGTGGCTGAGTGTGCTTCCATGGGTTTGGCAACTTGGCTGGAGC 1380
DB 1321 CTGACACCAAGCCGCTGGTGTGGCTGAGTGTGCTTCCATGGGTTTGGCAACTTGGCTGGAGC 1380

QY 1381 TGCAAGCTTCAGCTTGCCTTCAACTGGAACGACGACGCTGCAAAACCCGAAACCGTTACA 1440
DB 1381 TGCAAGCTTCAGCTTGCCTTCAACTGGAACGACGACGCTGCAAAACCCGAAACCGTTACA 1440

QY 1441 TCTGCCAGTTCGCGGAGGAGCACATCTCCGGTGGGGCCAGGGTCTGAGGCCGTGACCA 1500
DB 1441 TCTGCCAGTTCGCGGAGGAGCACATCTCCGGTGGGGCCAGGGTCTGAGGCCGTGACCA 1500

QY 1501 CATGGCTCCCTCGCTGCGCTGGGAGCACCGGCTCTGCTTACTGCTTGGCCACCTGTCT 1560
DB 1501 CATGGCTCCCTCGCTGCGCTGGGAGCACCGGCTCTGCTTACTGCTTGGCCACCTGTCT 1560

QY 1561 GGAACAGGGCCAGGTTAAGACACATGCTTCTTCCAAAGAGGTCTCAGACCTTGCAC 1620
DB 1561 GGAACAGGGCCAGGTTAAGACACATGCTTCTTCCAAAGAGGTCTCAGACCTTGCAC 1620

QY 1621 AATGCCAGAACTTGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1680
DB 1621 AATGCCAGAACTTGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1680

QY 1681 AGAAGAGCTGGGCGCTTCCGCTCTTGTATGGGAAGATGGGCTTCAATAGATGGC 1740
DB 1681 AGAAGAGCTGGGCGCTTCCGCTCTTGTATGGGAAGATGGGCTTCAATAGATGGC 1740

QY 1741 GAAGGAGAGGAGACCGCCAGTGTCCAAAGAGGCTCTCTTCCACCTGGCCAGACCC 1800
DB 1741 GAAGGAGAGGAGACCGCCAGTGTCCAAAGAGGCTCTCTTCCACCTGGCCAGACCC 1800

QY 1801 TGTGGGAGGAGGAGCTTCCCTGTGGCATGAACCCCAAGGGGTATTAATATCAATCAG 1860
DB 1801 TGTGGGAGGAGGAGCTTCCCTGTGGCATGAACCCCAAGGGGTATTAATATCAATCAG 1860

QY 1861 CTGAAAAAAGAAAAA 1876

Db 1861 CTGAAAAA 1876

RESULT 3

US-09-944-896-49
 ; Sequence 49, Application US/09944896
 ; Patent No. US20020168715A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin
 ; APPLICANT: Botstein, David
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gunney, Austin
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Kljavin, Ivar
 ; APPLICANT: Napier, Mary
 ; APPLICANT: Roy, Margaret
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P2548P1C1
 ; CURRENT APPLICATION NUMBER: US/09/944,896
 ; CURRENT FILING DATE: 2001-08-31
 ; PRIOR APPLICATION NUMBER: 09/866,028
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/069,334
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,335
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,278
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,425
 ; PRIOR FILING DATE: December 12, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,696
 ; PRIOR FILING DATE: December 16, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,694
 ; PRIOR FILING DATE: December 16, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,702
 ; PRIOR FILING DATE: December 16, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,870
 ; PRIOR FILING DATE: December 17, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,873
 ; PRIOR FILING DATE: December 17, 1997
 ; PRIOR APPLICATION NUMBER: 60/068,017
 ; PRIOR FILING DATE: December 18, 1997
 ; PRIOR APPLICATION NUMBER: 60/070,440
 ; PRIOR FILING DATE: January 5, 1998
 ; PRIOR APPLICATION NUMBER: 60/074,086
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/074,092
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/075,945
 ; PRIOR FILING DATE: February 25, 1998
 ; PRIOR APPLICATION NUMBER: 60/112,850
 ; PRIOR FILING DATE: December 16, 1998
 ; PRIOR APPLICATION NUMBER: 60/113,296
 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 60/146,222
 ; PRIOR FILING DATE: July 28, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US98/19330
 ; PRIOR FILING DATE: September 16, 1998
 ; PRIOR APPLICATION NUMBER: PCT/US98/25108
 ; PRIOR FILING DATE: December 1, 1998
 ; PRIOR APPLICATION NUMBER: 09/216,021
 ; PRIOR FILING DATE: December 16, 1998
 ; PRIOR APPLICATION NUMBER: 09/218,517

;
 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 09/254,311
 ; PRIOR FILING DATE: March 3, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252
 ; PRIOR FILING DATE: June 22, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: September 15, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28409
 ; PRIOR FILING DATE: No. US20020168715A1
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: No. US20020168715A1
 ; PRIOR APPLICATION NUMBER: PCT/US99/28301
 ; PRIOR FILING DATE: December 1, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: December 16, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US00/03565
 ; PRIOR FILING DATE: February 11, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: February 22, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841
 ; PRIOR FILING DATE: March 2, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/08439
 ; PRIOR FILING DATE: March 30, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/14042
 ; PRIOR FILING DATE: May 22, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/20710
 ; PRIOR FILING DATE: July 28, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678
 ; PRIOR FILING DATE: December 1, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520
 ; PRIOR FILING DATE: February 28, 2001
 ; NUMBER OF SEQ ID NOS: 120
 ; SEQ ID NO 49
 ; LENGTH: 1876
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-09-944-896-49

Query Match 100.0%; Score 1876; DB 9; Length 1876;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTCTTTTGTCCACGAGCCAGCCGCTGCTGAGATGTGAATAGCTCCATCCAGCCTG	60
Db	1	CTCTTTTGTCCACGAGCCAGCCGCTGCTGAGATGTGAATAGCTCCATCCAGCCTG	60
QY	61	AGAAACAAGCCGGTGGCTGAGCCAGGCTGTGCACGGAGACCTGACGGGGCCCAACAC	120
Db	61	AGAAACAAGCCGGTGGCTGAGCCAGGCTGTGCACGGAGACCTGACGGGGCCCAACAC	120
QY	121	CCATGCTGCATCCAGAGACCTCCCTGGCGGGGGCAATCTCTGGCTGTGCTTGGGCC	180
Db	121	CCATGCTGCATCCAGAGACCTCCCTGGCGGGGGCAATCTCTGGCTGTGCTTGGGCC	180
QY	181	TCCTTGGCACCACTGGGAGAGGTGTGGCCACCCAGCTGCGAGGAGCAGGCTCCGATGG	240
Db	181	TCCTTGGCACCACTGGGAGAGGTGTGGCCACCCAGCTGCGAGGAGCAGGCTCCGATGG	240
QY	241	CCGGAGCCCTGAACAGAGAGAGTTCTTGTCTCTCCCTGCAACCCGCTGGCGCA	300
Db	241	CCGGAGCCCTGAACAGAGAGAGTTCTTGTCTCTCCCTGCAACCCGCTGGCGCA	300
QY	301	GCTGGTCCAGCCCTGGGCTGACATGGGAGGTGGAGTGGAGTGGAGTGGAGTGGGCC	360
Db	301	GCTGGTCCAGCCCTGGGCTGACATGGGAGGTGGAGTGGAGTGGAGTGGAGTGGGCC	360
QY	361	AACTGGCTAAGCCAGGCGCCCTCTGTGGAAATCCAAACCCAGGCTGGCATCCGCGC	420
Db	361	AACTGGCTAAGCCAGGCGCCCTCTGTGGAAATCCAAACCCAGGCTGGCATCCGCGC	420
QY	421	TGTGGCGCACCTGCAAGTGGGCTGGAACATGCAGTGTGCTGCTGGGGGCTGGCGTCT	480
Db	421	TGTGGCGCACCTGCAAGTGGGCTGGAACATGCAGTGTGCTGCTGGGGGCTGGCGTCT	480

PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 49
LENGTH: 1876
TYPE: DNA
ORGANISM: Homo Sapien
US-09-944-944-49

Query Match 100.0%; Score 1876; DB 9; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTTTTGTCCACCGCCAGCCTGACCTCTGAGATTGTAAGTCTCCATCCAGCCCTG 60
Db 1 CTCCTTTTGTCCACCGCCAGCCTGACCTCTGAGATTGTAAGTCTCCATCCAGCCCTG 60

Qy 61 AGAAACAAGCGGGTGGTGTGACCGAGGCTGTGACCGAGCCTGTGACCGGCCCAACAGAC 120
Db 61 AGAAACAAGCGGGTGGTGTGACCGAGGCTGTGACCGAGCCTGTGACCGGCCCAACAGAC 120

121 CCATGCTGATCCAGAGACCTCCCTGGCGGGGGCATCTCTGGCTGTCTCTCTGCCCC 180
121 CCATGCTGATCCAGAGACCTCCCTGGCGGGGGCATCTCTGGCTGTCTCTCTGCCCC 180
181 TCCTTTGGCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGACAGGAGAGGCTCCGATGG 240
181 TCCTTTGGCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGACAGGAGAGGCTCCGATGG 240
241 CCGGAGCCCTGAACAGGAGAGAGTTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
241 CCGGAGCCCTGAACAGGAGAGAGTTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
301 GCTGGGTCCAGCCCTGCGGCTGACATGGGAGGTGGACTGGAGTGGAGTGGAGTGGAGTGG 360
301 GCTGGGTCCAGCCCTGCGGCTGACATGGGAGGTGGACTGGAGTGGAGTGGAGTGGAGTGG 360
361 AACTGGCTAAGCCAGGAGCCCTCTGTGGAAATCCAAACCCAGCTGGCATCCGAGCC 420
361 AACTGGCTAAGCCAGGAGCCCTCTGTGGAAATCCAAACCCAGCTGGCATCCGAGCC 420
421 TGTGGCGCACCCTGCAAGTGGGCTGGAACATGCAGTGTCTGCCCCGGGGTGGCGTCT 480
421 TGTGGCGCACCCTGCAAGTGGGCTGGAACATGCAGTGTCTGCCCCGGGGTGGCGTCT 480
481 TTGTTGAAGTGTGACGCTATGTTTGCAGAGGGGCGGTACAGCCAGCGGCGAGGAG 540
481 TTGTTGAAGTGTGACGCTATGTTTGCAGAGGGGCGGTACAGCCAGCGGCGAGGAG 540
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901 GCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 960
901 GCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 960
961 GCGTCTGTGACATCGGCTACGGGGGAGCCAGTGTGCCAGGAGTGTGCTTCCCTTCC 1020
961 GCGTCTGTGACATCGGCTACGGGGGAGCCAGTGTGCCAGGAGTGTGCTTCCCTTCC 1020
1021 ACACCTGTGACCTGAGGATCGACGAGACTGCTTATGTTGCTTTCAGAGGAGAGACCT 1080
1021 ACACCTGTGACCTGAGGATCGACGAGACTGCTTATGTTGCTTTCAGAGGAGAGACCT 1080
1081 ATTCAGAGCCAGATGAATGTTCAGAGAAAGCGGGGTGTGCCCCAGATCAAGAGCC 1140
1081 ATTCAGAGCCAGATGAATGTTCAGAGAAAGCGGGGTGTGCCCCAGATCAAGAGCC 1140
1141 AGAAGTGTGAGGATCTCTGCTTCTATCTGGCGGCTGTGAGAGCCACACAGAGGTGA 1200
1141 AGAAGTGTGAGGATCTCTGCTTCTATCTGGCGGCTGTGAGAGCCACCAAGAGGTGA 1200
1201 CTGACAGTGTGAGGAGAGGAACTTCTGTGCTGGGCTACCTTACAAGCCGCCAAGG 1260

1201 CTGACAGTGAAGTTCAGACAGGAACTTCTGATGGGCTCACTACAAGACGCCAAGG 1260
1261 ACTCTTCCGCTGGCCACAGGAGACACAGGAGCTTACAGTTTGTCTTTGGGAGC 1320
1261 ACTCTTCCGCTGGCCACAGGAGACACAGGAGCTTACAGTTTGTCTTTGGGAGC 1320
1321 CTGACAAACACGGGCTGGTGGCTGAGTGTCTGCTTACAGTTTGGCACTGCTGGAGC 1380
1321 CTGACAAACACGGGCTGGTGGCTGAGTGTCTGCTTACAGTTTGGCACTGCTGGAGC 1380
1381 TGCAGGCTTCACTGCTTCACTGGAAGACAGGAGCTTGAAGACCCGAAACGTTTACA 1440
1381 TGCAGGCTTCACTGCTTCACTGGAAGACAGGAGCTTGAAGACCCGAAACGTTTACA 1440
1441 TCTGCCAGTTTGGCCAGAGACATCTCCCGGTGGGGCCAGGGTCTGAGGCTTGACCA 1500
1441 TCTGCCAGTTTGGCCAGAGACATCTCCCGGTGGGGCCAGGGTCTGAGGCTTGACCA 1500
1501 CATGGCTCCCTCGCTGGGAGACCGGCTCTGCTTACCTGCTGCTGCTGCTGCTGCT 1560
1501 CATGGCTCCCTCGCTGGGAGACCGGCTCTGCTTACCTGCTGCTGCTGCTGCTGCT 1560
1561 GGAACAGGGCCAGGTTAAGACACATGCTCATGTCCAAAGAGGCTCAGACCTTGAC 1620
1561 GGAACAGGGCCAGGTTAAGACACATGCTCATGTCCAAAGAGGCTCAGACCTTGAC 1620
1621 AATGCCAGAGTTGGCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGTT 1680
1621 AATGCCAGAGTTGGCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGTT 1680
1681 AGAAGAAGCTGGGGCCCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
1681 AGAAGAAGCTGGGGCCCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
1741 GAAGAGAGGACACCGCCAGTGGTCCAAAGAGGCTGCTCTCTCCACCTGGCCAGACCC 1800
1741 GAAGAGAGGACACCGCCAGTGGTCCAAAGAGGCTGCTCTCTCTCCACCTGGCCAGACCC 1800
1801 TGTGGGGAGCGGAGCTTCCCTGTGCGATGACACCCAGCGGGTATTAAATTTATCAATCAG 1860
1801 TGTGGGGAGCGGAGCTTCCCTGTGCGATGACACCCAGCGGGTATTAAATTTATCAATCAG 1860
1861 CTGAAAAAAGAAAAA 1876
1861 CTGAAAAAAGAAAAA 1876

RESULT 5
US-09-866-028-49
; Sequence 49, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028

; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-09-866-028-49

Query Match 100.0%; Score 1876; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTTTGTCACACGCCAGCCTGACTCTCTGGAGATTGTGAATAGCTTCATCCAGCCTG 60
Db 1 CTCCTTTGTCACACGCCAGCCTGACTCTCTGGAGATTGTGAATAGCTTCATCCAGCCTG 60

Qy 61 AGAACAACCGGGTGGCTGAGCAGGCTGTGACGAGGACACCTGACGGGCCCAACAGAC 120
Db 61 AGAACAACCGGGTGGCTGAGCAGGCTGTGACGAGGACACCTGACGGGCCCAACAGAC 120

Qy 121 CCATGCTGATCAGAGACCTCCCTGCGGGGGGCACTCTCTTGGCTGTGCTTGGCCC 180
Db 121 CCATGCTGATCAGAGACCTCCCTGCGGGGGGCACTCTCTTGGCTGTGCTTGGCCC 180

Qy 181 TCCTTGGCACCACTTGGGACAGAGTGTGGCCACCCAGCTGACAGGAGAGGCTCCGATGG 240
Db 181 TCCTTGGCACCACTTGGGACAGAGTGTGGCCACCCAGCTGACAGGAGAGGCTCCGATGG 240

Qy 241 CCGGAGCCCTGACAGGAGAGGAGTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
Db 241 CCGGAGCCCTGACAGGAGAGGAGTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 300

Qy 301 GCTGGTCTCAGCCCTCGGCTGACATGCGAGGCTGAGTGGAGTGGAGTGGAGTGGAGT 360
Db 301 GCTGGTCTCAGCCCTCGGCTGACATGCGAGGCTGAGTGGAGTGGAGTGGAGTGGAGT 360

Qy 361 AACTGGCTCAAGCCAGGAGGAGCCTCTGTGGAATCCCAACCCAGAGCTGGATCCGGCC 420
Db 361 AACTGGCTCAAGCCAGGAGGAGCCTCTGTGGAATCCCAACCCAGAGCTGGATCCGGCC 420

Qy 421 TGTGGCGCACCTTGAAGTGGCTGGAACATGACAGTGTCTGCGCGGGGCTTGGGCTCTCT 480
Db 421 TGTGGCGCACCTTGAAGTGGCTGGAACATGACAGTGTCTGCGCGGGGCTTGGGCTCTCT 480

Qy 481 TTGTTGAAGTGGTCAAGCTTATGTTTGCAGAGGAGGAGTGTGACAGGAGGAGGAGGAG 540
Db 481 TTGTTGAAGTGGTCAAGCTTATGTTTGCAGAGGAGGAGTGTGACAGGAGGAGGAGGAG 540

Qy 541 AGTGTGCTCGAAGCCACCTGACCCACTACAGCAGCTCTGTGGGCGCACCTCAAGCC 600
Db 541 AGTGTGCTCGAAGCCACCTGACCCACTACAGCAGCTCTGTGTGGGCGCACCTCAAGCC 600

Qy 601 AGCTGGCTGTGGGCGCACCTGTCTGCGAGGCGACAGCAGCTAGAGGCTTGTGTCT 660
Db 601 AGCTGGCTGTGGGCGCACCTGTCTGCGAGGCGACAGCAGCTAGAGGCTTGTGTCT 660

Qy 661 GTGCTACTCCCCCGAGGCAACTGGGAGTCAACGGGAGAGCAATATATCCCTATAAGA 720
Db 661 GTGCTACTCCCCCGAGGCAACTGGGAGTCAACGGGAGAGCAATATATCCCTATAAGA 720

Qy 721 AGGCTGCTGTGTGCTGTGACAGCAGTGTCTCAGGCTGTCTCAAGGCTTGGGACC 780
Db 721 AGGCTGCTGTGTGCTGTGACAGCAGTGTCTCAGGCTGTCTCAAGGCTTGGGACC 780

Qy 781 ATCAGGGGGCTGTGTGAGGTCCTCCAGGATCTTGTGCGATGAGTGCAGAACCATG 840
Db 781 ATCAGGGGGCTGTGTGAGGTCCTCCAGGATCTTGTGCGATGAGTGCAGAACCATG 840

Qy 841 GAGCTCTCAACATCAGCAGCCTGCCACTGCCACTGTCCCTGTCCCTGTCCCTGTCCCTGT 900
Db 841 GAGCTCTCAACATCAGCAGCCTGCCACTGCCACTGTCCCTGTCCCTGTCCCTGTCCCTGT 900

Qy 901 GCCAAGTGAAGTGCAGCCTGCAGTGTGTGCAGCGCGGTTCCGGAGGAGGAGTGTCTGT 960
Dbb 901 GCCAAGTGAAGTGCAGCCTGCAGTGTGTGCAGCGCGGTTCCGGAGGAGGAGTGTCTGT 960
Qy 961 GGGTGTGTGACATCGGCTACGGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCC 1020
Dbb 961 GGGTGTGTGACATCGGCTACGGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCC 1020
Qy 1021 ACACCTGTGACTGTAGGATCGAGGAGTGTCTTCTATGTGTGTCTTTCAGAGGAGGAGCCT 1080
Dbb 1021 ACACCTGTGACTGTAGGATCGAGGAGTGTCTTCTATGTGTGTCTTTCAGAGGAGGAGCCT 1080
Qy 1081 ATTACAGAGCCAGGATGAATGTACAGAGGAAAGCGGGGTGTGCCCCAGATCAAGAGCC 1140
Dbb 1081 ATTACAGAGCCAGGATGAATGTACAGAGGAAAGCGGGGTGTGCCCCAGATCAAGAGCC 1140
Qy 1141 AGAAGTGCAGGACATCTTCGGCTTCTATCTGGGCGGCTTGGAGACCAACAGAGGTGA 1200
Dbb 1141 AGAAGTGCAGGACATCTTCGGCTTCTATCTGGGCGGCTTGGAGACCAACAGAGGTGA 1200
Qy 1201 CTGACAGTGAATCTGAGACCAAGGAACTTCTGGATCGGCTCACCTACAAGACCGCAAGG 1260
Dbb 1201 CTGACAGTGAATCTGAGACCAAGGAACTTCTGGATCGGCTCACCTACAAGACCGCAAGG 1260
Qy 1261 ACTCCTTCGGCTGGCCACAGGGGAGCACCAGGCTTTCACAGTTTGGGCGAGC 1320
Dbb 1261 ACTCCTTCGGCTGGCCACAGGGGAGCACCAGGCTTTCACAGTTTGGGCGAGC 1320
Qy 1321 CTGACACACCGGCTGT 1380
Dbb 1321 CTGACACACCGGCTGT 1380
Qy 1381 TGCAGCTTCAGTCTGCTTCACTGGAAGCAGCAGCGCTGCAAAACCGGTTTACA 1440
Dbb 1381 TGCAGCTTCAGTCTGCTTCACTGGAAGCAGCAGCGCTGCAAAACCGGTTTACA 1440
Qy 1441 TGTGCGAGTTTCCCGAGGAGCACATCTCCCGTGGGGCCGAGGCTCTGAGGCTTGACCA 1500
Dbb 1441 TGTGCGAGTTTCCCGAGGAGCACATCTCCCGTGGGGCCGAGGCTCTGAGGCTTGACCA 1500
Qy 1501 CATGGCTCCTCGCTGGGAGCAGCGGCTCTGTCTTACCTGTCTGCCCCACCTGTCT 1560
Dbb 1501 CATGGCTCCTCGCTGGGAGCAGCGGCTCTGTCTTACCTGTCTGCCCCACCTGTCT 1560
Qy 1561 GAACAAGGCGCAGGTAAAGACACATGCTCATGTCCAAAGAGTCTCAGACCTTGAC 1620
Dbb 1561 GAACAAGGCGCAGGTAAAGACACATGCTCATGTCCAAAGAGTCTCAGACCTTGAC 1620
Qy 1621 AATGCCAGAAGTTGGSCAGAGAGGAGGAGGCGGCGAGTGAAGGCGGAGGTGAGTGT 1680
Dbb 1621 AATGCCAGAAGTTGGSCAGAGAGGAGGAGGCGGCGAGTGAAGGCGGAGGTGAGTGT 1680
Qy 1681 AGAAGAGTGGGCGCTTCGGCTGCTTTTGTATGGAGAGATGGGCTCAATTAGATGGC 1740
Dbb 1681 AGAAGAGTGGGCGCTTCGGCTGCTTTTGTATGGAGAGATGGGCTCAATTAGATGGC 1740
Qy 1741 GAAGGAGAGGACCCCGCAGTGTGCAAAAGGCTCTCTCTCCACCTGGCCGAGACCC 1800
Dbb 1741 GAAGGAGAGGACCCCGCAGTGTGCAAAAGGCTCTCTCTCCACCTGGCCGAGACCC 1800
Qy 1801 TGTGGGCGAGGAGTCTCCCTGTGGCATGAACCCACCGGGTATTAAATTAATGAATCAG 1860
Dbb 1801 TGTGGGCGAGGAGTCTCCCTGTGGCATGAACCCACCGGGTATTAAATTAATGAATCAG 1860
Qy 1861 CTGAAAAAATAAAAA 1876
Dbb 1861 CTGAAAAAATAAAAA 1876

RESULT 6

US-09-944-449-49

; Sequence 49, Application US/09944449

; Patent No. US20020102647A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944, 449
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067, 411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069, 334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/068, 017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070, 440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075, 945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112, 850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146, 222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218, 517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254, 311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090

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; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-09-944-449-49

Query Match      100.0%; Score 1876; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTTTGTCACAGCCAGCCGCTGACTCTCTGGAGATTGTAATAGCTTCATCAGCCCTG 60
Db 1 CTCCTTTGTCACAGCCAGCCGCTGACTCTCTGGAGATTGTAATAGCTTCATCAGCCCTG 60
Qy 61 AGAAACAAGCCGGTGCTGAGCCAGGCTGTGCAGGAGACCTGACGGGGCCCAACAGAC 120
Db 61 AGAAACAAGCCGGTGCTGAGCCAGGCTGTGCAGGAGACCTGACGGGGCCCAACAGAC 120
Qy 121 CCATGCTGCATCCAGAGACCTCCCTGGCCGGGGGATCTCCTGGCTGTGCTCTGGCCC 180
Db 121 CCATGCTGCATCCAGAGACCTCCCTGGCCGGGGGATCTCCTGGCTGTGCTCTGGCCC 180
Qy 181 TCCTTGGCACCAGCTGGGAGAGGTTGGCCACCCAGCTGCAGGAGAGCTCCGATGG 240
Db 181 TCCTTGGCACCAGCTGGGAGAGGTTGGCCACCCAGCTGCAGGAGAGCTCCGATGG 240
Qy 241 CCGGAGCCCTGAACAGAGAGGAGTTTCTGCTCTCCCTGCACAAACCCCTGCGCA 300
Db 241 CCGGAGCCCTGAACAGAGAGGAGTTTCTGCTCTCCCTGCACAAACCCCTGCGCA 300
Qy 301 GCTGGGTCCAGCCCTGGCGGCTGACATGCGGAGGCTGGAGTGCAGCCCTGGCCC 360
Db 301 GCTGGGTCCAGCCCTGGCGGCTGACATGCGGAGGCTGGAGTGCAGCCCTGGCCC 360
Qy 361 AACTGCTCAAGCCAGGAGCCCTCTGTGGAATCCAAACCCAGGCTGCATCCGCCC 420
Db 361 AACTGCTCAAGCCAGGAGCCCTCTGTGGAATCCAAACCCAGGCTGCATCCGCCC 420
Qy 421 TGTGGCGCACCTGCAAGTGGGTGGAACATGCAAGCTGTGCGCGGGCTTGGCGTCT 480
Db 421 TGTGGCGCACCTGCAAGTGGGTGGAACATGCAAGCTGTGCGCGGGCTTGGCGTCT 480
Qy 481 TTGTTGAAGTGTGAGCCTATGTTTTCAGAGGGGAGCGGTACAGCCACCGCGCAGGAG 540
Db 481 TTGTTGAAGTGTGAGCCTATGTTTTCAGAGGGGAGCGGTACAGCCACCGCGCAGGAG 540
Qy 541 AGTGTGCTCGCAACGCCACCTGACCCACTACAGCGAGCTCGTGGGCCACCTCAAGCC 600
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Db 1621 AATGCCAGAGTTGGCAGAGAGGAGGAGGAGCCAGTGGAGCCAGGAGTGGTGT 1680
QY 1681 AGAAGAGCTGGGCGCTTCGCTGCTTTTCATTTGGGAAGATGGCTTCAATTAGATGCC 1740
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QY 1741 GAAGGAGAGACACCGGCACTGGTCCAAAAGGCTGCTCTTCCACCTGCCCGCAGACCC 1800
Db 1741 GAAGGAGAGACACCGGCACTGGTCCAAAAGGCTGCTCTTCCACCTGCCCGCAGACCC 1800
QY 1801 TGTGGGACGCGAGCTTCCTGTGGCATGAACCCACGCGGCTATTAAATATGAATCAG 1860
Db 1801 TGTGGGACGCGAGCTTCCTGTGGCATGAACCCACGCGGCTATTAAATATGAATCAG 1860
QY 1861 CTGAAAAA 1876
Db 1861 CTGAAAAA 1876

RESULT 7

US-09-944-457-49
; Sequence 49, Application US/09944457
; Patent No. US20020110859A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998

; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-457-49
Query Match 100.0%; Score 1876; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTCTTTTGTCCACAGCCCGCTGACTCTGGAGATTGTGAATAGCTTCATCCAGCCTG 60
Db 1 CTCTTTTGTCCACAGCCCGCTGACTCTGGAGATTGTGAATAGCTTCATCCAGCCTG 60
QY 61 AGAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGAC 120
Db 61 AGAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGAC 120
QY 121 CCATGCTGCATCCACAGACACCTCCCTGGCGGGGGGCATCTCCTGGCTGTGCTTGGGCC 180
Db 121 CCATGCTGCATCCACAGACACCTCCCTGGCGGGGGGCATCTCCTGGCTGTGCTTGGGCC 180
QY 181 TCCTTGGCACCACTGGGCGAGAGTGTGGCCACCCACCTGCAGGAGGCTCCGATGG 240
Db 181 TCCTTGGCACCACTGGGCGAGAGTGTGGCCACCCACCTGCAGGAGGCTCCGATGG 240

181	TCC	TGGCACCACCTCGGCGAGAGGTGTGGCCACCCACGCTGCAGGAGCAGGCTTCCGATGG	240	
QY	241	CCGAGGCCCTGAACAGGAGGAGTTTCCTGCTCTCCTCTCCCTGCACAACCGCCTCGCA	300	
	241			
	241	CCGAGGCCCTGAACAGGAGGAGATTTCCTGCTCTCCTCTCCCTTGCAACACCGCCTGGCA	300	
QY	301	GCTGGGTCCAGCCCCTCGGGCTGACATGCGGAGGCTGACTGGAGTGACAGCCTGGCCC	360	
	301			
	301	GCTGGGTCCAGCCCCCTCGGCTGACATGCGGAGGCTGACTGGAGTGACAGCCTGGCCC	360	
QY	361	AAC	TGGCTCAAAGCCAGGCGAGCCCTCTGTGGAATCCAAACCCGAGCCCTGGCATCCGGCC	420
	361			
	361	AAC	TGGCTCAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCGAGCCTTGGCATCCGGCC	420
QY	421	TGTGGGCACCCCTGCAAGTGGGCTGGAAATGCACATGCAGCTGCTGCCCGCGGCTTGGCGTCC	480	
	421			
	421	TGTGGGCACCCCTGCAAGTGGGCTGGAAATGCAGCTGCTGCCCGCGGCTTGGCGTCC	480	
QY	481	TTGTTGAAGTGGTCAGCCCTATGGTTTGAGAGGGCACGCGTACAGCCACGCGCGCAGGAG	540	
	481			
	481	TTGTTGAAGTGGTCAGCCCTATGGTTTGAGAGGGCACGCGTACAGCCACGCGCGCAGGAG	540	
QY	541	AGTGTGCTCGCAAGCCACCTGCACCCACTACACGACAGCTCGTGTGGGCGACCTCAAGCC	600	
	541			
	541	AGTGTGCTCGCAAGCCACCTGCACCCACTACACGACAGCTCGTGTGGGCGACCTCAAGCC	600	
QY	601	AGCTGGGCTGTGGCGGCACCTGTGCTCTGCAGGCGCAGACGGGATAGAGCCTTTGTCT	660	
	601			
	601	AGCTGGGCTGTGGCGGCACCTGTGCTCTGCAGGCGCAGACGGGATAGAGCCTTTGTCT	660	
QY	661	GTGCTACTCCCCGGAGGCAACTGGGAGGTCAAGGGGAAGAACAATCATCCCCATAAGA	720	
	661			
	661	GTGCTACTCCCCGGAGGCAACTGGGAGGTCAAGGGGAAGAACAATCATCCCCATAAGA	720	
QY	721	AGSGTGCTGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAGCGCTGGGACC	780	
	721			
	721	AGSGTGCTGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAGCGCTGGGACC	780	
QY	781	ATGCAGGGGGGCTCTGTGAGTGTCCCGAAGAACCTTTGTCGATGAGCTGCCAAGCAATG	840	
	781			
	781	ATGCAGGGGGGCTCTGTGAGTGTCCCGAAGAACCTTTGTCGATGAGCTGCCAAGCAATG	840	
QY	841	GACGTCTCAACATCAGACCTGCGCACTGCGCACTGTCCCGCTGGCTACAGGGGAGATACT	900	
	841			
	841	GACGTCTCAACATCAGACCTGCGCACTGCGCACTGTCCCGCTGGCTACAGGGGAGATACT	900	
QY	901	GCCAAGTCAGGTGCAGCCTGCAGTGTGTGCAGCGCGGTTCGCGGAGGAGGAGTGCTCGT	960	
	901			
	901	GCCAAGTCAGGTGCAGCCTGCAGTGTGTGCAGCGCGGTTCGCGGAGGAGGAGTGCTCGT	960	
QY	961	CGGTCTGTGACATCGGCTPACGGGGGAGCCCACTGTGCCAACCAAGGTGCAATTTTCCCTTC	1020	
	961			
	961	CGGTCTGTGACATCGGCTPACGGGGGAGCCCACTGTGCCAACCAAGGTGCAATTTTCCCTTC	1020	
QY	1021	ACACCTGTGACCTGAGGATCGACGAGACTGCTTTCATGGTGCTTCAGAGGCGAGACACT	1080	
	1021			
	1021	ACACCTGTGACCTGAGGATCGACGAGACTGCTTTCATGGTGCTTCAGAGGCGAGACACT	1080	
QY	1081	ATTACAGAGCCAGGATGAAATGTACAGAGGAAGCGGGGTGCTGCCCCAGATCAAGAGCC	1140	
	1081			
	1081	ATTACAGAGCCAGGATGAAATGTACAGAGGAAGCGGGGTGCTGCCCCAGATCAAGAGCC	1140	
QY	1141	AGRAAGTGCAGGACATCCTCGCCCTTCTATCTTGGGCGCGCTGGAGACACCAACAGGTGA	1200	
	1141			
	1141	AGRAAGTGCAGGACATCCTCGCCCTTCTATCTTGGGCGCGCTGGAGACCAACCAAGGTGA	1200	
QY	1201	CTGACAGTGACTTCGAGACCAGGAACCTTCTGGATCGGCTCACTTACAGACCGCCAAG	1260	
	1201			
	1201	CTGACAGTGACTTCGAGACCAGGAACCTTCTGGATCGGCTCACTTACAGACCGCCAAG	1260	
QY	1261	ACTCCTTCGGTGGGCCACAGGGGAGCACAGGCGCTTCAACAGTTTTTGCCTTTGGGCAGC	1320	
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	1261	ACTCCTTCGGTGGGCCACAGGGGAGCACAGGCGCTTCAACAGTTTTTGCCTTTGGGCAGC	1320	

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RESULT 8
US - 09-945-587-49
: Sequence 49, Application US/09945587
: Patent No. US20020127643A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fliviaroff, Ellen
: APPLICANT: Geritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kljavin, Ivay
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TR
: TITLE OF INVENTION: ACIDS ENCODING
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/9-26
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 09/866,021
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/067,411
: PRIOR FILING DATE: December 3, 1997
: PRIOR APPLICATION NUMBER: 60/069,331

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, PRIOR FILING DATE: December 11, 1997
, PRIOR APPLICATION NUMBER: 60/069335
, PRIOR FILING DATE: December 11, 1997
, PRIOR APPLICATION NUMBER: 60/069,278
, PRIOR FILING DATE: December 11, 1997
, PRIOR APPLICATION NUMBER: 60/069,425
, PRIOR FILING DATE: December 12, 1997
, PRIOR APPLICATION NUMBER: 60/069,696
, PRIOR FILING DATE: December 16, 1997
, PRIOR APPLICATION NUMBER: 60/069,694
, PRIOR FILING DATE: December 16, 1997
, PRIOR APPLICATION NUMBER: 60/069,702
, PRIOR FILING DATE: December 16, 1997
, PRIOR APPLICATION NUMBER: 60/069,870
, PRIOR FILING DATE: December 17, 1997
, PRIOR APPLICATION NUMBER: 60/069,873
, PRIOR FILING DATE: December 17, 1997
, PRIOR APPLICATION NUMBER: 60/068,017
, PRIOR FILING DATE: December 18, 1997
, PRIOR APPLICATION NUMBER: 60/070,440
, PRIOR FILING DATE: January 5, 1998
, PRIOR APPLICATION NUMBER: 60/074,086
, PRIOR FILING DATE: February 9, 1998
, PRIOR APPLICATION NUMBER: 60/074,092
, PRIOR FILING DATE: February 9, 1998
, PRIOR APPLICATION NUMBER: 60/075,945
, PRIOR FILING DATE: February 25, 1998
, PRIOR APPLICATION NUMBER: 60/112,850
, PRIOR FILING DATE: December 16, 1998
, PRIOR APPLICATION NUMBER: 60/113,296
, PRIOR FILING DATE: December 22, 1998
, PRIOR APPLICATION NUMBER: 60/146,222
, PRIOR FILING DATE: July 28, 1999
, PRIOR APPLICATION NUMBER: PCT/US98/19330
, PRIOR FILING DATE: September 16, 1998
, PRIOR APPLICATION NUMBER: PCT/US98/25108
, PRIOR FILING DATE: December 1, 1998
, PRIOR APPLICATION NUMBER: 09/216,021
, PRIOR FILING DATE: December 16, 1998
, PRIOR APPLICATION NUMBER: 09/218,517
, PRIOR FILING DATE: December 22, 1998
, PRIOR APPLICATION NUMBER: 09/254,311
, PRIOR FILING DATE: March 3, 1999
, PRIOR APPLICATION NUMBER: PCT/US99/12252
, PRIOR FILING DATE: June 22, 1999
, PRIOR APPLICATION NUMBER: PCT/US99/21090
, PRIOR FILING DATE: September 15, 1999
, PRIOR APPLICATION NUMBER: PCT/US99/28409
, PRIOR FILING DATE: NO. US2002012763A1enber 30, 1999
, PRIOR APPLICATION NUMBER: PCT/US99/28313
, PRIOR FILING DATE: NO. US2002012763A1enber 30, 1999
, PRIOR APPLICATION NUMBER: PCT/US99/28301
, PRIOR FILING DATE: December1, 1999
, PRIOR APPLICATION NUMBER: PCT/US99/30095
, PRIOR FILING DATE: December 16, 1999
, PRIOR APPLICATION NUMBER: PCT/US00/03565
, PRIOR FILING DATE: February 11, 2000
, PRIOR APPLICATION NUMBER: PCT/US00/04414
, PRIOR FILING DATE: February 22, 2000
, PRIOR APPLICATION NUMBER: PCT/US00/05841
, PRIOR FILING DATE: March 2, 2000
, PRIOR APPLICATION NUMBER: PCT/US00/08439
, PRIOR FILING DATE: March 30, 2000
, PRIOR APPLICATION NUMBER: PCT/US00/14042
, PRIOR FILING DATE: May 22, 2000
, PRIOR APPLICATION NUMBER: PCT/US00/20710
, PRIOR FILING DATE: July 28, 2000
, PRIOR APPLICATION NUMBER: PCT/US00/32678
, PRIOR FILING DATE: December 1, 2000
, PRIOR APPLICATION NUMBER: PCT/US01/06520
, PRIOR FILING DATE: February 28, 2001
, NUMBER OF SEQ ID NOS: 120
, SEQ ID NO 49

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; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-945-587-49

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Query Match 100.0%; Score 1876; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0;
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1	QY	1	CTCTTTTGTCCACAGCCGAGCCTGACTCCTGGAGATTGTAATAGTCCATCCAGCCTG	60
1	Db	1	CTCTTTTGTCCACAGCCGAGCCTGACTCCTGGAGATTGTAATAGTCCATCCAGCCTG	60
61	QY	61	AGAAACAAGCCGGTGGCTGAGCCAGGCTGTCACGGAGCACCTGACGGGCCACACAGAC	120
61	Db	61	AGAAACAAGCCGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCACACAGAC	120
121	QY	121	CCATGCTGATCCAGAGACCTCCCTTGGCCGGGGGCATCTCCTGGCTGTGCTCTGGCCC	180
121	Db	121	CCATGCTGATCCAGAGACCTCCCTTGGCCGGGGGCATCTCCTGGCTGTGCTCTGGCCC	180
181	QY	181	TGCTTTGGACACACTGGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGTCCGATGG	240
181	Db	181	TGCTTTGGACACACTGGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGTCCGATGG	240
241	QY	241	CGGGAGCCCTGAACAGGAAGAGAGTTTCTTCTCCTCTCCCTGTCACACCCGCTTCGCGCA	300
241	Db	241	CGGGAGCCCTGAACAGGAAGAGAGTTTCTTCTCCTCTCCCTGTCACACCCGCTTCGCGCA	300
301	QY	301	GCTGGTCCAGCCCTCGCGCTGACATCGGAGGCTGGACGTGGAGTGCACGCTTGGCCC	360
301	Db	301	GCTGGTCCAGCCCTCGCGCTGACATCGGAGGCTGGACGTGGAGTGCACGCTTGGCCC	360
361	QY	361	AACTGGCTCAAGCCAGGCGAGCCCTCTGTGGAAATCCCAACCCGAGCCTTGGCATCCG	420
361	Db	361	AACTGGCTCAAGCCAGGCGAGCCCTCTGTGGAAATCCCAACCCGAGCCTTGGCATCCG	420
421	QY	421	TGTGGCGCACCTGCAAGTGGCTGGAACATGCAGCTGCTGCCGGGGCTTGGGCTCT	480
421	Db	421	TGTGGCGCACCTGCAAGTGGCTGGAACATGCAGCTGCTGCCGGGGCTTGGGCTCT	480
481	QY	481	TTGTTGAAGTGTGACCCCTATGTTTGCAGAGGGCAGCGGTACAGCCACGCGGCGAGGAG	540
481	Db	481	TTGTTGAAGTGTGACCCCTATGTTTGCAGAGGGCAGCGGTACAGCCACGCGGCGAGGAG	540
541	QY	541	AGTGTGCTCGCAAGCCACCTGCACCCACTACAGGAGCTCTGTGGGCCACCTCAAGCC	600
541	Db	541	AGTGTGCTCGCAAGCCACCTGCACCCACTACAGGAGCTCTGTGGGCCACCTCAAGCC	600
601	QY	601	AGCTGGGCTGTGGCGGCACCTGTGCTCTGCAGGGCCAGACGCGATAGAAAGCCTTTGCT	660
601	Db	601	AGCTGGGCTGTGGCGGCACCTGTGCTCTGCAGGGCCAGACGCGATAGAAAGCCTTTGCT	660
661	QY	661	GTGCCTACTCCCCCGGAGGCAACTGGGAGGTCAAGGGGAAGACAATCATCCCTATAAGA	720
661	Db	661	GTGCCTACTCCCCCGGAGGCAACTGGGAGGTCAAGGGGAAGACAATCATCCCTATAAGA	720
721	QY	721	AGGGTGCCTGTGTTCCTCTGCACAGCCAGTGTCTCAGGCTGTCTAAAGCCTGGGACC	780
721	Db	721	AGGGTGCCTGTGTTCCTCTGCACAGCCAGTGTCTCAGGCTGTCTAAAGCCTGGGACC	780
781	QY	781	ATGCAGGGGGGCTGTGTAGGTTCCCGAGGAATCTTGTGCGATGAGCTGCCAGAACCATG	840
781	Db	781	ATGCAGGGGGGCTGTGTAGGTTCCCGAGGAATCTTGTGCGATGAGCTGCCAGAACCATG	840
841	QY	841	GAGGCTCAACATCAGCACCTGCCACTGGCACTGTCCCTGGCTACACGGGCAGATACT	900
841	Db	841	GAGGCTCAACATCAGCACCTGCCACTGGCACTGTCCCTGGCTACACGGGCAGATACT	900
901	QY	901	GCCAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCGGGTTCCGGGAGGAGTAGTCTCGT	960
901	Db	901	GCCAGTGAGGTGCAGCCTGCAGTGTGTGTGCACGGCGGGTTCCGGGAGGAGTAGTCTCGT	960

Qy 961 GCGTCTGTGACATCGGCTACGGGGAGGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCC 1020
Db 961 GCGTCTGTGACATCGGCTACGGGGAGGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCC 1020
Qy 1021 ACACCTGTGACCTGAGGATCGACGAGACTGCTTCATGTGTCTTTCAGAGGCAGACACCT 1080
Db 1021 ACACCTGTGACCTGAGGATCGACGAGACTGCTTCATGTGTCTTTCAGAGGCAGACACCT 1080
Qy 1081 ATTACAGAGCCAGGATGAATCTCAGAGAAAGCGGGGTGCTGGCCACAGTCAAGAGCC 1140
Db 1081 ATTACAGAGCCAGGATGAATCTCAGAGAAAGCGGGGTGCTGGCCACAGTCAAGAGCC 1140
Qy 1141 AGAAAGTCAGAGACATCTCGCTTCTATCTGGGCGCCCTGGAGACCAACCAAGAGTGA 1200
Db 1141 AGAAAGTCAGAGACATCTCGCTTCTATCTGGGCGCCCTGGAGACCAACCAAGAGTGA 1200
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Qy 1261 ACTCCTTCGGCTGGGCCACAGGGAGCACCAGGCTTTCACAGTCTTTCGCTTTGGGCAGC 1320
Db 1261 ACTCCTTCGGCTGGGCCACAGGGAGCACCAGGCTTTCACAGTCTTTCGCTTTGGGCAGC 1320
Qy 1321 CTGACAAACAGGGCTGGTGTGGCTGAGTGTGCTGCCATGGGGTTTGGCACTGCGTGGAGC 1380
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Db 1381 TGCAGGCTTCAGTCCCTTCAACTGGAACGACGCGCTGCAAAACCCGAAACCGTTACA 1440
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Qy 1501 CATGCTCCCTCGCTCGCTGGGAGCAGCGGCTGTGCTTACCTGTGCTCCACCTGTCT 1560
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Db 1801 TGTGGGGCAGCGAGCTTCCCTGTGTCATGAACCCACCGGGTATTAAATATTGAATCAG 1860
Qy 1861 CTGAAAAAATAAAAAA 1876
Db 1861 CTGAAAAAATAAAAAA 1876

RESULT 9

US-09-945-015-49
; Sequence 49, Application US/09945015
; Patent No. US20020132768A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,015
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313

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; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/703565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-09-945-015-49

Query Match      100.0%; Score 1876; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 TCCCTGGCACCACCTGGCAGAGGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGG 240
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RESULT 10
US-09-944-396-49
; Sequence 49, Application US/09944396
; Patent No. US20020132981A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerriksen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,396
; CURRENT FILING DATE: 2001-09-25
; PRIORITY APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998

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QY 361 AACTGGCTCAAGCAGGAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCC 420
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QY 421 TGTGGCCACCCCTGCAAGTGGCTGGACATGCACTGCTGCCCGGGCTTGGCTCCT 480
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RESULT 11

US-09-944-097-49

; Sequence 49, Application US/09944097

; Patent No. US20020133675A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/944, 097

; CURRENT FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: 09/866, 028

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/069, 334

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069335

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069, 278

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069, 425

PRIOR FILING DATE: December 12, 1997
 PRIOR APPLICATION NUMBER: 60/069,696
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,694
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,702
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069,873
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/068,017
 PRIOR FILING DATE: December 18, 1997
 PRIOR APPLICATION NUMBER: 60/070,440
 PRIOR FILING DATE: January 5, 1998
 PRIOR APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/074,092
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/075,945
 PRIOR FILING DATE: February 25, 1998
 PRIOR APPLICATION NUMBER: 60/112,850
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 60/113,296
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 60/146,222
 PRIOR FILING DATE: July 28, 1999
 PRIOR APPLICATION NUMBER: PCT/US98/19330
 PRIOR FILING DATE: September 16, 1998
 PRIOR APPLICATION NUMBER: PCT/US98/25108
 PRIOR FILING DATE: December 1, 1998
 PRIOR APPLICATION NUMBER: 09/216,021
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 09/218,517
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 09/254,311
 PRIOR FILING DATE: March 3, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: June 22, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: September 15, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28409
 PRIOR FILING DATE: No. US20020133675alembor 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: No. US20020133675alembor 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28301
 PRIOR FILING DATE: December 1, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: December 16, 1999
 PRIOR APPLICATION NUMBER: PCT/US00/03565
 PRIOR FILING DATE: February 11, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: February 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR FILING DATE: March 2, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/08439
 PRIOR FILING DATE: March 30, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/14042
 PRIOR FILING DATE: May 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: July 28, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: December 1, 2000
 PRIOR APPLICATION NUMBER: PCT/US01/06520
 PRIOR FILING DATE: February 28, 2001
 NUMBER OF SEQ ID NOS: 120
 SEQ ID NO 49
 LENGTH: 1876
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-09-944-097-49

Query Match 100.0%; Score 1876; DB 10; Length 1876;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 CTCCTTTTGTCCACACGCCAGCTGACTCCTCTGGAGATTGTGAATAGCTCCATCCAGCCGTG 60
 Qy 61 AGAAACAAGCCGGTGGCTGAGCAGAGCTGTGCAGGAGCACCCTGACGGGCCACACAGAC 120
 Db 61 AGAAACAAGCCGGTGGCTGAGCAGAGCTGTGCAGGAGCACCCTGACGGGCCACACAGAC 120
 Qy 121 CCATGCTGCATCCAGAGACCTCCCTGCGGGGGGCTCTCTCTGCTGTGCTCTGCTGCCCC 180
 Db 121 CCATGCTGCATCCAGAGACCTCCCTGCGGGGGGCTCTCTCTGCTGTGCTCTGCTGCCCC 180
 Qy 181 TCCTTTGGCACCACTGGGCGAGAGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGG 240
 Db 181 TCCTTTGGCACCACTGGGCGAGAGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGG 240
 Qy 241 CCGGAGCCCTGAACAGGAGAGAGTTTCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
 Db 241 CCGGAGCCCTGAACAGGAGAGAGTTTCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
 Qy 301 GCTGGGTCCAGCCCTCTGCGGCTGACATGCGGAGGCTGGAGTGGAGTGCAGAGCTGGCCC 360
 Db 301 GCTGGGTCCAGCCCTCTGCGGCTGACATGCGGAGGCTGGAGTGGAGTGCAGAGCTGGCCC 360
 Qy 361 AACTGGCTCAAGCCAGGCGACCCCTCTGTGGAAATCCCAACCCAGAGCTGGCATCCGGCC 420
 Db 361 AACTGGCTCAAGCCAGGCGACCCCTCTGTGGAAATCCCAACCCAGAGCTGGCATCCGGCC 420
 Qy 421 TGTGGCGCACCCCTGCAAGTGGGCTGGACATGCGAGCTGCTGCCCCGGGCTTGGCGCTCT 480
 Db 421 TGTGGCGCACCCCTGCAAGTGGGCTGGACATGCGAGCTGCTGCCCCGGGCTTGGCGCTCT 480
 Qy 481 TTCTTGAAGTGGTCAGCCTATGTGTTGCAGAGGGGACGGGTACAGCCACGCGGCGAGGAG 540
 Db 481 TTCTTGAAGTGGTCAGCCTATGTGTTGCAGAGGGGACGGGTACAGCCACGCGGCGAGGAG 540
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 Db 661 GTCCCTACTCCCCGGGAGGCAACTGGGAGGTCAACGGGAAGACAAATCATCCCTATAAGA 720
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 Db 781 ATGAGGGGGGCTCTGTGAGTCCCCAGGAATCTTGTGCGCATGAGCTGCCAGAACATG 840
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Db 1081 ATTACAGAGCAGGATGAATATGTCAGAGGAAGCGGGGTGCTGCCCCAGATCAAGAGCC 1140
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Db 1381 TGCAGGCTTCAGCTGCGCTTCAACTGGAACGACAGCGCTGCAAAACCGCAACCGTTACA 1440
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Db 1741 GAAGAGAGGAGACCGCCAGTGGTCCAAAAGGCTGCTCTTCCACCTGGCCCGAGCC 1800
QY 1801 TGTGGGCGAGGAGCTTCCCTGTGGCATGACCCCGAGGCTATTAATATGATGATCAG 1860
Db 1801 TGTGGGCGAGGAGCTTCCCTGTGGCATGACCCCGAGGCTATTAATATGATGATCAG 1860
QY 1861 CTGAAAAAATAAAAAA 1876
Db 1861 CTGAAAAAATAAAAAA 1876

RESULT 12

US-09-944-432-49
; Sequence 49, Application US/09944432
; Patent No. US20020142419A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,432
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,378
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 15, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020142419A1, September 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020142419A1, September 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565


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; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-432-49

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Query Match      100.0%; Score 1876; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	61	AGAAACAAGCGGTTGGCTGAGCCAGGCTGTGCACGAGCACTGACGGGCCCAACAGAC	120
Db	61	AGAAACAAGCGGTTGGCTGAGCCAGGCTGTGCACGAGCACTGACGGGCCCAACAGAC	120
Qy	121	CCATGTGCAATCCAGAGACCTCCCTGGCGGGGGCATCTCTGGCTGTGCTCTCTGGCC	180
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Db	181	TCCTTTGGACCACTGGGAGAGGTTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGG	240
Qy	241	CCGGAGCCCTGAACAGAGGAGAGTTCTTGCTCTCTCTCCCTGCAACACCGCTTCGCA	300
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Qy	301	GCTGGGTTCACAGCCCTCGGGCTGACATCGGAGGCTGCACCTGGAGTGACAGCTGGCCC	360
Db	301	GCTGGGTTCACAGCCCTCGGGCTGACATCGGAGGCTGCACCTGGAGTGACAGCTGGCCC	360
Qy	361	AACCTGCTCAAGCCAGGCGACCCCTCTGTGGAATCCCAACCCCGAGCCTTGGCATCCGGCC	420
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Qy	421	TGTGGCGCACCTTGCAAGTGGGTGAAACATGCAGCTGCTGCCCGGGGCTTGGGTCTCT	480
Db	421	TGTGGCGCACCTTGCAAGTGGGTGAAACATGCAGCTGCTGCCCGGGGCTTGGGTCTCT	480
Qy	481	TTGTTGAAGTGTGCAGCCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACGCGGACGAG	540
Db	481	TTGTTGAAGTGTGCAGCCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACGCGGACGAG	540
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Db	661	GTGCTACTCCCCGGAGGCACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGA	720

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 Db 1801 TGTGGGCGAGCGAGTTCCTGTGTCATGAACCCACGGGTATTAAATTAATGAATCAG 1860
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 QY 1861 CTGAAAAA 1876
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 Db 1861 CTGAAAAA 1876
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RESULT 13
 US-09-943-762-49
 ; Sequence 49, Application US/09943762
 ; Patent No. US20020142958A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin
 ; APPLICANT: Botstein, David
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Kljavin, Ivar
 ; APPLICANT: Napier, Mary
 ; APPLICANT: Roy, Margaret
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P2548P1C1
 ; CURRENT FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US/09/943,762
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/067,411
 ; PRIOR FILING DATE: December 3, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,334
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,335
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,378
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,425
 ; PRIOR FILING DATE: December 12, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,696
 ; PRIOR FILING DATE: December 16, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,694
 ; PRIOR FILING DATE: December 16, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,702
 ; PRIOR FILING DATE: December 16, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,870
 ; PRIOR FILING DATE: December 17, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,873
 ; PRIOR FILING DATE: December 17, 1997
 ; PRIOR APPLICATION NUMBER: 60/068,017
 ; PRIOR FILING DATE: December 18, 1997
 ; PRIOR APPLICATION NUMBER: 60/070,440
 ; PRIOR FILING DATE: January 5, 1998
 ; PRIOR APPLICATION NUMBER: 60/074,086
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/074,092
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/075,945
 ; PRIOR FILING DATE: February 25, 1998
 ; PRIOR APPLICATION NUMBER: 60/112,850
 ; PRIOR FILING DATE: December 16, 1998
 ; PRIOR APPLICATION NUMBER: 60/113,296
 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 60/146,222
 ; PRIOR FILING DATE: July 28, 1999

; PRIOR APPLICATION NUMBER: PCT/US98/19330
 ; PRIOR FILING DATE: September 16, 1998
 ; PRIOR APPLICATION NUMBER: PCT/US98/25108
 ; PRIOR FILING DATE: December 1, 1998
 ; PRIOR APPLICATION NUMBER: 09/216,021
 ; PRIOR FILING DATE: December 16, 1998
 ; PRIOR APPLICATION NUMBER: 09/218,517
 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 09/254,311
 ; PRIOR FILING DATE: March 3, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252
 ; PRIOR FILING DATE: June 22, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: September 15, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28409
 ; PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28301
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 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: December 16, 1999
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 ; PRIOR FILING DATE: February 11, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: February 22, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841
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 ; PRIOR APPLICATION NUMBER: PCT/US00/32678
 ; PRIOR FILING DATE: December 1, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520
 ; PRIOR FILING DATE: February 28, 2001
 ; NUMBER OF SEQ ID NOS: 120
 ; SEQ ID NO 49
 ; LENGTH: 1876
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-09-943-762-49

Query Match 100.0%; Score 1876; DB 10; Length 1876;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCCTTTTGTCCACCGCCAGCCTGACTCCTGGAGATTGTGAATAGTCCATCCAGCCTG 60
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 Db 1 CTCCTTTTGTCCACCGCCAGCCTGACTCCTGGAGATTGTGAATAGTCCATCCAGCCTG 60
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QY 1321 CTGACAAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Db 1321 CTGACAAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 TCGAGCTTTCAGTGTCTTCACTGGAACAGCAGGCTGCAAAACCCGAAACCGTTTACA 1440
Db 1381 TCGAGCTTTCAGTGTCTTCACTGGAACAGCAGGCTGCAAAACCCGAAACCGTTTACA 1440
QY 1441 TCTGCCAGTTTGGCCAGGACACATCTCCGGTGGGCGCCCGAGGCTGTGAGGCGTGACCA 1500

Db 1441 TCTGCCAGTTTGGCCAGGACACATCTCCCGGTGGGGCCCGAGGCTCTGAGGCTTGACCA 1500
QY 1501 CATGGCTCCCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCT 1560
Db 1501 CATGGCTCCCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCT 1560
QY 1561 GGAACAGGCGCCAGGTAAAGACACATGCCTCATGTCCAAAGAGGTCTCAGACCTTGAC 1620
Db 1561 GGAACAGGCGCCAGGTAAAGACACATGCCTCATGTCCAAAGAGGTCTCAGACCTTGAC 1620
QY 1621 AATGCCAGAAAGTTGGGCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGT 1680
Db 1621 AATGCCAGAAAGTTGGGCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGT 1680
QY 1681 AGAAGAGCTGGGGCCCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
Db 1681 AGAAGAGCTGGGGCCCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
QY 1741 GAAGAGAGGAGACACCGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
Db 1741 GAAGAGAGGAGACACCGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
QY 1801 TGTGGGCGAGCGAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
Db 1801 TGTGGGCGAGCGAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
QY 1861 CTGAAAAAAGAAAAA 1876
Db 1861 CTGAAAAAAGAAAAA 1876

RESULT 14

US-09-944-654-49
; Sequence 49, Application US/09944654
; Patent No. US20020142959A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944, 654
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866, 028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067, 411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069, 334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069, 696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 694

PRIOR FILING DATE:	December 16, 1997
PRIOR APPLICATION NUMBER:	60/069,702
PRIOR FILING DATE:	December 16, 1997
PRIOR APPLICATION NUMBER:	60/069,870
PRIOR FILING DATE:	December 17, 1997
PRIOR APPLICATION NUMBER:	60/069,873
PRIOR FILING DATE:	December 17, 1997
PRIOR APPLICATION NUMBER:	60/068,017
PRIOR FILING DATE:	December 18, 1997
PRIOR APPLICATION NUMBER:	60/070,440
PRIOR FILING DATE:	January 5, 1998
PRIOR APPLICATION NUMBER:	60/074,086
PRIOR FILING DATE:	February 9, 1998
PRIOR APPLICATION NUMBER:	60/074,092
PRIOR FILING DATE:	February 9, 1998
PRIOR APPLICATION NUMBER:	60/075,945
PRIOR FILING DATE:	February 25, 1998
PRIOR APPLICATION NUMBER:	60/112,850
PRIOR FILING DATE:	December 16, 1998
PRIOR APPLICATION NUMBER:	60/113,296
PRIOR FILING DATE:	December 22, 1998
PRIOR APPLICATION NUMBER:	60/146,222
PRIOR FILING DATE:	July 28, 1999
PRIOR APPLICATION NUMBER:	PCT/US98/19330
PRIOR FILING DATE:	September 16, 1998
PRIOR APPLICATION NUMBER:	PCT/US98/25108
PRIOR FILING DATE:	December 1, 1998
PRIOR APPLICATION NUMBER:	09/216,021
PRIOR FILING DATE:	December 16, 1998
PRIOR APPLICATION NUMBER:	09/218,517
PRIOR FILING DATE:	December 22, 1998
PRIOR APPLICATION NUMBER:	09/254,311
PRIOR FILING DATE:	March 3, 1999
PRIOR APPLICATION NUMBER:	PCT/US99/12252
PRIOR FILING DATE:	June 22, 1999
PRIOR APPLICATION NUMBER:	PCT/US99/21090
PRIOR FILING DATE:	September 15, 1999
PRIOR APPLICATION NUMBER:	PCT/US99/28409
PRIOR FILING DATE:	No. US20020142959A1ember 30, 1999
PRIOR APPLICATION NUMBER:	PCT/US99/28313
PRIOR FILING DATE:	No. US20020142959A1ember 30, 1999
PRIOR APPLICATION NUMBER:	PCT/US99/28301
PRIOR FILING DATE:	December 1, 1999
PRIOR APPLICATION NUMBER:	PCT/US99/30095
PRIOR FILING DATE:	December 16, 1999
PRIOR APPLICATION NUMBER:	PCT/US00/03565
PRIOR FILING DATE:	February 11, 2000
PRIOR APPLICATION NUMBER:	PCT/US00/04414
PRIOR FILING DATE:	February 22, 2000
PRIOR APPLICATION NUMBER:	PCT/US00/05841
PRIOR FILING DATE:	March 2, 2000
PRIOR APPLICATION NUMBER:	PCT/US00/08439
PRIOR FILING DATE:	March 30, 2000
PRIOR APPLICATION NUMBER:	PCT/US00/14042
PRIOR FILING DATE:	May 22, 2000
PRIOR APPLICATION NUMBER:	PCT/US00/20710
PRIOR FILING DATE:	July 28, 2000
PRIOR APPLICATION NUMBER:	PCT/US00/32678
PRIOR FILING DATE:	December 1, 2000
PRIOR APPLICATION NUMBER:	PCT/US01/06520
PRIOR FILING DATE:	February 28, 2001
NUMBER OF SEQ ID NOS:	120
SEQ ID NO 49	
LENGTH:	1876
TYPE:	DNA
ORGANISM:	Homo Sapien
US-09-944-654-49	
Query Match	100.0%; Score 1876; DB 10; Length 1876;
Best Local Similarity	100.0%; Pred.No. 0;
Matches 1876; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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Db	1081	ATTACAGACCAGATGAATGT	CAGAGGAAGGGGGGTGCTGGCCACAGTCAAGAGCC	1114
QY	1141	AGAAAGTCAGGACATCTTCGCTTCTATCTGGCGCGCTTGAGACACCAACAGAGTGA	1200	
Db	1141	AGAAAGTCAGGACATCTTCGCTTCTATCTGGCGCGCTTGAGACACCAACAGAGTGA	1200	
QY	1261	CTGACAGTGACTTCGAGACCGAGAACTTCTGATGGGTCACTTAAAGACGCCCAAGG	1260	
Db	1201	CTGACAGTGACTTCGAGACCGAGAACTTCTGATGGGTCACTTAAAGACGCCCAAGG	1260	
QY	1261	ACTCCTCCGCTGGCCACAGGGGAGCACCAGGCCTTACACAGTTTGGCTTTGGCGAGC	1320	
Db	1261	ACTCCTCCGCTGGCCACAGGGGAGCACCAGGCCTTACACAGTTTGGCTTTGGCGAGC	1320	
QY	1321	CTGACAACACGGGCTGTGTGGCTGAGTGTGCCATGGGTTTGGCAACTCGCTGGAGC	1380	
Db	1321	CTGACAACACGGGCTGTGTGGCTGAGTGTGCCATGGGTTTGGCAACTCGCTGGAGC	1380	
QY	1381	TGCAGGCTTCAAGTCCCTTCAACTGGAACGACACCGCTGCAAAACCCGAACCCGTTACA	1440	
Db	1381	TGCAGGCTTCAAGTCCCTTCAACTGGAACGACACCGCTGCAAAACCCGAACCCGTTACA	1440	
QY	1441	TCTGCCAGTTTGGCCAGGAGCACATCTCCCGTGGGGCCAGGTCCTGAGGCGTGACCA	1500	
Db	1441	TCTGCCAGTTTGGCCAGGAGCACATCTCCCGTGGGGCCAGGTCCTGAGGCGTGACCA	1500	
QY	1501	CATGCTCCCTCGCTGCGCTGGGAGCACCGGCTCTGCTTACCTGTCTCCCACTGTCT	1560	
Db	1501	CATGCTCCCTCGCTGCGCTGGGAGCACCGGCTCTGCTTACCTGTCTCCCACTGTCT	1560	
QY	1561	GGACAAGGGCCAGGTTAAGACACATGCCTATGTCCAAAGAGTCTCAGACCTTGCAC	1620	
Db	1561	GGACAAGGGCCAGGTTAAGACACATGCCTATGTCCAAAGAGTCTCAGACCTTGCAC	1620	
QY	1621	AATGCCAGAAGTTGGCCACAGAGAGGCGAGGCGCAGTGAGGGCCAGGAGCTGT	1680	
Db	1621	AATGCCAGAAGTTGGCCACAGAGAGGCGAGGCGCAGTGAGGGCCAGGAGCTGT	1680	
QY	1681	AGAAAGCTGGGCGCTTCGCCCTGCTTTGATGGGAAGATGGCTTCAATTAGATGGC	1740	
Db	1681	AGAAAGCTGGGCGCTTCGCCCTGCTTTGATGGGAAGATGGCTTCAATTAGATGGC	1740	
QY	1741	GAAGSAGGAGACCGCCAGTGGTCCAAAAGGCTGCTCTTCCACCTTGCCCCAGACC	1800	
Db	1741	GAAGSAGGAGACCGCCAGTGGTCCAAAAGGCTGCTCTTCCACCTTGCCCCAGACC	1800	
QY	1801	TGTGGGCGAGGGAGCTTCCCTGTGGCATGAACCCACGGGTATTAATTATGAATCAG	1860	
Db	1801	TGTGGGCGAGGGAGCTTCCCTGTGGCATGAACCCACGGGTATTAATTATGAATCAG	1860	
QY	1861	CTGAAAAAANAANAANA 1876		
Db	1861	CTGAAAAAANAANAANA 1876		

RESULT 15	
US-09-943-851A-49	
Sequence 49, Application US/09943851A	
Patent No. US20020150976A1	
GENERAL INFORMATION:	
APPLICANT: Baker, Kevin	
APPLICANT: Botstein, David	
APPLICANT: Eaton, Dan	
APPLICANT: Ferrara, Napoleone	
APPLICANT: Filvaroff, Ellen	
APPLICANT: Gerritsen, Mary	
APPLICANT: Goddard, Audrey	
APPLICANT: Godowski, Paul	
APPLICANT: Grimaldi, Christopher	
APPLICANT: Gurney, Austin	
APPLICANT: Hillan, Kenneth	
APPLICANT: Kijavini, Iivar	
APPLICANT: Napier, Mary	
PRIOR APPLICATION NUMBER: 09/254,311	
PRIOR FILING DATE: March 3, 1999	
PRIOR APPLICATION NUMBER: PCT/US99/12252	
PRIOR FILING DATE: June 22, 1999	
PRIOR APPLICATION NUMBER: PCT/US99/21090	
PRIOR FILING DATE: September 15, 1999	
PRIOR APPLICATION NUMBER: PCT/US99/28409	
PRIOR FILING DATE: No. US20020150976A1member 30, 1999	
PRIOR APPLICATION NUMBER: PCT/US99/28313	
PRIOR FILING DATE: No. US20020150976A1member 30, 1999	
PRIOR APPLICATION NUMBER: PCT/US99/28301	
PRIOR FILING DATE: December 1, 1999	
PRIOR APPLICATION NUMBER: PCT/US99/30095	
PRIOR FILING DATE: December 16, 1999	
PRIOR APPLICATION NUMBER: PCT/US00/03565	
PRIOR FILING DATE: February 11, 2000	
PRIOR APPLICATION NUMBER: PCT/US00/04414	
PRIOR FILING DATE: February 22, 2000	
PRIOR APPLICATION NUMBER: PCT/US00/05841	

QY	1861	CTGAAAAAAAAAAAA	1876
Db	1861	CTGAAAAAAAAAAAA	1876

Search completed: December 28, 2002, 23:04:18
Job time : 104.538 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 16:45:43 ; Search time 329.93 Seconds
(without alignments)
12124.644 Million cell updates/sec

Title: US-09-944-896-49_COPY_201_447

Perfect score: 247

Sequence: 1 gaggtgtggccaccagct.....cacctgcaagtggcgctga 247

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rtd:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	245.4	99.4	463	9	AI792411
2	245.4	99.4	1076	13	BM547887
3	242.2	98.1	1034	14	BM924615
4	232.6	94.2	710	13	BI760121
5	230.2	93.2	709	13	BI759120
6	230.2	93.2	928	13	BI517774

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7	228.6	92.6	939	13	BI757380
8	223	90.3	500	13	BI761101
9	219.8	89.0	852	13	BI762690
10	216	87.4	836	13	BI764403
11	190.4	77.1	916	13	BI759333
12	163.6	66.2	521	13	BI340175
13	162	65.6	392	10	AW437073
14	135.6	54.9	321	13	BI359591
15	124.4	50.4	523	10	AW786132
16	118	47.8	634	10	BB602462
17	87.2	35.3	457	13	BI759735
18	43.2	17.5	1101	17	CNS01751
19	42.8	17.3	515	10	BE481031
20	42.2	17.1	529	12	BF079457
21	42	17.0	893	11	AK005860
22	41.2	16.7	1175	13	BI912306
23	40.8	16.5	925	17	CNS0091P
24	40	16.2	665	10	BE369422
25	40	16.2	925	17	CNS0091P
26	39.8	16.1	734	17	BH839844
27	39.8	16.1	749	17	BH839110
28	39.2	15.9	680	13	BI911002
29	39	15.8	233	10	AW382986
30	38.8	15.7	977	14	BQ710623
31	38.2	15.5	738	12	BF026829
32	37.6	15.2	323	14	BM705204
33	37.6	15.2	364	10	BE487038
34	37.6	15.2	407	12	BG592644
35	37.6	15.2	428	10	AW863268
36	37.6	15.2	448	12	BE846302
37	37.6	15.2	451	12	BF074630
38	37.6	15.2	454	10	BE479205
39	37.6	15.2	454	10	BE480335
40	37.6	15.2	498	12	BG688440
41	37.6	15.2	515	10	BE484486
42	37.6	15.2	518	10	BE480835
43	37.6	15.2	528	10	BE480319
44	37.6	15.2	532	10	BE480502
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ALIGNMENTS

RESULT 1
AI792411
LOCUS
DEFINITION
AI792411 463 bp mRNA linear EST 02-JUL-1999
an34b09.y5 Gessler Wilms tumor Homo sapiens cDNA clone
IMAGE:1700537 5' similar to TR:043692 O43692 25 KDA TRYPSIN
INHIBITOR. ; mRNA sequence.
AI792411 GI:5340127
EST.
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 463)
NCI/NIDR-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation
information
This 5' resequenced clone has no previous 5' data to verify this
new read against
Seq primer: -40RP from Gibco
High quality sequence stop: 429.

BI757380 603029310
BI761101 603043573
BI762690 603048444
BI764403 603046141
BI759333 603043013
BI340175 365365 MA
AW437073 77836 MAR
BI359591 384181 MA
AW786132 118625 MA
BB602462 BB602462
BI759735 603045609
AL108460 Drosophila
BE481031 166323 BA
BF079457 230060 MA
AK005860 Mus muscu
BI912306 603068842
AL053013 Drosophila
BE369422 601220824
AL053013 Drosophila
BH839844 LMCRI5000
BH839110 LMCRI5000
BI911002 603068720
AW382986 PNO-HF034
BQ710623 AGENCOURT
BF026829 601670724
BM705204 UI-E-C11-
BE487038 175565 BA
BG592644 342421 BA
AW863268 MR3-SN000
BE46302 231986 BA
BF074630 222090 MA
BE479205 163817 BA
BE480335 165384 BA
BG688440 336061 BA
BE484486 171120 BA
BE480835 166077 BA
BE480319 165365 BA
BE480502 165605 BA
AL703236 DKFZp686H

FEATURES
source

Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:1700537"
/clone_lib="Gessler Wilms tumor"
/sex="pooled (6)"
/lab_host="DH10B"
/note="vector: pSPORT1; Site_1: SalI; Site_2: NotI; RNA
was prepared from a pool of 6 anonymous Wilms' tumor RNAs.
RNA was prepared by acid-phenol, followed by one round of
oligo dt selection. cDNA library preparation was with
the BRL/Life Tech. Superscript plasmid system. An
oligo-dt NotI primer for first strand synthesis generated
gcggccccc(t)n at the 3' end of the clones. A 5' SalI
adaptor was used with sequence 5'-gtcgaccacgctccg-3'.
Resulting cDNAs were size selected (average size 2 kb),
NotI digested, and ligated into NotI/SalI-cut pSPORT1.
Library was constructed by Dr. Manfred Gessler."

BASE COUNT
ORIGIN

80 a 163 c 143 g 77 t

Query Match 99.4%; Score 245.4; DB 9; Length 463;
Best Local Similarity 99.6%; Pred. No. 9.3e-49;
Matches 246; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCCCTGACAGGAAG 60
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DB 205 GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCCCTGACAGGAAG 264
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QY 61 GAGAGTTTCTTCTCTCTCCCTGCACACCGCTGCGCAGCTGGTCCAGCCCCCTTGGC 120
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DB 265 GAGAGTTTCTTCTCTCTCCCTGCACACCGCTGCGCAGCTGGTCCAGCCCCCTTGGC 324
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QY 121 GCTGACATGCGGAGGTGGAGTGGAGTGCAGCTGGCCCACTGGCTCAAGCCAGGGCA 180
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DB 325 GCTGACATGCGGAGGTGGAGTGGAGTGCAGCTGGCCCACTGGCTCAAGCCAGGGCA 384
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QY 181 GCCCTCTGTGGAATCCCAACCCGAGCGCTGGCATCCGCGCTGTGGCCACCCCTCAAGTG 240
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DB 385 GCCCTCTGTGGAATCCCAACCCGAGCGCTGGCATCCGCGCTGTGGCCACCCCTCAAGTG 444
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QY 241 GGCTGGA 247
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DB 445 GGCTGGA 451

RESULT 2
BM547887
LOCUS

DEFINITION BM547887 1076 bp mRNA linear EST 20-FEB-2002
AGENCOURT_6531767 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5732633
5', mRNA sequence.

ACCESSION BM547887
VERSION BM547887.1 GI:18782034
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1076)

REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI2735 row: a column: 18

FEATURES
source

High quality sequence start: 9
High quality sequence stop: 677.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5732633"
/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
(destroyed); Site_2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dt primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

BASE COUNT 192 a 358 c 338 g 182 t 6 others
ORIGIN

Query Match 99.4%; Score 245.4; DB 13; Length 1076;
Best Local Similarity 99.6%; Pred. No. 1e-48;
Matches 246; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCCCTGACAGGAAG 60
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DB 334 GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCCCTGACAGGAAG 393
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QY 61 GAGAGTTTCTTCTCTCTCTCCCTGCACACCGCTGCGCAGCTGGTCCAGCCCCCTTGGC 120
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DB 394 GAGAGTTTCTTCTCTCTCTCCCTGCACACCGCTGCGCAGCTGGTCCAGCCCCCTTGGC 453
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QY 121 GCTGACATGCGGAGGTGGAGTGGAGTGCAGCTGGCCCACTGGCTCAAGCCAGGGCA 180
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DB 454 GCTGACATGCGGAGGTGGAGTGGAGTGCAGCTGGCCCACTGGCTCAAGCCAGGGCA 513
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QY 181 GCCCTCTGTGGAATCCCAACCCGAGCGCTGGCATCCGCGCTGTGGCCACCCCTCAAGTG 240
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DB 514 GCCCTCTGTGGAATCCCAACCCGAGCGCTGGCATCCGCGCTGTGGCCACCCCTCAAGTG 573
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QY 241 GGCTGGA 247
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DB 574 GGCTGGA 580

RESULT 3
BM924615
LOCUS

DEFINITION BM924615 1034 bp mRNA linear EST 12-MAR-2002
AGENCOURT_6767842 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5761001
5', mRNA sequence.

ACCESSION BM924615
VERSION BM924615.1 GI:19374994
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1034)

REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI2808 row: o column: 18
High quality sequence stop: 685.

FEATURES
source

Location/Qualifiers
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/clone="IMAGE:5761001"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"

/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon, 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

BASE COUNT 186 a 336 c 321 g 189 t 2 others
ORIGIN

Query Match 98.1%; Score 242.2; DB 14; Length 1034;
Best Local Similarity 98.8%; Pred. No. 5,8e-48;
Matches 244; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGGTGTGCCACCCAGCTGCAGGAGGCTCCGATGGCCGGAGCCCTGAACAGGAAG 60
|||||
Db 198 GAGGTGTGCCACCCAGCTGCAGGAGGCTCCGATGGCCGGAGCCCTGAACAGGAAG 257
QY 61 GAGAGTTTCTTGTCTCTCCCTGCACAAACCCCTGCCAGCTGGTCCAGCCCTCGG 120
|||||
Db 258 GAGAGTTTCTTGTCTCTCCCTGCACAAACCCCTGCCAGCTGGTCCAGCCCTCGG 317
QY 121 GCTGACATCGGAGGCTGGAGTGGAGTGACAGCCCTGGCCCACTGGCTCAAGCCAGGGCA 180
Db 318 GCTGACATCGGAGGCTGGAGTGGAGTGACAGCCCTGGCCCACTGGCTCAAGCCAGGGCA 377
QY 181 GCCCTCTGTGGAATCCCAACCCCGAGCTGGCATCCGCGCTGTGGCGCACCCCTGCAAGT 240
|||||
Db 378 GCCCTCTGTGGAATCCCAACCCCGAGCTGGCATCCGCGCTGTGGCGCACCCCTGCAAGT 437
QY 241 GGCTGGA 247
|||||
Db 438 GGCTGGA 444

RESULT 4
BI760121
LOCUS
DEFINITION
603044615F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5184962 5',
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
human.
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11461 row: n column: 03
High quality sequence stop: 704.

FEATURES
source

Location/Qualifiers
1..710
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5184962"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"

/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon, 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

BASE COUNT 131 a 228 c 226 g 125 t
ORIGIN

Query Match 94.2%; Score 232.6; DB 13; Length 710;
Best Local Similarity 98.3%; Pred. No. 1.1e-45;
Matches 235; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 GCCACCCAGCTGCAGGAGGCTCCGATGGCCGGAGCCCTGAACAGGAAGAGTTT 68
|||||
Db 6 GCCACCCAGCTGCAGGAGGCTCCGATGGCCGGAGCCCTGAACAGGAAGAGTTT 65
QY 69 CTTGCTCTCTCCCTGCACAAACCCCTGCCAGCTGGTCCAGCCCTCGCGCTGACAT 128
|||||
Db 66 CTTGCTCTCTCCCTGCACAAACCCCTGCCAGCTGGTCCAGCCCTCGCGCTGACAT 125
QY 129 GCGGAGCTGGAGTGGAGTGACAGCCCTGGCCCACTGGCTCAAGCCAGGAGCCCTCG 188
Db 126 GCGGAGCTGGAGTGGAGTGACAGCCCTGGCCCACTGGCTCAAGCCAGGAGCCCTCG 185
QY 189 TGAATCCCAACCCCGAGCTGGCATCCGCGCTGTGGCGCACCCCTGCAAGTGGGTGGA 247
|||||
Db 186 TGAATCCCAACCCCGAGCTGGCATCCGCGCTGTGGCGCACCCCTGCAAGTGGGTGGA 244

RESULT 5
BI759120
LOCUS
DEFINITION
603042530F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5182999 5',
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
human.
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11456 row: 1 column: 08
High quality sequence stop: 709.

FEATURES
source

Location/Qualifiers
1..709
/organism="Homo sapiens"
/db_xref="taxon:9606"

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/clonelib="IMAGE:5182999"
/clonelib="NIH_MGC_116"
/lab_host="DH10B"
/Note="Organ: pooled colon, kidney, stomach; Vector:
PCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT 124 a 240 c 220 g 125 t
ORIGIN

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```

Query Match 93.2%; Score 230.2; DB 13; Length 709;
Best Local Similarity 98.4%; Pred. No. 4.1e-45;
Matches 243; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 GAGGTGTGGCCACCCAGCTGCAGGAGGCTCCGATGGCGGAGCCCTGAACAGGAAG 60
Db 248 GAGGTGTGGCCACCCAGCTGCAGGAGGCTCCGATGGCGGAGCCCTGAACAGGAAG 307
QY 61 GAGAGTTTCTTGTCTCTCCCTGCACACCGCTGCGAGCTGGTCCAGCCCTCGG 120
Db 308 GAGAGTTTCTTGTCTCTCCCTGCACACCGCTGCGAGCTGGTCCAGCCCTCGG 367
QY 121 GCTGACATGCGGAGGCTGAGTGGAGTACAGCTGGCCCACTGGCTCAAGCCAGGCA 180
Db 368 GCTGACATGCGGAGGCTGAGTGGAGTACAGCTGGCCCACTGGCTCAAGCCAGGCA 426
QY 181 GCCCTCTGTGGAATCCACACCGAGCTTGGATCGGCTGCGGAGCCCTGCAAGTG 240
Db 427 GCCCTCTGTGGAATCCACACCGAGCTTGGATCGGCTGCGGAGCCCTGCAAGTG 486
QY 241 GGCTGGA 247
Db 487 GGCTGGA 493

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RESULT 6
BI517774
LOCUS 603042018F1 NIH_MGC_116 928 bp mRNA linear EST 29-AUG-2001
DEFINITION 603042018F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5182997 5',
mRNA sequence.
ACCESSION BI517774
VERSION BI517774.1 GI:15342566
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 928)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1455 row: c column: 06
High quality sequence stop: 860.
FEATURES
source
Location/Qualifiers
1..928
/organism="Homo sapiens"
/db_xref="taxon:9606"

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/clonelib="IMAGE:5182397"
/clonelib="NIH_MGC_116"
/lab_host="DH10B"
/Note="Organ: pooled colon, kidney, stomach; Vector:
PCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT 169 a 293 c 307 g 159 t
ORIGIN

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```

Query Match 93.2%; Score 230.2; DB 13; Length 928;
Best Local Similarity 98.4%; Pred. No. 4.2e-45;
Matches 243; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 GAGGTGTGGCCACCCAGCTGCAGGAGGCTCCGATGGCGGAGCCCTGAACAGGAAG 60
Db 140 GAGGTGTGGCCACCCAGCTGCAGGAGGCTCCGATGGCGGAGCCCTGAACAGGAAG 199
QY 61 GAGAGTTTCTTGTCTCTCCCTGCACACCGCTGCGAGCTGGTCCAGCCCTCGG 120
Db 200 GAGAGTTTCTTGTCTCTCCCTGCACACCGCTGCGAGCTGGTCCAGCCCTCGG 259
QY 121 GCTGACATGCGGAGGCTGAGTGGAGTACAGCTGGCCCACTGGCTCAAGCCAGGCA 180
Db 260 GCTGACATGCGGAGGCTGAGTGGAGTACAGCTGGCCCACTGGCTCAAGCCAGGCA 318
QY 181 GCCCTCTGTGGAATCCACACCGAGCTTGGATCGGCTGCGGAGCCCTGCAAGTG 240
Db 319 GCCCTCTGTGGAATCCACACCGAGCTTGGATCGGCTGCGGAGCCCTGCAAGTG 378
QY 241 GGCTGGA 247
Db 379 GGCTGGA 385

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RESULT 7
BI757380
LOCUS 603029310F1 NIH_MGC_114 939 bp mRNA linear EST 25-SEP-2001
DEFINITION 603029310F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5199674 5',
mRNA sequence.
ACCESSION BI757380
VERSION BI757380.1 GI:15748958
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 939)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1500 row: c column: 03
High quality sequence stop: 778.
FEATURES
source
Location/Qualifiers
1..939
/organism="Homo sapiens"
/db_xref="taxon:9606"

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/clone="IMAGE:5198674"
/clone_lib="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
BASE COUNT      168 a   286 c   320 g   165 t
ORIGIN

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Query Match      92.6%; Score 228.6; DB 13; Length 939;
Best Local Similarity 98.0%; Pred. No. 1e-44;
Matches 242; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCGGAGCCCTGAACAGGAAG 60
Db 128 GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCGGAGCCCTGAACAGGAAG 187
QY 61 GAGAGTTTCTTGCTCTCTCCCTGCACAAACCGCTGCAGCTGGGTCCAGCCCCCTGCG 120
Db 188 GAGAGTTTCTTGCTCTCTCCCTGCACAAACCGCTGCAGCTGGGTCCAGCCCCCTGCG 247
QY 121 GCTGACATGCGGAGGCTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGCA 180
Db 248 GCTGACATGCGGAGGCTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGCA 306
QY 181 GCCTCTGTGGAATCCCAACCCGAGGCTGGCATCCGCGCTGGCGGAGCCCTGCAAGTG 240
Db 307 GCCTCTGTGGAATCCCAACCCGAGGCTGGCATCCGCGCTGGCGGAGCCCTGCAAGTG 366
QY 241 GCGTGA 247
Db 367 GCGTGA 373

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```

RESULT 8
BI761101
LOCUS      BI761101
DEFINITION 60304373F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:518398 5',
mrna sequence.
ACCESSION  BI761101
VERSION     BI761101.1
KEYWORDS    EST
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1459 row: a column: 19
High quality sequence stop: 480.
Location/Qualifiers
1..500
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:518398"
/clone_lib="NIH_MGC_116"

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FEATURES
Source

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/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT      84 a   180 c   151 g   85 t
ORIGIN

```

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Query Match      90.3%; Score 223; DB 13; Length 500;
Best Local Similarity 97.5%; Pred. No. 2.1e-43;
Matches 237; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCGGAGCCCTGAACAGGAAG 60
Db 215 GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCGGAGCCCTGAACAGGAAG 274
QY 61 GAGAGTTTCTTGCTCTCTCCCTGCACAAACCGCTGCAGCTGGGTCCAGCCCCCTGCG 120
Db 275 GAGAGTTTCTTGCTCTCTCCCTGCACAAACCGCTGCAGCTGGGTCCAGCCCCCTGCG 334
QY 121 GCTGACATGCGGAGGCTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGCA 180
Db 335 GCTGACATGCGGAGGCTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGCA 394
QY 181 GCCTCTGTGGAATCCCAACCCGAGGCTGGCATCCGCGCTGGCGGAGCCCTGCAAGTG 239
Db 395 GCCTCTGTGGAATCCCAACCCGAGGCTGGCATCCGCGCTGGCGGAGCCCTGCAAGTG 454
QY 240 GGG 242
Db 455 TGG 457

```

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RESULT 9
BI762690
LOCUS      BI762690
DEFINITION 60304844F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188643 5',
mrna sequence.
ACCESSION  BI762690
VERSION     BI762690.1
KEYWORDS    EST
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1471 row: g column: 12
High quality sequence stop: 849.
Location/Qualifiers
1..852
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5188643"
/clone_lib="NIH_MGC_116"

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FEATURES
Source

```

/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
PCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dt primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT 146 a 283 c 269 g 154 t
ORIGIN

Query Match 89.0%; Score 219.8; DB 13; Length 852;
Best Local Similarity 98.4%; Pred. No. 1.3e-42;
Matches 243; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
QY 1 GAGGTGTGGCCACCCAGCTGCAGAGCAGGCTCCGATGGCCGGAGCCCTGACACGAAG 60
Db 336 GAGGTGTGGCCACCCAGCTGCAGAGCAGGCTCCGATGGCCGGAGCCCTGACACGAAG 395
QY 61 GAGAGTTTCTGCTCTCCCTGCACAAACGCGCTGGCTGGCTCCAGCCCTCGG 120
Db 396 GAGAGTTTCTGCTCTCCCTGCACAAACGCGCTGGCTGGCTCCAGCCCTCGG 455
QY 121 GCTGACATGCGAGGCTGGAGTGGAGTGCAGAGCCTGGCCCACTGGCTCAAGCCAGGCA 180
Db 456 GCTGACAGGCGGAGGCTGGAGTGGAGTGCAGAGCCTGG-CCAACTGGCTCAAGCA-GGCA 513
QY 181 GCCCTCTGTGAATCCCAACCCGAGCTGGCATCGGCTGFGGCGACCCCTGCAAGTG 240
Db 514 GCCCTCTGTGAATCCCAACCCGAGCTGGCGTCCGGCTGTGGCGACCCCTGCAAGTG 573
QY 241 GGCTGGA 247
Db 574 GGCTGGA 580

RESULT 10
BI764403
LOCUS 603046141F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186219 5',
DEFINITION mRNA sequence.
ACCESSION BI764403 836 bp mRNA linear EST 25-SEP-2001
VERSION BI764403
KEYWORDS EST.
SOURCE BI764403.1 GI:15755981
ORGANISM human.
REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL 1 (bases 1 to 836)
COMMENT NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL1465 row: b column: 12
High quality sequence stop: 761.
Location/Qualifiers

1. .836
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5186219"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"

FEATURES
source

/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
PCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dt primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT 157 a 255 c 271 g 153 t
ORIGIN

Query Match 87.4%; Score 216; DB 13; Length 836;
Best Local Similarity 97.8%; Pred. No. 1e-41;
Matches 219; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 24 GGAGCAGGCTCCGATGGCCGGAGCCCTGAACAGAGGAGAGTTTCTTGTCTCTCCCT 83
Db 1 GGAGCAGGCTCCGATGGCCGGAGCCCTGAACAGAGGAGAGTTTCTTGTCTCTCCCT 60
QY 84 GCACAAACCCCTGCGCAGCTGGTCCAGCCCTGCGGCTGACATGCGGAGGCTGGACTG 143
Db 61 GCACAAACCCCTGCGCAGCTGGTCCAGCCCTGCGGCTGACATGCGGAGGCTGGACTG 120
QY 144 GAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCC 203
Db 121 GAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCC 180
QY 204 GAGCTGGCATCCGGCTGTGGCGCACCCCTGCAAGTGGCTGGA 247
Db 181 GAGCTGGCATCCGGCTGTGGCGCACCCCTGCAAGTGGCTGGA 224

RESULT 11
BI759353
LOCUS 603043013F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183330 5',
DEFINITION mRNA sequence.
ACCESSION BI759353 916 bp mRNA linear EST 25-SEP-2001
VERSION BI759353.1 GI:15750931
KEYWORDS EST.
SOURCE BI759353
ORGANISM human.
REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL 1 (bases 1 to 916)
COMMENT NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL1457 row: j column: 03
High quality sequence stop: 723.
Location/Qualifiers

1. .916
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5183330"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"

FEATURES
source

female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

BASE COUNT 153 a 306 c 278 g 178 t 1 others
ORIGIN

Query Match 77.18; Score 190.4; DB 13; Length 916;
Best Local Similarity 97.68; Pred. No. 1.3e-35;
Matches 246; Conservative 0; Mismatches 1; Indels 5; Gaps 5;

QY 1 GAGGTGTGGCCACC-CCAGCTGCA-GGACGAGGCTCCGATGCCGAGGCCCTGAACAGGA 58
|||||
Db 223 GAGGTGTGGCCACCACCAGCTGATGAGCAGGCTCCGATGCCGAGGCCCTGAACAGGA 282
|||||
QY 59 AGGAGAGTTTCTGCTCTCTCTCTGTCACAAACCGGCTG-CGACGCTGGGTCCAGCCCTCT 117
|||||
Db 283 AGGAGAGTTTCTGCTCTCTCTCTGTCACAAACCGGCTGTCGACGCTGGGTCCAGCCCTCT 342
|||||
QY 118 GCGG-CTGACATCGGAGGCTGGACTGGAGTGACA-GCCTGGCCCAACTGGCTCAAGCCA 175
|||||
Db 343 GCGGCTGACATCGGAGGCTGGACTGGAGTGACATGCTGCGCCCAACTGGCTCAAGCCA 402
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QY 176 GGGCAGCCCTCTGTGGAAATCCCAACCCGAGCCTGGCATCGGCTGTGGCCACCCCTGC 235
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Db 403 GGGCAGCCCTCTGTGGAAATCCCAACCCGAGCCTGGCATCGGCTGTGGCCACCCCTGC 235
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QY 236 AAGTGGGCTGGA 247
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Db 463 AAGTGGGCTGGA 474

RESULT 12
BI340175 521 bp mRNA linear EST 30-JUL-2001
LOCUS
DEFINITION 365365 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BI340175
VERSION BI340175.1 GI:15033458
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
AUTHORS 1 (bases 1 to 521)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keelle,J.W.

TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 104 row: P column: 4
Seq primer: ATTAGTGACACATATAG.

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/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"

/tissue_type="pooled"
/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site.1: NotI; Site.2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT 92 a 188 c 160 g 81 t
ORIGIN

Query Match 66.28; Score 163.6; DB 13; Length 521;
Best Local Similarity 81.28; Pred. No. 3.1e-29;
Matches 203; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY 1 GAGGTGTGGCCACCCAGCTGCAGG---AGCAGGCTCCGATGCCGAGGCCCTGAACAGG 57
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Db 138 GAAGTGACGACCACTTCAGCTCCAGGAGAGCAGGTTCCTCAATGCCGAGGCCCTGAGCAGG 197
|||||
QY 58 AAGGAGAGTTTCTGCTCTCTCTCTGCTGCAACACCGCTGCGCAGCTGGGTCCAGCCCTCT 117
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Db 198 AAGGAGAGTTTCTGCTCTCTCTGCTGCAACACCGCTGCGCAGCTGGGTCCAGCCCTCT 257
|||||
QY 118 GCGGCTGACATCGGAGGCTGGACTGGAGTGACAACCGCTGCGCAGCGCGGTCCACCCCT 177
|||||
Db 258 GCAGCCCAACATGACAGAAATGGACTGGAGCAGAGGCTGGCTCAACAGGCTCAGACCCAGG 317
|||||
QY 178 GCAGCCCTCTGTGGAAATCCCAACCCGAGCCTGGCATCGGCTGTGGCGACCCCTGCAA 237
|||||
Db 318 GCGGCCCTTTGTGGCGCCCGCAGCCCCAAGCCTGGCTTCCATCTCTCCGGGCGCCACCCCAA 377
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QY 238 GTGGGCTGGA 247
|||||
Db 378 GTGGGCTGGA 387

RESULT 13
AW437073

LOCUS AW437073 392 bp mRNA linear EST 09-JUL-2000
DEFINITION 77836 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION AW437073
VERSION AW437073.1 GI:6972379
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa

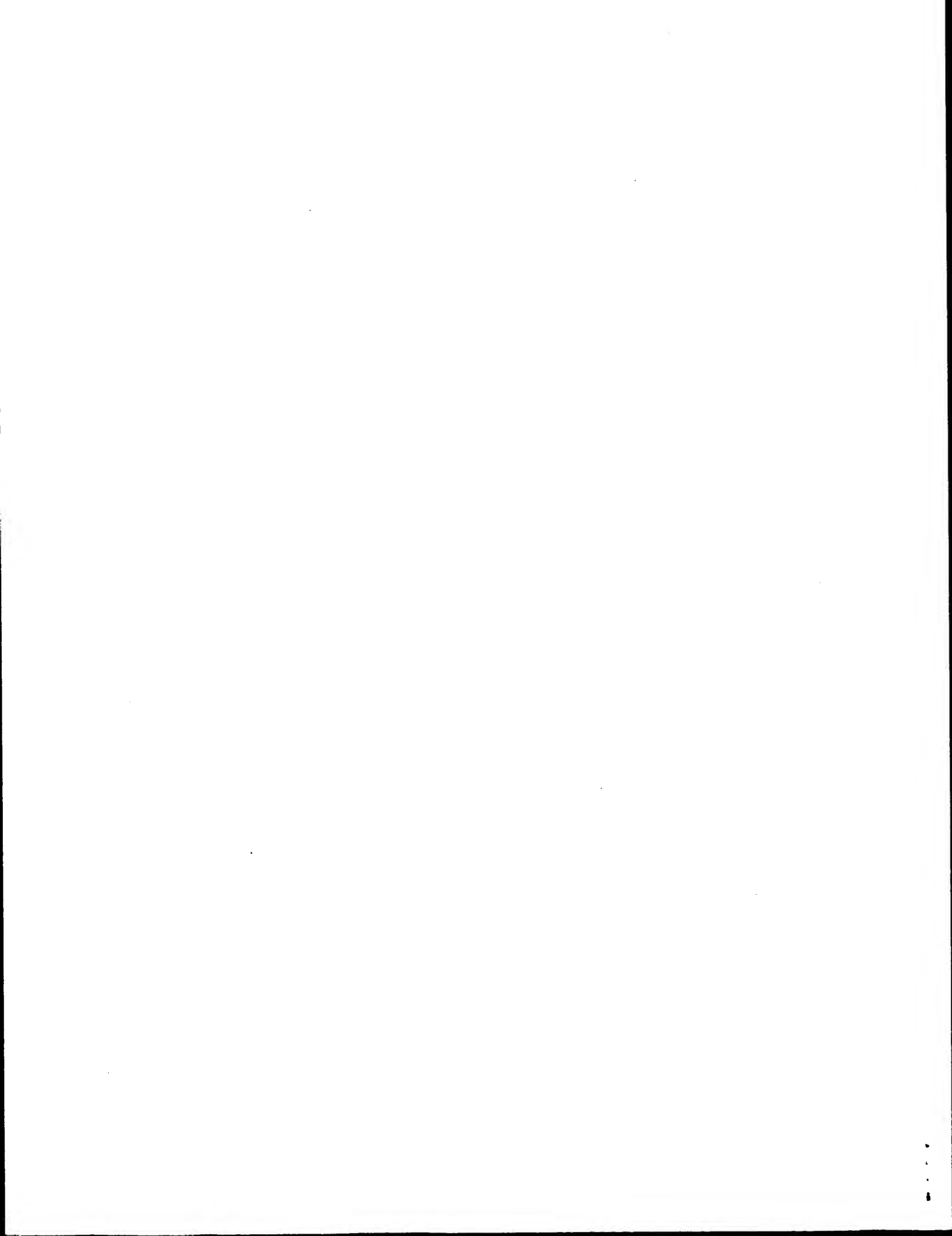
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
AUTHORS 1 (bases 1 to 392)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keelle,J.W.

TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 37 row: H column: 9
Seq primer: ATTAGTGACACATATAG.

FEATURES
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/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"

/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site.1: NotI; Site.2: SalI;



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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 16:45:43 ; Search time 2505.87 Seconds
(without alignments)
12124.644 Million cell updates/sec

Title: US-09-944-896-49

Perfect score: 1876

Sequence: 1 ctctttgtccaccagccca.....tcagctgaaaaaaaaa 1876

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estcov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	861.6	45.9	1034	14	BM924615
2	790.6	42.1	1076	13	BM547887
3	771.8	41.1	928	13	BI517774
4	754	40.2	836	13	BI764403
5	679.6	36.2	939	13	BI757380
6	676	36.0	710	13	BI760121

7	636.6	33.9	709	13	BI759120
8	622.2	33.2	645	14	BM695392
9	610.2	32.5	916	13	BI759353
10	589	31.4	852	13	BI762690
c 11	580	30.9	617	9	AI307814
c 12	579.8	30.9	704	9	AL040183
c 13	568.6	30.3	612	12	BF057185
c 14	564.4	30.1	744	14	BQ006636
c 15	564	30.1	611	10	BM929257
c 16	556.4	29.7	612	14	BQ446805
c 17	513.8	27.4	578	14	BQ720124
c 18	490.2	26.1	495	9	AI989724
c 19	487.6	26.0	494	9	AI433291
c 20	487.4	26.0	490	10	AW001740
c 21	487	26.0	509	9	AI627475
c 22	453.4	24.2	460	10	AW451907
c 23	448.4	23.9	481	9	AA976491
c 24	444.8	23.7	463	9	AI792411
c 25	443.8	23.7	447	12	BG150347
c 26	439	23.4	460	9	AI150446
c 27	432	23.0	445	9	AI589178
c 28	419.8	22.4	500	13	BI761101
c 29	410.8	21.9	492	9	AI827695
c 30	402.6	21.5	409	10	BE552150
c 31	401.8	21.4	405	14	BM708158
c 32	376.2	20.1	385	10	AW137750
c 33	352.2	18.8	396	9	AI863534
c 34	339	18.1	383	9	AA903561
c 35	328	17.5	756	12	BF527554
c 36	325.2	17.3	330	9	AA812725
c 37	313.4	16.7	429	12	BF198258
c 38	304	16.2	312	9	AI657201
c 39	293.2	15.9	521	13	BI340175
c 40	287.2	15.8	411	14	W79362
c 41	286.4	15.3	288	9	AA582202
c 42	271.6	14.5	339	12	BG608968
c 43	265	14.1	470	10	AW972808
c 44	257	13.7	457	13	BI759735
c 45	241	12.8	264	9	AI942280

ALIGNMENTS

RESULT 1
BM924615
LOCUS
DEFINITION AGENCOURT_6767842 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5761001 linear EST 12-MAR-2002
5', mRNA sequence.
ACCESSION BM924615
VERSION BM924615.1 GI:19374994
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1034)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM12808 row: o column: 18
High quality sequence stop: 685.
Location/Qualifiers 1. .1034

/organism="Homo sapiens"
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/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

BASE COUNT 186 a 336 c 321 g 189 t 2 others
ORIGIN

Query Match 45.9%; Score 861.6; DB 14; Length 1034;
Best Local Similarity 93.6%; Pred. No. 1.2e-183;
Matches 953; Conservative 0; Mismatches 56; Indels 9; Gaps 5;

QY 4 TTTTGTCCACGACCCAGCTGACTCTGGAGATTGTAATAGCTCCATCCAGCCTGAGA 63
DB 1 TTTCTCTGTGACGCCAGCTGACTCTCTGGAGATTGTAATAGCTCCATCCAGCCTGAGA 60
QY 64 AACAGCCGGTGGCTGAGCCAGCTGTGCACGAGACCTGACGGGCCCAACAGACCCA 123
DB 61 AACAGCCGGTGGCTGAGCCAGCTGTGCACGAGACCTGACGGGCCCAACAGACCCA 120
QY 124 TGTGTATCCAGAGACCTCCCTGGCCGGGGGATCTCTCTGGCTGTGCTGGCCCTCC 183
DB 121 TGTGTATCCAGAGACCTCCCTGGCCGGGGGATCTCTCTGGCTGTGCTGGCCCTCC 180
QY 184 TTGGCACCACCTGGGAGAGGTGTGGCCACCCAGCTGCAGGAGAGGCTCGGATGGCGG 243
DB 181 TTGGCACCACCTGGGAGAGGTGTGGCCACCCAGCTGCAGGAGAGGCTCGGATGGCGG 240
QY 244 GAGCCCTGAACAGAGGAGATTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 303
DB 241 GAGCCCTGAACAGAGGAGATTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 304 GGCTCAGCCCTCGCGGCTGACATGCGGAGGCTGGAGTGCAGTGCAGCCTGGCCCAAC 363
DB 301 GGCTCAGCCCTCGCGGCTGACATGCGGAGGCTGGAGTGCAGCCTGGCCCAAC 360
QY 364 TGCTCAAGCCAGGCGACCTCTGTGGAATCCCAACCCAGCCTGGCATCCGCGCTGT 423
DB 361 TGCTCAAGCCAGGCGACCTCTGTGGAATCCCAACCCAGCCTGGCATCCGCGCTGT 420
QY 424 GGCGCACCTTGAAGTGGCTGGAACATGACGCTGCTCCCGCGGCTTGGCTCTCTTTG 483
DB 421 GGCGCACCTTGAAGTGGCTGGAACATGACGCTGCTCCCGCGGCTTGGCTCTCTTTG 480
QY 484 TTGAAGTGTGACGCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACCGCGCAGGAGT 543
DB 481 TCGAAGTGTGACGCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACCGCGCAGGAGT 540
QY 544 GTGCTGCAAGCCACCTGACCCACTACAGCAGCTGCTGTGGGCCACCTCAAGCCAGC 603
DB 541 GTGCTGCAAGCCACCTGACCCACTACAGCAGCTGCTGTGGGCCACCTCAAGCCAGC 600
QY 604 TGGGCTGTGGGGCAGCTGTGCTCTCAGGCCAGACGCGATAGAAGCTTTTGTCTGTG 663
DB 601 TGGGCTGTGGGGCAGCTGTGCTCTCAGGCCAGACGCGATAGAAGCTTTTGTCTGTG 660
QY 664 CTTACTCCCCGGAGGCAACTGGGAGTTC-AACGGGAAGACAATCATCCCTTATAAGAAG 722
DB 661 CTTACTCCCCGGAGGCAACTGGGAGTTC-AACGGGAAGACAATCATCCCTTATAAGAAG 720
QY 723 GGTGCTGTGTTGCTGTGACAGCCAGTGTCTCAGGCTGTTCAAGCCTGGGACCAT 782

DB 721 GGTGCCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCANAGCCCTGGGACCAT 780
QY 783 GCA-GGGGGGCTCTGTGAGGTCCCGAGGAATCTTTGTTCGATGAGCTGCCAAGACCATGG 841
DB 781 GCAGGGGGGCTCTGTGAGGTCCCGAGGATCTTTGTCATGAGTGCCTCAAAATGG 839
QY 842 ACCTCTCAACATCAGCAGCTGCCACTGTCACATGTCCTCCCTGGCTACACGGGCGAGTACTG 901
DB 840 ACCTCTCAACATCAGCAGCTGCCACTGTCACATGTCCTCCCTGGCTACACGGGCGAGTACTG 899
QY 902 CCAAGTCAAGTGCAG-CCTGCAGTGTGTCACGGCGGTTCCGGG-AGGAGGAGTG 955
DB 900 CCAAGTCAAGTGCAGCCCTGCANTGTGTCACGCCGTTTCCGGGAAGGAATGCTTC 959
QY 956 CTGCTGCTGTGACATCGCTACGGGGGAGCCAGTGTGCCACCAAGTGCATTTT 1013
DB 960 TTGCTCTCTTAACATCGGCTAGGGGGGGAACCCAGGCTGCCCCAGGGGCGATTT 1017

RESULT 2
LOCUS BM547887
DEFINITION BM547887 1076 bp mRNA linear EST 20-FEB-2002
AGENCOURT_6531767 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5732633
5', mRNA sequence.
ACCESSION BM547887
VERSION BM547887.1 GI:18782034
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1076)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L1AM12735 row: a column: 18
High quality sequence start: 9
High quality sequence stop: 677.

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/clone_lib="NIH_MGC_124"
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
BASE COUNT 192 a 358 c 338 g 182 t 6 others
ORIGIN

Query Match 42.1%; Score 790.6; DB 13; Length 1076;
Best Local Similarity 93.4%; Pred. No. 1.2e-167;
Matches 846; Conservative 0; Mismatches 57; Indels 3; Gaps 2;
QY 9 TCCACACGCGGCTGACTCTCTGGAGATTGTAATAGCTCCATCCAGCTGAGAAACA 68
DB 142 TCAGGGGGCGGCTGACTCTCTGGAGATTGTAATAGCTCCATCCAGCTGAGAAACA 201


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mRNA sequence.
BI757380
VERSION BI757380.1 GI:15748958
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 939)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1500 row: c column: 03
High quality sequence stop: 778.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5199674"
/clone_lib="NIH-MGC_114"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH-MGC Library."
BASE COUNT 168 a 286 c 320 g 165 t
ORIGIN
Query Match 36.2%; Score 679.6; DB 13; Length 939;
Best Local Similarity 96.2%; Pred. No. 1.2e-142;
Matches 718; Conservative 0; Mismatches 24; Indels 4; Gaps 2;

QY 74 GTGGCTGAGCAGGCTGTGCAGGAGCAGCTGACGGGCGCCACACAGCCATGCTGCATCC 133
D 1 GTGGCTGAGCAGGCTGTGCAGGAGCGCCCTGACGGGCGCCACACAGCCATGCTGCATCC 60
QY 134 AGAGACCTCCCTGGCGGGGCGATCTCTGGCTGTGCTCTGCTGCGCCCTCTTGGCACCAC 193
D 61 AGAGACCTCCCTGGCGGGGCGATCTCTGGCTGTGCTCTGCTGCGCCCTCTTGGCACCAC 120
QY 194 CTGGGCGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCGGAGCCCTGAA 253
D 121 CTGGGCGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCGGAGCCCTGAA 180
QY 254 CAGGAAGGAGAGTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 313
D 181 CAGGAAGGAGAGTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 314 CCGTGGGCTGACATGCGAGGCTGAGTGTGAGTGACAGCAGCTGGCCCAACTGGCTCAAGC 373
D 241 CCGTGGGCTGACATGCGAGGCTGAGTGTGAGTGACAGCAGCTGGCCCAACTGGCTCAAGC 300
QY 374 CAGGCGAGCCCTCTGTGGAATCCCAACCCGAGCCCTGGCATCCGGCCCTGTGGCGCACCT 433
D 301 CA-GGACCCCTCTGTGGAACCCCAACCCGAGCCCTGGCGCTCCGGCCCTGTGGCGCACCT 359
QY 434 GCAAGTGGGCTGGACATGACAGCTGCTGCGCGCGGCTTGGCGTCTTTGTTGAAGTGT 493
D 360 GCAAGTGGGCTGGACATGACAGCTGCTGCGCGCGGCTTGGCGTCTTTGTTGAAGTGT 419

RESULTS
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LOCUS 603044615F1 NIH-MGC_116 Homo sapiens cDNA clone IMAGE:5184962 5',
DEFINITION mRNA sequence.
ACCESSION BI760121
VERSION BI760121.1 GI:15751699
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 710)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 704.
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/clone="IMAGE:5184962"
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/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH-MGC Library."
BASE COUNT 131 a 228 c 226 g 125 t
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Location/Qualifiers
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/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH-MGC Library."
BASE COUNT 131 a 228 c 226 g 125 t
ORIGIN
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Query Match 36.0%; Score 676; DB 13; Length 710;
Best Local Similarity 98.4%; Pred. No. 7.2e-142;
Matches 693; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 209 GCCACCCAGCTGCAGGAGCAGCTCCGATGCCGAGCCCTGAACAGGAGAGAGTTT 268
DB 6 GGCACCCAGCTGCAGGAGCAGCTCCGATGCCGAGCCCTGAACAGGAGAGAGTTT 65

QY 269 CTTGTCTCTCTCCCTGCACAAACCGCTGGCGAGCTGGTCCAGCCCTCGCGGTGACAT 328
DB 66 CTTGTCTCTCTCCCTGCACAAACCGCTGGCGAGCTGGTCCAGCCCTCGCGGTGACAT 125

QY 329 GCGGAGGTGGACTGGAGTACAGCCTGGCCCAACTGGCTCAAGCCAGGCGCCCTCTG 388
DB 126 GCGGAGGTGGACTGGAGTACAGCCTGGCCCAACTGGCTCAAGCCAGGCGCCCTCTG 185

QY 389 TGGATCCCAACCCGAGCTGGCATCCGGCTGTGGCGACCTGCAAGTGGCTGGAA 448
DB 186 TGGAAACCCCAACCCGAGCTGGCGTCCGGCTGTGGCGACCTGCAAGTGGCTGGAA 245

QY 449 CATGAGCTGTCTGCCGCGGCTTGGCTCTCTTTGTTGAAGTGGTCAAGCTATGTTTGC 508
DB 246 CATGAGCTGTCTGCCGCGGCTTGGCTCTCTTTGTTGAAGTGGTCAAGCTATGTTTGC 305

QY 509 AGAGGGCAGCGGTACAGCCACGCGGAGGAGTGTGCTCGCAACGCCACCTSCACCCA 568
DB 306 AGAGGGCAGCGGTACAGCCACGCGGAGGAGTGTGCTCGCAACGCCACCTSCACCCA 365

QY 569 CTACAGCAGCTGTGTGGCCACCTCAAGCAGCTGGGTGTGGCGGACCTGTGCTC 628
DB 366 CTACAGCAGCTGTGTGGCCACCTCAAGCAGCTGGGTGTGGCGGACCTGTGCTC 425

QY 629 TGCAGGCCAGACGATAGAAGCCTTTGCTGTGCTTACTCTCCCGAGGCAACTGGGA 688
DB 426 TGCAGGCCAGCAGATAGAAGCCTTTGCTGTGCTTACTCTCCCGAGGCAACTGGGA 485

QY 689 GGTCAACGGGAAGACAATCATCCCTATTAAGAGGCTGCTGTGTTGCTCTGCACAGC 748
DB 486 GGTCAACGGGAAGACAATCATCCCTATTAAGAGGCTGCTGTGTTGCTCTGCACAGC 545

QY 749 CAGTGTCTCAGCTGCTCAAGACCTGGGACCATGACGAGGGGCTCTGTAGGTCCCCAG 808
DB 546 CAGTGTCTCAGCTGCTCAAGACCTGGGACCATGACGAGGGGCTCTGTAGGTCCCCAG 605

QY 809 GAATCTTGTGCATGAGTGCAGAACCATGACGCTCTCAACATCAGACCTGCCACTG 868
DB 606 GAATCTTGTGCATGAGTGCAGAACCATGACGCTCTCAACATCAGACCTGCCACTG 665

QY 869 CCATGTCTCCCTGCTACAC - GGGCAGATACCTGCCAAGTGAGG 911
DB 666 CCATGTCTCCCTGCTACACGGGCGAGATACCTGCCAAGTGAGG 709

RESULT 7
B1759120
LOCUS 603042530F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5182999 5',
DEFINITION B1759120 709 bp mRNA linear EST 25-SEP-2001
mRNA sequence.
ACCESSION B1759120
VERSION B1759120.1 GI:15750698
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 709)
REFERENCE
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11456 row: 1 column: 08
High quality sequence stop: 709.

FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5182999"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

BASE COUNT 124 a 240 c 220 g 125 t
ORIGIN

Query Match 33.9%; Score 636.6; DB 13; Length 709;
Best Local Similarity 98.5%; Pred. No. 5.5e-133;
Matches 653; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1 CTCCTTTTCCACAGCCAGCTGACTCTGGAGATTGTGAATAGCTCCATCCAGCCG 60
DB 48 CTCCTTTTCCACAGCCAGCTGACTCTGGAGATTGTGAATAGCTCCATCCAGCCG 107

QY 61 AGAAACAAGCCGGTGGCTGAGCCAGCTGTGSCAGGAGCACCTGACGGGCCCCAACAGAC 120
DB 108 AGAAACAAGCCGGTGGCTGAGCCAGCTGTGSCAGGAGCCCTGACGGGCCCCAACAGAC 167

QY 121 CCATGCTGATCCAGAGACCTCCCTGGCGGGGGCATCTCTTGGCTGTGCTGGGCC 180
DB 168 CCATGCTGATCCAGAGACCTCCCTGGCGGGGGCATCTCTTGGCTGTGCTGGGCC 227

QY 181 TCCTTGGCACCACCTGGGCGAGGTGGCCACCCACCTGACGAGGAGGCTCCGATGG 240
DB 228 TCCTTGGCACCACCTGGGCGAGGTGGCCACCCACCTGACGAGGAGGCTCCGATGG 287

QY 241 CCGGAGCCCTGAACAGGAGAGAGTTTCTTGTCTCTCTCCCTGCACAAACCCCTGCGCA 300
DB 288 CCGGAGCCCTGAACAGGAGAGAGTTTCTTGTCTCTCTCCCTGCACAAACCCCTGCGCA 347

QY 301 GCTGGTCCAGCCCTGCGGCTGACATGCGGAGGTGGAGTGGAGTGAACGCTGGGCC 360
DB 348 GCTGGTCCAGCCCTGCGGCTGACATGCGGAGGTGGAGTGGAGTGAACGCTGGGCC 407

QY 361 AACTGGCTCAAGCCAGGCGAGCCCTCTGTGAATCCCAACCCCGAGCTGGCATCGGCC 420
DB 408 AGCTGGCTCAAGCCA - GGCAGCCCTCTGTGAACCCCAACCCCGAGCTGGCGTCCGGCC 466

QY 421 TGTGGCGCACCCCTGCAAGTGGGCTGGAACATGCAAGTGTCTGCCCGGGGCTTGGGCTCT 480
DB 467 TGTGGCGCACCCCTGCAAGTGGGCTGGAACATGCAAGTGTCTGCCCGGGGCTTGGGCTCT 526

QY 481 TTGTTGAAGTGTGACGCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACGCGGAGGAG 540
DB 527 TTGTTGAAGTGTGACGCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACGCGGAGGAG 586

QY 541 AGTGTCTCGCAACGCCACCTGCACCCACCTACACGAGCTCTGTGTGGGCCACCTCAAGCC 600
DB 587 AGTGTCTCGCAACGCCACCTGCACCCACCTACATGCAAGTGTGTGGGCCACCTCAAGCC 646


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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B"
/Note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT 153 a 306 c 278 g 178 t 1 others
ORIGIN

Query Match 32.5%; Score 610.2; DB 13; Length 916;
Best Local Similarity 91.6%; Pred. No. 5.1e-127;
Matches 822; Conservative 0; Mismatches 58; Indels 17; Gaps 16;

QY 1 CTCCTTTGTCCACGACCCAGCTGACTCTCTGGAGATTGTAATAGCTCCATCCAGCCTG 60
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QY 61 AGAACAAAGCGGGTGGCTGAGCAGGCTGTGACGAGGACCTGACGGGGCCCAACAGAC 120
Db 81 AGAACAAAGCGGGTGGCTGAGCAGGCTGTGACGAGGACCTGACGGGGCCCAACAGAC 140
QY 121 CCATGCTGCATCAGAGACCTCCCTGCGCGGGGCGCATCTCCTG-GTGTGCTCTCTGGCC 179
Db 141 CCATGCTGCATCAGAGACCTCCCTGCGCGGGGCGCATCTCCTGAGCTGTGCTCTGGCC 200
QY 180 CTCCTTTG-GCACCACCTGGGCGAGGTTGGCCAGC-CCAGCTGCA-GGAGCGCTCCG 236
Db 201 CTCCTTTGCGACCACTGGGCGAGGTTGGCCAGGCTGTGACGAGGCTGTGAGGAGCTCCG 260
QY 237 ATGGCGGGAGCCTGACAGGAGGAGTTTCTGCTCTCCCTGCGACAAACCGCCTG 296
Db 261 ATGGCGGGAGCCTGACAGGAGGAGTTTCTGCTCTCCCTGCGACAAACCGCCTG 320
QY 297 -CGCAGCTGGTCCAGCCCTCGG-CTGACATGCGGAGCTGGAGTGCATGACATGC 353
Db 321 TCGCAGCTGGTCCAGCCCTCGG-CTGACATGCGGAGCTGGAGTGCATGACATGC 380
QY 354 CTGGCCCAACTGGCTCAAGCGAGGAGCCTCTGTGGAATCCCAACCCCGAGCCTGGCA 413
Db 381 CTGGCCCAACTGGCTCAAGCGAGGAGCCTCTGTGGAATCCCAACCCCGAGCCTGGCG 440
QY 414 TCGGGCTGTGGCGACCTGCAAGTGGGCTGGAACA-TGCAGTGTGTCGGCGGGGCTT 472
Db 441 TCGGGCTGTGGCGACCTGCAAGTGGGCTGGAACATTGCAGTGTGTCGGCGGGGCTT 500
QY 473 GCGCTCTTTGTGAAGTGTGAGCTATGTTTGA- -GAGGGGACGGGTACAGCCAC 530
Db 501 GCGCTCTTTGTGAAGTGTGAGCTATGTTTGA- -GAGGGGACGGGTACAGCCAC 560
QY 531 GCGGCGAGGAGA-GTGTGCTGCG- -AACGCCACCTGCAACCCACTACAGCAGCTGTGTGGG 588
Db 561 GCGGCGAGGAGATGTGTGCTCGGAAGCCAGCTGGAGCCCACTACAGCAGCTGTGTGGG 620
QY 589 CCACCTCAAGCAGCTGGGCTGTGGGGGACCC- -TGTGCTCTCGAGGCCAGAGCCATA 647
Db 621 CCA-CTCAAGCCAGCTGGGCTGTGGGGGACCCCTTGTGCTCTCGAGGCCAGAGCCATA 679
QY 648 GAAGCCTTTGCTGTGCTCTACTCCCGGAGGCAACTGGGAGGTCAACGGGGAACACATC 707
Db 680 GAAGCCTTTGCTGTGCTCTACTCCCGGAGGCACTGGGAGGTCAACGGGGAACACATC 739
QY 708 ATCCCCCTATAAGAGGGTGCCTGCTTTCGCTC-TGCACAGCCAGTGTCTCAGGCTGCTT 766
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Db 740 ATCCCCCTATAAGAGGGTGCCTGCTTCTTGACAGCCAGTGTCTCAGGCTGCTT 799
QY 767 CAAGGCTGGGACCATGCAGGGGGCTCTGTGAGGTCCCGAGGAATCCTTGTCCCATGAG 826
Db 800 C-AAGGCTGTGGACCTGCGGGGGCTCTGTGAGGTCCCGAGGAATCCTTGTCCGCATGA 858
QY 827 CTGCCAGAACCA-TGGACGTCTCAACATCAGCAGCCTGCCACTGCCACTGTCCCGCTG 882
Db 859 CTGCCAGAACCATGTCAGCTCTCCGCATCGCTCTGCCATTGCCATGGTGGTCCCGCTG 915

RESULT 10
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LOCUS 603048444F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188643 5',
DEFINITION mRNA sequence.
ACCESSION BI762690
VERSION BI762690.1 GI:15754256
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 852)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999),
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Inceyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11471 row: g column: 12
High quality sequence stop: 849.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5188643"
/lab_lib="NIH_MGC_116"
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/Note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT 146 a 283 c 269 g 154 t
ORIGIN

Query Match 31.4%; Score 589; DB 13; Length 852;
Best Local Similarity 96.0%; Pred. No. 3e-122;
Matches 679; Conservative 0; Mismatches 20; Indels 8; Gaps 7;

QY 1 CTCCTTTGTCCACGACCCAGCCTGACTCTCTGGAGATTGTGAATAGCTCCATCCAGCCTG 60
Db 136 CTCCTTTGTCCACGACCCAGCCTGACTCTCTGGAGATTGTGAATAGCTCCATCCAGCCTG 195
QY 61 AGAACAAAGCGGGTGGCTGAGCAGGCTGTGACGAGGACCTGACGGGGCCCAACAGAC 120
Db 196 AGAACAAAGCGGGTGGCTGAGCAGGCTGTGACGAGGAGTGTGACGGGGCCCAACAGAC 255
QY 121 CCATGCTGCATCCAGAGACCTCCCTGCGCGGGGCGCATCTCCTGCTGTGCTCTCTGGCCC 180
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Db 256 CCATGTGTCATCAGAGACCTCCCTCGCGGGGCACTCTCTGGCTGTGCTCTCTGCGCC 315
QY 181 TCCTTGGCACCACCTGGGCGAGAGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGG 240
Db 316 TCCTTGGCACCAGCTGGGCGAGAGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGG 375
QY 241 CCGGAGCCCTGACAGGAAGAGAGTTCTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
Db 376 CCGGAGCCCTGACAGGAAGAGAGTTCTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 435
QY 301 GCTGGGTCACAGCCCTCGGCTGACATGCGGAGGCTGGAGTGAGTGACAGCCCTGGCC 360
Db 436 GCTGGGTCACAGCCCTCGGCTGACAGGCGGAGGCTGGAGTGAGTGACAGCCCTGG-CC 494
QY 361 AACTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCC 420
Db 495 AACTGGCTCAAGCCA-GGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCGTCCGGCC 553
QY 421 TGTGGCGCACCCTCAAGTGGGCTGGACATGCAGCTG-CTGCGCGGGGCTTGGCGTCC 479
Db 554 TGTGGCGCACCCTCAAGTGGGCTGGAAATGCAAGTGCAGCTGCTGCGCGGGGCTTGGCGTCC 613
QY 480 TTTCTTGAAGT-GGTCAGCCCTATGTTTGCAGAGGGGCGAGCGGTACAGCCACGGCGG-CAG 537
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QY 655 TTGCTGTGCTACTTCCCGGAGCAACTGGGAGGTCAACGGGAAG 701
Db 794 TTGCTGTGCTACTTCCCGGAGGCACTGGGAGGTCAACGGGAAG 840

RESULT 11
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mRNA sequence.
ACCESSION AI307814
VERSION AI307814.1 GI:4002418
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 617)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 725 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 451.
Location/Qualifiers
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/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid5 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(CloneIDs 1323912-1325831, 1471368-1472903 and
1492104-1493255). Subtraction by Bento Soares and M.
Fatima Bonaldo."
BASE COUNT 118 a 182 c 179 g 138 t
ORIGIN
Query Match 30.9%; Score 580; DB 9; Length 617;
Best Local Similarity 95.8%; Pred. No. 3e-120;
Matches 617; Conservative 0; Mismatches 0; Indels 27; Gaps 1;
QY 1227 TTCGTGATCGGCTCACCTACAAGACCCCAAGGACTCTTCCGCTGGGCCACACGGGAG 1286
Db 617 TTCGTGATCGGCTCACCTACAAGACCCCAAGGACTCTTCCGCTGGGCCACACGGGAG 558
QY 1287 CACGAGGCTTCCACAGTTTGGCCCTTGGGCAAGCTGCAACACCGGCTGTGGCTG 1346
Db 557 CACGAGGCTTCCACAGTTTGGCCCTTGGGCAAGCTGCAACACCGGCTGTGGCTG 513
QY 1347 AGTGTGCTATGGGCTTGGCAACTGCGTGGAGCTGACAGCTTTCAGCTGCTTCAACTGG 1406
Db 512 -----GGCTTTGGCAACTGCGTGGAGCTGACAGCTTTCAGCTGCTTCAACTGG 465
QY 1407 AACGAGGCTGCAAAACCCGAAACCTTACACTGCTTGGCCAGGAGCACATC 1466
Db 464 AACGAGGCTGCAAAACCCGAAACCTTACACTGCTTGGCCAGGAGCACATC 405
QY 1467 TCCCGGTGGGCGCCAGGGTCTGAGGCTTGACCATGCTCCCTGCTGCTGCTGGGAG 1526
Db 404 TCCCGGTGGGCGCCAGGGTCTGAGGCTTGACCATGCTCCCTGCTGCTGCTGGGAG 345
QY 1527 CACCGGCTGCTGTACCTGCTGCGCCACTGTCTGGAACAGGGCCAGGTTAAGACCAC 1586
Db 344 CACCGGCTGCTGTACCTGCTGCGCCACTGTCTGGAACAGGGCCAGGTTAAGACCAC 285
QY 1587 TGCCTCATGTCACAAAGAGGCTCTCAGACCTTGACCAATGCCAAGTTGGCGAGAGAGG 1646
Db 284 TGCCTCATGTCACAAAGAGGCTCTCAGACCTTGACCAATGCCAAGTTGGCGAGAGAGG 225
QY 1647 CAGGAGGCTAGTGGGCGCAGGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 1706
Db 224 CAGGAGGCTAGTGGGCGCAGGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 165
QY 1707 TTTTGTATGGGAAGATGGCTTCAATTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 1766
Db 164 TTTTGTATGGGAAGATGGCTTCAATTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 105
QY 1767 AAAAGGCTGCTCTCTTCCACCTGGCCCGAGACCTGCTGGGCGCAGGAGGCTTCCCTGTGG 1826
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DEFINITION DKFZp434F2413 5', mRNA sequence.
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ACCESSION AL040183 GI:5409148
VERSION AL040183.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Koehler, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Koehler K
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
SI sequence also available.
This clone (DKFZp34F2413) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
BASE COUNT 150 a 207 c 207 g 139 t 1 others
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Source
Location/Qualifiers
1..704
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/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
Query Match 30.9%; Score 579.8; DB 9; Length 704;
Best Local Similarity 97.1%; Pred. No. 3.4e-120;
Matches 604; Conservative 0; Mismatches 13; Indels 7; Gaps 7;
QY 657 GTCTGTGCTTACTCCCGGAGGCACTGGGAGGTCAACGGGAAGACAATCATCCCTAT 716
DB 1 GTCTGTGCTTACTCCCGGAGGCACTGGGAGGTCAACGGGAAGACAATCGTCCCTAT 60
QY 717 AACAAAGGTCCTGGTGTGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAGCCCTGG 776
DB 61 AAGAAAGGTGCCCTGGTGTGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAGCCCTGG 120
QY 777 GACCATGCAGGGGGGCTCTGTGAGGTCCCGAGGAATCTTGTGCGATGAGTGCAGAAC 836
DB 121 GACCATGCAGGGGGGCTCTGTGAGGTCCCGAGGAATCTTGTGCGATGAGTGCAGAAC 180
QY 837 CATGGACGTCTCAACATCAGCACTGCCACTGTCACCTGTCCTCCCTGGCTACACGGGCGA 896
DB 181 CAGGACGTCTCAACATCAGCACTGCCACTGTCACCTGTCCTCCCTGGCTACACGGGCGA 240
QY 897 TACTGCCAAGTAGGTCAGCTGTCAGTGTGTCACGGCCGGTTCGGGAGGAGGATGC 956
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QY 957 TCGTGGCTGTGACATCGGCTACGGGGAGCCAGTGTGCCACCAAGTGCAATTTCCC 1016
DB 301 TCGTGGCTGTGACATCGGCTAC -GGGAGGCCAGTGTGCCACCAAGTGCAATTTCCC 359
QY 1017 TTCCACACCTGTGACCTGAGGATCGACGAGACTGCTTCATGTTGTCTTC -AGAGGCGA 1075
DB 360 TTCCACACCTGTGACCTGAGGATCGACGAGACTGCTTCATGTTGTCTTC -CAAGAGGCGA 419
QY 1076 CACCTATTACAGCCAGGATGAATGTTCAGAGAAAGCGGGTGTCTGCCCCAGATCAA 1135
DB 420 CACCTATTACAGGCA -GATGAATGTTCAGAGAAA -CGGGGGTGTCTGCCCCAGATCAA 477

QY 1136 GAGCCAGAAAGTGC -AGGACATCTCGCTTCTATCTATCTGGGCGGCTTGAGACCACCAACG 1194
DB 478 GAGCCAGAAAGTGC -AANGACATCTCGCTTCTATCTATCTGGGCGGCTTGAGACCACCAACG 537
QY 1195 AGGTGACTGACAGTACTTCGAGACGAGGAATCTTCTGGATCGGCTCACTTACAGACCG 1254
DB 538 AGGTGATTGACAGTACTTCGAGACCA -GAATCTTGGATCGGCTCACTTACAGACCG 596
QY 1255 CAAAGGACTCTTCCGCTGGGCCACAGGGGAGCAGGAGCCTTCAACAGTTTGGCTTTG 1314
DB 597 CC -AGGACTCTTCCGCTGGGCCACAGGGGAGCAGGAGCCTTCAACAGTTTGGCTTTG 655
QY 1315 GGCAGCTGACAAACCGGGCTGG 1338
DB 656 GGCAGCTGACAAACCGGGTTTG 679

RESULT 13
BF057185/c
LOCUS
DEFINITION
7k17b07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:344444 3'
similar to SW:MANR_HUMAN P22897 MACROPHAGE MANNOSSE RECEPTOR
PRECURSOR. ; mRNA sequence.
ACCESSION BF057185
VERSION BF057185
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS NCI - CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 446.
Location/Qualifiers
1..612
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:344444"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI_CGAP_GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonids
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 117 a 181 c 179 g 135 t
ORIGIN
Query Match 30.3%; Score 568.6; DB 12; Length 612;
Best Local Similarity 95.1%; Pred. No. 1.1e-117;
Matches 608; Conservative 0; Mismatches 4; Indels 27; Gaps 1;
QY 1227 TTCTGGATCGGGCTCACCTACAAGACCGCAAGGACTCTTCGGCTGGGCCACAGGGGAG 1286

Db 47 CCACGGGTATTAAATTATGATCAGCTGAAAAA 6

RESULT 15
AW299257/c
LOCUS
DEFINITION
x548f01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2772889 3',
similar to SW:MANR_HUMAN P22897 MACROPHAGE MANNOSE RECEPTOR
PRECURSOR. ; mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 458.

FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2772889"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloned IDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."

BASE COUNT 117 a 181 c 179 g 132 t 2 others
ORIGIN

Query Match 30.1%; Score 564; DB 10; Length 611;
Best Local Similarity 94.7%; Pred. No. 1.2e-116;
Matches 604; Conservative 0; Mismatches 7; Indels 27; Gaps 1;

QY 1227 TTCTGGATCGGCTCACCCTACAGACCGCCCAAGGACTCCTCCGCTGGGCCACAGGGGAG 1286
Db 611 TTTCTGGATCGGGCTCACNTACAGACCGCCCAAGGACTCCTCGGCTGGGCCACAGGGGAG 552

QY 1287 CACCAGGCTTCACACAGTTTTCCTTTGGCGAGCTGACAAACACAGGGCTGGTGGCTG 1346
Db 551 CACCAGGCTTCACACAGTTTTCCTTTGGCGAGCTGACAAACACAGGGCTGGTGGCTG 507

QY 1347 AGTGTGCATGGGTTTGGCACTGCTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGG 1406
Db 506 -----GGGTTTGGCACTGCTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGG 459

QY 1407 AACGACGAGCGCTGCAAAACCGGAACCGTTACATCTGCCAGTTTGGCCGAGGACATC 1466
Db 458 AACGACGAGCGCTGCAAAACCGGAACCGTTACATCTGCCAGTTTGGCCGAGGACATC 399

QY 1467 TCCCGGTGGGGCCAGGGTCTCTGAGGCCTGACCATGAGTCCCTCGCCTCCCTGGGAG 1526
Db 398 TCCCGGTGGGGCCAGGGTCTCTGAGGCCTGACCATGAGTCCCTCGCCTCCCTGGGAG 339

QY 1527 CACCGGCTCTGCTTACTGCTGCCACCTGCTCTGGAAACAAGGCCAGGTTAAACACCA 1586
Db 338 CACCGGCTCTGCTTACTGCTGCCACCTGCTCTGGAAACAAGGCCAGGTTAAACACCA 279

QY 1587 TGCTCATGTCCAAAGAGGTTCTCAGACCTTGCACAATGCCAAGAGTTGGGCAGAGAGG 1646
Db 278 TGCTCATGTCCAAAGAGGTTCTCAGACCTTGCACAATGCCAAGAGTTGGGCAGAGAGG 219

QY 1647 CAGGAGGCGCAGTGCAGGGCCAGGAGTGAAGTGTAGNAGAAGCTGGGGCCCTTCGCCTGC 1706
Db 218 CAGGAGGCGCAGTGCAGGGCCAGGAGTGAAGTGTAGNAGAAGCTGGGGCCCTTCGCCTGC 159

QY 1707 TTTGATTGGGAAGATGGGCTTCAATTAGATGGCGAAGAGAGACACCGCCAGTGGTCC 1766
Db 158 TTTGATTGGGAAGATGGGCTTCAATTAGATGGCGAAGAGAGAGACACCGCCAGTGGTCC 99

QY 1767 AAAAAGGCTGCTCTCTTCCACCTGGCCCGAGACCTGTGGGGCAGCGGAGCTTCCTCTGG 1826
Db 98 AAAAAGGCTGCTCTCTTCCACCTGGCCCGAGACCTGTGGGGCAGCGGAGCTTCCTCTGG 39

QY 1827 CATGAACCCACGGGCTATTAAATTAATGATCAGCTGA 1864
Db 38 CACCAACCCACGGGCTATTAAATTAATGATCAGCTGA 1

Search completed: December 28, 2002, 20:45:31
Job time : 2518.87 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 16:48:37 ; Search time 75.0618 Seconds
(without alignments)
7664.697 Million cell updates/sec

Title: US-09-944-896-49
Perfect score: 1876
Sequence: 1 ctcctttgtccaccagccca.....tcagctgaaaaaaaaaaaaa 1876

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 382724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	672.8	35.9	690	4	US-09-404-879A-321
2	47.8	2.5	582	4	US-09-433-248A-3
3	43.4	2.3	1155	2	US-08-387-942C-18
4	43.4	2.3	12588	2	US-08-387-942C-1
5	42.6	2.3	3259	5	PCT-US95-03747-1
6	40.8	2.2	4724	1	US-08-404-665-3
7	40.8	2.2	4724	1	US-08-404-671-3
8	40.8	2.2	4724	1	US-08-404-781-3
9	39.4	2.1	1176	2	US-08-387-942C-17
10	39.2	2.1	4403765	4	US-09-103-840A-2
11	39	2.1	7218	1	US-08-232-463-14
12	38.6	2.1	1155	2	US-08-387-942C-21
13	37.4	2.0	2335	4	US-09-387-574-9
14	37.4	2.0	2335	4	US-09-668-096-9
15	37.2	2.0	1070	4	US-09-470-443-7
16	37.2	2.0	3726	1	US-08-173-497-1
17	37.2	2.0	3726	1	US-08-286-889-1
18	37.2	2.0	3726	1	US-08-485-618-1
19	37.2	2.0	3726	1	US-08-362-652-1
20	37.2	2.0	3726	1	US-08-605-672-1
21	37.2	2.0	3726	2	US-08-482-293A-1
22	37.2	2.0	3726	2	US-08-943-363-1
23	37.2	2.0	3726	4	US-09-193-043-1
24	37.2	2.0	3726	4	US-09-688-307A-1
25	37.2	2.0	3785	1	US-08-485-618-98
26	37.2	2.0	3785	1	US-08-605-672-98
27	37.2	2.0	3785	2	US-08-482-293A-98

28	37.2	2.0	3785	2	US-08-943-363-98	Sequence 98, Appl	
29	37.2	2.0	3785	4	US-09-193-043-98	Sequence 98, Appl	
30	37.2	2.0	3785	4	US-09-688-307A-98	Sequence 98, Appl	
31	37.2	2.0	3956	1	US-08-485-618-97	Sequence 97, Appl	
32	37.2	2.0	3956	1	US-08-605-672-97	Sequence 97, Appl	
33	37.2	2.0	3956	2	US-08-482-293A-97	Sequence 97, Appl	
34	37.2	2.0	3956	2	US-08-943-363-97	Sequence 97, Appl	
35	37.2	2.0	3956	4	US-09-193-043-97	Sequence 97, Appl	
36	37.2	2.0	3956	4	US-09-688-307A-97	Sequence 97, Appl	
37	37	2.0	749	4	US-09-257-583-12	Sequence 12, Appl	
c	38	37	2.0	2348	4	US-08-990-823-61	Sequence 61, Appl
39	36.4	1.9	1227	3	US-09-074-912-3	Sequence 3, Appl	
40	36.4	1.9	1227	4	US-09-290-136-3	Sequence 3, Appl	
41	36.2	1.9	970	2	US-08-773-368-2	Sequence 2, Appl	
42	36.2	1.9	970	3	US-09-199-887-2	Sequence 2, Appl	
c	43	36.2	1.9	1436	4	US-09-471-396-2	Sequence 2, Appl
44	36.2	1.9	13842	4	US-09-105-537-30	Sequence 30, Appl	
45	36.2	1.9	36778	4	US-09-105-537-5	Sequence 5, Appl	

ALIGNMENTS

RESULT 1
US-09-404-879A-321
; Sequence 321, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404, 879A
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 321
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(690)
; OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-321

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Best Local Similarity	99.3%	Pred. No.	4.2e-162;				
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						Gaps	1;
QY	604	TGGGCTGTGGGGGCGACCTGTGCTCTGCGAGGAGTCAACGGGAGACCAATCATCCCTTATAGAAGG	663				
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QY	664	CTTACTCTCCCGGAGGCACTGGGAGGTCAACGGGAGACCAATCATCCCTTATAGAAGG	723				
DB	61	CTTACTCTCCCGGAGGCACTGGGAGGTCAACGGGAGACCAATCATCCCTTATAGAAGG	120				
QY	724	GTCCCTGTGTTCGCTCTGCGAGGAGTCAACGGGAGACCAATCATCCCTTATAGAAGG	783				
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QY	784	CAGGGGGGCTGTGAGGTCCTGCGAGGAGTCAACGGGAGACCAATCATCCCTTATAGAAGG	843				
DB	181	CAGGGGGGCTGTGAGGTCCTGCGAGGAGTCAACGGGAGACCAATCATCCCTTATAGAAGG	240				
QY	844	GTCTCAACATCAGCACCTGCCACTGTCCCTTATAGAAGGAGTCAACGGGAGACCAATCATCCCTTATAGAAGG	903				
DB	241	GTCTCAACATCAGCACCTGCCACTGTCCCTTATAGAAGGAGTCAACGGGAGACCAATCATCCCTTATAGAAGG	300				
QY	904	AAGTGAGGTGCAGCCTGCAGTGTGTGACACGGCCGGTTCGGGAGGAGGAGTCTCGTGGG	963				

Db 301 AAGTGGAGTGCAGCCTGCAGTGTGTGCACGCCGCGTTCGGGAGGAGAGTGCCTCGTGG 360
QY 964 TCTGTGACATCGGCTACGGGGGAGCCAGTGTGCCACCAAGGTGCATTTCCTTCCACCA 1023
Db 361 TCTGTGACATCGGCTACGGGGGAGCCAGTGTGCCACCAAGGTGCATTTCCTTCCACCA 420
QY 1024 CCGTGTGACCTGAGGATCGAGCGGAGACTGCTTCATGTGTCTTTCAGAGCGACACCTATT 1083
Db 421 CCGTGTGACCTGAGGATCGAGCGGAGACTGCTTCATGTGTCTTTCAGAGCGACACCTATT 480
QY 1084 ACAG-AGCCAGGATGAATGTACAGAGGAAGGGGGTGTGGCCCGACAGTCAAGAGCCAG 1142
Db 481 ACAGAGCCAGGATGAATGTACAGAGGAATGGCGGGTGTGGCCCGACAGTCAAGAGCCAG 540
QY 1143 AAAGTCAGGACATCTCGGCTTCTATCTGGCGCGCTGGAGACACCAAGAGGTGACT 1202
Db 541 AAAGTCAGGACATCTCGGCTTCTATCTGGCGCGCTGGAGACACCAAGAGGTGACT 600
QY 1203 GACAGTACTTCGAGACCGAGGAACCTTCTGGATCGGGCTACCTACAAGACCGCCAAAGGAC 1262
Db 601 GACAGTACTTCGAGACCGAGGAACCTTCTGGATNGGGCTACCTACAAGACCGCCAAAGGAC 660
QY 1263 TCCTTCGCTGGGCCACAGGGGAGCACCAG 1292
Db 661 TCCTTCGCTGGGCCACAGGGGAGCACCAG 690

RESULT 2
US-09-433-248A-3
; Sequence 3, Application US/09433248A
; Patent No. 6355462
; GENERAL INFORMATION:
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Han, Feng
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Disease Resistance Factors
; FILE REFERENCE: BB1252 US NA
; CURRENT APPLICATION NUMBER: US/09/433,248A
; CURRENT FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,242
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (337)
; NAME/KEY: unsure
; LOCATION: (370)
; NAME/KEY: unsure
; LOCATION: (421)
; NAME/KEY: unsure
; LOCATION: (437)
; NAME/KEY: unsure
; LOCATION: (481)
; NAME/KEY: unsure
; LOCATION: (484)
; NAME/KEY: unsure
; LOCATION: (502)
; NAME/KEY: unsure
; LOCATION: (511)
; NAME/KEY: unsure
; LOCATION: (542)
; NAME/KEY: unsure
; LOCATION: (547)
; NAME/KEY: unsure
; LOCATION: (564)
; NAME/KEY: unsure

; LOCATION: (571)
US-09-433-248A-3
Query Match 2.5%; Score 47.8; DB 4; Length 582;
Best Local Similarity 50.2%; Pred. No. 0.0047;
Matches 118; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
QY 1210 ACTTCGAGACAGGAACTTCTGGATCGGGCTCACCTACAGACCGCCAAAGGACTCTCTCC 1269
Db 1 ACATCTGAAACGGACCATCGCATGGACACCTCCAAAGGCCACCTCCGACTACGCTCC 60
QY 1270 GCTGGCCACAGGGAGCACCAGGCTTCACCAAGTTTTGCTTTGGGACGCTGACAACC 1329
Db 61 GGCAAGCCATCGCGAGGACACGTGGAGCGCCATCTTCGGGTGGTGGCGCGGCCCAACG 120
QY 1330 AGGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1389
Db 121 CGGGCTGATGATCTGTCGGACCGCTAGCGGCGGACATCGGCAGCTGGCGAGCGGCGCG 180
QY 1390 CAGCTGCGCTTCAACTGGAACGACGAGCGCTGCAAAACCGGAAACCGTTACATCTG 1444
Db 181 CGCGCTTCCGACCGCGCGGCTGCTCTACAACATCCAGTACATGAACTTCTG 235

RESULT 3
US-08-387-942C-18
; Sequence 18, Application US/08387942C
; Patent No. 5939289
; GENERAL INFORMATION:
; APPLICANT: ERTESVAG, HELGA
; APPLICANT: VALLA, SVEIN
; APPLICANT: SKJAK-BRAEK, GUDMUND
; APPLICANT: LARSEN, BJORN
; TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
; TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: P.O. BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,942C
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1809-106P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-387-942C-18

Query Match 2.3%; Score 43.4; DB 2; Length 1155;
Best Local Similarity 49.8%; Pred. No. 0.081;
Matches 110; Conservative 0; Mismatches 111; Indels 0; Gaps 0;
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Db 297 CTTGGCATGAGCGACCTGACCTCGAGCGCAACCGCGACACCTGTCCGCCAAGGTGCA 356
QY 1076 CACCTATTACAGCAGCAGGATGAATGTACAGAGAAAGCGGGTCTGCGCCAGATCAA 1135
Db 357 CGGCTGGTTCAACGGCTACATCCCGCGCAGGACGCGCGCATCGGACGTGACCCCTGGA 416
QY 1136 GAGCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGCGCGCCTGGAGACCAACCA 1195
Db 417 CGGGTGAATCCGAGATGTCGCGTACCGTTTCGACCCCCAGGACGACGACCATCAA 476
QY 1196 GGTGACTGACAGTACTTCGAGACCAAGAACTTCTGGATCG 1236
Db 477 CTTGACGATCGGACAGCGTGGCCCGCAGCAACAGCCTCG 517

RESULT 4

US-08-387-942C-1
; Sequence 1, Application US/08387942C
; Patent No. 5939289

GENERAL INFORMATION:
APPLICANT: ERTESVAG, HELGA

APPLICANT: VALLA, SVEIN
APPLICANT: SKJAK-BRAEK, GUDMUND

APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES

TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP

STREET: P.O. BOX 747
CITY: FALLS CHURCH

STATE: VA
COUNTRY: USA

ZIP: 22042
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,942C

FILING DATE: 09-MAY-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.

REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1809-106P

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000

TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 12588 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

ORGANISM: Azotobacter vinelandii
STRAIN: E

FEATURE:
NAME/KEY: CDS

LOCATION: 290..1951
FEATURE:

NAME/KEY: CDS
LOCATION: 2227..6438

NAME/KEY: CDS
LOCATION: 6702..9695

NAME/KEY: CDS
LOCATION: 9973..12588

US-08-387-942C-1

Query Match 2.3%; Score 43.4; DB 2; Length 12588;
Best Local Similarity 49.8%; Pred. No. 0.2; Mismatches 0; Gaps 0;

Matches 110; Conservative 0; Indels 11; Gaps 0;

QY 1016 CTTCCACACCTGTGACCTGAGGATCGACGAGACTGCTTCTATGTTCTTTCAGAGCAGA 1075
Db 2523 CTTCCGATGAGCGACCTGACCTCGACGCGCAACCGCAGACACTGTCCGCCAAGGTGCA 2582

QY 1076 CACCTATTACAGCAGGATGAATGTACAGAGAAAGCGGGTCTGCGCCAGATCAA 1135
Db 2583 CGGCTGGTTCAACGGCTACATCCCGCGCAGGACGCGCGCATCGACGCTGACCCCTGGA 2642

QY 1136 GAGCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGCGCGCCTGGAGACCAACCA 1195
Db 2643 CGGGTGAATCCGAGATGTCGCGGTACGGTTTCGACCCCCAGGACGACCATCAA 2702

QY 1196 GGTGACTGACAGTACTTCGAGACCAAGAACTTCTGGATCG 1236
Db 2703 CTTGACGATCGGACAGCGTGGCCCGCAGCAACAGCCTCG 2743

RESULT 5

PCT-US95-03747-1

; Sequence 1, Application PC/TUS9503747

GENERAL INFORMATION:

APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
TITLE OF INVENTION: Brevecan, A Gliol Cell Proteoglycan

NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego
STATE: California

COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/03747
FILING DATE: 27-MAR-1995

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Imbra, Richard J.
REGISTRATION NUMBER: 37,643

REFERENCE/DOCKET NUMBER: PP-LJ 1453
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 3259 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS

LOCATION: 112..2848
PCT-US95-03747-1

Query Match 2.3%; Score 42.6; DB 5; Length 3259;
Best Local Similarity 53.0%; Pred. No. 0.19;

Matches 115; Conservative 0; Mismatches 99; Indels 3; Gaps 1;

QY 944 GGAGGAGAGTCTGCTGCTGCTGTGACATCGGCTACGGGGGAGCCAGTGTGCCACCAA 1003
Db 2106 GGAGGAGGGGTGCTGCTGCTGTGTTGCTGCTATGGGGGACCTGTGCGATTTGG 2165

QY 1004 GGTGCAATTTCCCTTCCACACCTGTGACCTGAGGATCGAGGAGACTGCTTCATGTTGTC 1063

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Db 2166 CTCCACTTCTGACGCCCGGTTGGGAC---GCCTCCAGGGTGCTGTCAAGCACTT 2222
Qy 1064 TTCAGAGGCACACCTATTACAGAGCCAGGATGAAATGTGAGAGGAAGCGGGGTGCT 1123
Db 2223 TTCTGCCGAGGAGCTGGGAGGAGCGGAGACAAAGTCGGGATGTACGGCGGCACT 2282
Qy 1124 GCGCCAGATCAGAGCCAGCAAAAGTGAGGACATGCTC 1160
Db 2283 GCGCAGCATCAGCACGCGGAGGAGGAACAGGACTTCATC 2319

RESULT 6
US-08-404-665-3
; Sequence 3, Application US/08404665
; Patent No. 5591583
; GENERAL INFORMATION:
; APPLICANT: Reid, Robert A.
; APPLICANT: Ackley, Rhonda L.
; APPLICANT: Hemperly, John J.
; TITLE OF INVENTION: HUMAN RESTRICTIN AND NUCLEIC ACID
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,665
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3341
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4724 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-404-665-3

Query Match 2.2%; Score 40.8; DB 1; Length 4724;
Best Local Similarity 52.3%; Pred. No. 0.63;
Matches 90; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy 827 CTGCCAACAACCATGGACGTCTCAACATCAGCACCTGCCACTGTCCTCCCTGGCTA 886
Db 987 CTGCAGTGGCCACGCAACTTTAGCTTTGAGTCTGTGGCTGCATCTGCAACGAGGCTG 1046
Qy 887 CACGGGCAGATCTGCGGAGCCCTACTGCCGAGCCCTACTGCCGCTGGTGTCTCCAGCGGGGGTGTG 946
Db 1047 GTTTGGCAAGATTTGCTCGGAGCCCTACTGCCGCTGGTGTCTCCAGCGGGGGTGTG 1106
Qy 947 GGAGGAGTGTCTGTGCTGTGACATCGGTACGGGGGAGCCCACTGTGCC 998
Db 1107 TGTGGATGCCAGTGCATCTGTGACAGCGAGTACAGCGGGGATGACTGTTC 1158

RESULT 7
US-08-404-671-3
; Sequence 3, Application US/08404671
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; Patent No. 5635360
; GENERAL INFORMATION:
; APPLICANT: Reid, Robert A.
; APPLICANT: Ackley, Rhonda L.
; APPLICANT: Hemperly, John J.
; TITLE OF INVENTION: HUMAN RESTRICTIN AND NUCLEIC ACID
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,671
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3341
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4724 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-404-671-3

Query Match 2.2%; Score 40.8; DB 1; Length 4724;
Best Local Similarity 52.3%; Pred. No. 0.63;
Matches 90; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy 827 CTGCCAACAACCATGGACGTCTCAACATCAGCACCTGCCACTGTCCTCCCTGGCTA 886
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Qy 887 CACGGGCAGATCTGCGGAGCCCTACTGCCGAGCCCTACTGCCGCTGGTGTCTCCAGCGGGGGTGTG 946
Db 1047 GTTTGGCAAGATTTGCTCGGAGCCCTACTGCCGCTGGTGTCTCCAGCGGGGGTGTG 1106
Qy 947 GGAGGAGTGTCTGTGCTGTGACATCGGTACGGGGGAGCCCACTGTGCC 998
Db 1107 TGTGGATGCCAGTGCATCTGTGACAGCGAGTACAGCGGGGATGACTGTTC 1158

RESULT 8
US-08-404-781-3
; Sequence 3, Application US/08404781
; Patent No. 5681931
; GENERAL INFORMATION:
; APPLICANT: Reid, Robert A.
; APPLICANT: Ackley, Rhonda L.
; APPLICANT: Hemperly, John J.
; TITLE OF INVENTION: HUMAN RESTRICTIN AND NUCLEIC ACID
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
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; ZIP: 07417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,781
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3341
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4724 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-404-781-3

Query Match 2.2%; Score 40.8; DB 1; Length 4724;
Best Local Similarity 52.3%; Pred. No. 0.63;
Matches 90; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 827 CTGCAGAACCATGGACGTCTCAACATCAGACCTGCCACTGCCACTGTCCCTGGGTA 886
Db 987 CTGCAGTGGCCAGCAACTTTAGCTTTGAGTCTGTGCTGCATCTGCAACGAAGGCTG 1046
QY 887 CACGGGAGATACATGCCAAGTGAGGTGAGCTGCAGTGTGTGCACGGCGGTTCCGGGA 946
Db 1047 GTTTGGCAAGAATTTGCTGGAGCCCTACTGCCCGCTGGTCTGCACGGCGGGGTGTG 1106
QY 947 GGAGGAGTCTGCTGGCTGTGACATCGGCTACGGGGGAGCCAGTGTGCC 998
Db 1107 TGTGATGCCAGTGTGATCTGTGACGAGTACAGCGGGGATGACTGTTC-1158

RESULT 9
US-08-387-942C-17
; Sequence 17, Application US/08387942C
; Patent No. 5939289
; GENERAL INFORMATION:
; APPLICANT: ERTESVAG, HELGA
; APPLICANT: VALLA, SVEIN
; APPLICANT: SKJAK-BRAEK, GUDMUND
; APPLICANT: LARSEN, BJORN
; TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
; TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: P.O. BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,942C
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1809-106P
; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1176 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-387-942C-17

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Best Local Similarity 52.1%; Pred. No. 0.85;
Matches 88; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 1133 CAAGAGCCAGAAAGTGCAGGACATCTCGCTTCTATCTGGCGCGCTGGAGACCACCAA 1192
Db 873 CGACAAACGCGCAGCGCGCGCTGCCGAGTCTCTGTCAGTCTCTTCGACGATACCGC 932
QY 1193 CGAGGTGACTGACAGTGCAGTTCGAGACGAGGAAGTCTTGGATCGGCTCACCTACAAGAC 1252
Db 933 CGGGGCGTCCGGCACCTACTACAGCACCTGTAACACCCGGATCGAGGCAACACCATCAG 992
QY 1253 CGCCAAGGACTCTTCGCTGGGCCACAGGGGAGCACACGACCCCTTCACC 1301
Db 993 CGGCTCGGCCAACTCCACCTACGCGATCCAGGAGCGCAACGACGCGACC 1041

RESULT 10
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
; US-09-103-840A-2

Query Match 2.1%; Score 39.2; DB 4; Length 4403765;
Best Local Similarity 53.2%; Pred. No. 18;
Matches 83; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

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Db 3994090 CCCGTCACGCGCGCGCGCGCTCGCGCCAGAGAGAGCGCGCGCGCAACAGCACCG 3994031
QY 461 GCCCGCGGCTTGGCGTCTTTGTGAAGTGTGACGCTATGTTGTGCAGAGGGGCGAGCG 520
Db 3994030 GCGCGCGGCTCGGTCCAAGATGTCGGTGGCTTCTGTGGCGGTGTAGCGGGTGTCAAG 3993971
QY 521 GTACAGCCACGCGGCGAGGAGTGTGCTCGCAACGC 556
Db 3993970 GCACACCGCGCGCGCGCTGGTGGATCGCCAGGC 3993935

RESULT 11
US-08-232-463-14/c
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 15:40:17 ; Search time 262.586 Seconds
(without alignments)
11372.097 Million cell updates/sec

Title: US-09-944-896-49_COPY_123_1448

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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1326	100.0	1876	20	AAK87260
2	1326	100.0	1876	20	AAK80053
3	1326	100.0	1876	21	AAA46918
4	1326	100.0	1876	21	AAA49561
5	1254	94.6	1338	20	AAZ23300
6	1254	94.6	1775	22	AAD12570
7	1254	94.6	1856	20	AAZ23299
8	1254	94.6	1856	24	AAD33531
9	1254	94.6	1923	22	AAF24152

10	1246	94.0	1786	22	AAK94246	Human full-length
11	1205.6	90.9	1934	23	AAK91790	DNA encoding novel
12	889.4	67.1	1519	23	AAK76344	DNA encoding novel
13	672.8	50.7	690	21	AAK70010	Human ovarian carc
14	672.8	50.7	690	24	ABN72904	Ovarian carcinoma
15	657.2	49.6	906	23	AAK76343	DNA encoding novel
16	518	39.1	602	23	AAK81209	DNA encoding novel
17	496.6	37.5	855	21	AAZ50926	Human protease and
18	362.2	27.3	512	22	AAK91830	Human CDNA 5'-end
19	362.2	27.3	512	22	AAK93233	Human CDNA clone r
20	332.2	25.1	517	22	AAH98469	Human EST-derived
21	234.8	17.7	792	23	AAK76345	DNA encoding novel
22	191.2	14.4	3660	23	AAK88505	DNA encoding novel
23	191.2	14.4	3660	23	AAK89242	DNA encoding novel
24	144.8	10.9	3660	23	AAK88505	DNA encoding novel
25	144.8	10.9	3660	23	AAK89242	DNA encoding novel
26	137.4	10.4	480	23	AAK81207	DNA encoding novel
27	133.2	10.0	1482	23	AAK81210	DNA encoding novel
28	129.4	9.8	168	23	AAK91789	DNA encoding novel
29	95.8	7.2	915	23	AAK81206	DNA encoding novel
30	89.6	6.8	1239	23	AAK73137	DNA encoding novel
31	56.8	4.3	759	24	ABL57727	Human sbg1002620TI
32	56.8	4.3	1494	24	ABL57728	Human sbg1002620TI
33	56.8	4.3	3483	24	AAH38692	Human LP095 secret
34	55.2	4.2	939	22	AAH98687	Rat EST-derived co
35	55.2	4.2	1491	22	AAF77686	Human protease-inh
36	55.2	4.2	1669	22	AAD17765	Human novel trypsi
37	55.2	4.2	1690	22	AAH15690	Human CDNA sequenc
38	55.2	4.2	1824	24	ABK33563	CDNA encoding huma
39	55.2	4.2	2272	22	AAF77687	Human protease-inh
40	55.2	4.2	3836	24	AAK39682	Human secreted pro
41	55.2	4.2	4877	22	AAK60871	Human cancer agent
42	55.2	4.2	4877	22	AAK60872	Human cancer agent
43	55.2	4.2	4877	22	AAK60883	Human cancer agent
44	55	4.1	2403	22	AAD17766	Human novel trypsi
45	54.6	4.1	840	22	AAH05058	Human CDNA clone (

ALIGNMENTS

RESULT 1
AAK87260
ID AAK87260 standard; CDNA; 1876 BP.
XX
AC AAK87260;
XX
27-SEP-1999 (first entry)
XX
CDNA clone encoding human PRO347, amplified in tumour cells.
DE
XX
XX
KW PRO347; UNQ306; cancer; tumour; diagnosis; therapy; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 123..1490
FT sig_peptide /*tag= a
FT FT 123..200
FT mat_peptide /*tag= b
FT FT 201..1487
FT FT /*tag= c
XX
PN WO9935170-A2.
XX
PD 15-JUL-1999.
XX
PF 05-JAN-1999; 99WO-US00106.
XX
PR 20-NOV-1998; 98US-0109304.
PR 05-JAN-1998; 98US-0070440.
PR 29-APR-1998; 98US-0083500.
PR 22-MAY-1998; 98US-0086414.

PR 10-JUN-1998; 98US-0088742.
PR 10-NOV-1998; 98US-0107783.
PA (GETH) GENENTECH INC.
PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
PI Roy MA, Wood WI;
XX WPI: 1999-430385/36.
DR P-PSDB: AAY06483.
XX
PT Antibody against proteins expressed in neoplastic cells, useful for
PT tumor diagnosis and treatment
XX
PS Example 1; Fig 13; 162pp; English.
XX
CC This is the nucleotide sequence of cDNA clone DNA44176 (ATCC 209532)
CC coding for human PRO347 (UN0306) (see AAY06482). The clone was
CC isolated from a foetal kidney library. Amplification of DNA44176
CC occurs in various tumours, suggesting an association with tumour
CC formation or growth. Antagonists (e.g. antibodies) directed against
CC PRO347 may have use in cancer therapy. The invention identifies 14
CC genes (see AX87254-67) that are amplified in the genome of tumour
CC cells. Such amplification is expected to be associated with
CC overexpression of the gene product and to contribute to
CC tumorigenesis. The encoded proteins (see AAY06477-90) may be useful
CC targets for the diagnosis and/or treatment (including prevention)
CC of certain cancers, and may act as predictors of the prognosis of
CC tumour treatment.
XX
SQ Sequence 1876 BP; 387 A; 568 C; 574 G; 347 T; 0 other;
Query Match 100.0%; Score 1326; DB 20; Length 1876;
Best Local Similarity 100.0%; Pred. No. 7.8e-299;
Matches 1326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCTGCATCCAGAGACCTCCCTGCGGGGGGAGTCTCTGGCTGTGCTGCGCCCTC 60
Db 123 ATGCTGCATCCAGAGACCTCCCTGCGGGGGGAGTCTCTGGCTGTGCTGCGCCCTC 182
Qy 61 CTGTGCACACCTGGCAGAGGTGCGCCACCCAGCTGCAGGAGCAGGCTCCGATGCCC 120
Db 183 CTGTGCACACCTGGCAGAGGTGCGCCACCCAGCTGCAGGAGCAGGCTCCGATGCCC 242
Qy 121 GGAGCCCTGAACAGGAAGAGAGTTCCTGCTCTCTCCCTGCACACCGCCTCGCGCAG 180
Db 243 GGAGCCCTGAACAGGAAGAGAGTTCCTGCTCTCTCCCTGCACACCGCCTCGCGCAG 302
Qy 181 TGGGTCCAGCCCTGCGGCTGCATGCGGAGCTGGAGCTGGAGTGACAGCTGGCCCAA 240
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Db 363 CTGGCTCAAGCCAGGCGACCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCGGCTG 422
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Db 423 TGGCGCACCTGCAGTGGGCTGGAACATGCAGCTGCTGCCCGGGGCTTGGCGTCCCTTT 482
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Db 543 TGTGCTCGCAACGCCACCTGCACCCACTACACGAGCTCTGTGGGCGACCTCAAGCCAG 602
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Db 603 CTGGGCTGTGGGCGGACCTGTGCTCTGAGGGCGAGACGAGATAGAGCCTTTGCTCTGT 662
Qy 541 GCCTACTCCCCGGAGGCACTGGGAGGTCAACGGGAGACAATCATCCCCCTATAAGAAG 600

Db 663 GCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAGACAATCATCCCCCTATAAGAAG 722
Qy 601 GGTGCTGTGTGCTGTGCACAGCCAGTGTCTCAGGCTGCTTCAAGACCTGGGACCAT 660
Db 723 GGTGCTGTGTGCTGTGCACAGCCAGTGTCTCAGGCTGCTTCAAGACCTGGGACCAT 782
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Qy 781 CAAGTCAGGTGTCAGCTGTGTCACGCGCGGTTCCGGGAGGAGAGTGTCTGCTGC 840
Db 903 CAAGTCAGGTGTCAGCTGTGTCACGCGCGGTTCCGGGAGGAGAGTGTCTGCTGC 962
Qy 841 GTCTGTACATCGGCTACGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCAC 900
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Db 1023 ACTGTGACCTGAGGTGTCAGGAGACTGCTTCATGTGTCTTTCAGAGGCGACACCTAT 1082
Qy 961 TACAGAGCCAGGATGAATGTTCAGAGGAAGGCGGGTGTGCGCCAGATCAAGAGCCAG 1020
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Qy 1021 AAAGTCAGGACATCTCTCGCTTCTATCTGGGCGCGCTGGAGACCAACAGAGGTGACT 1080
Db 1143 AAAGTCAGGACATCTCTCGCTTCTATCTGGGCGCGCTGGAGACCAACAGAGGTGACT 1202
Qy 1081 GACAGTGACTTCAGAGCCAGAACTTCTGGATCGGGCTCACTTACAGACCCGCCAAGGAC 1140
Db 1203 GACAGTGACTTCAGAGCCAGAACTTCTGGATCGGGCTCACTTACAGACCCGCCAAGGAC 1262
Qy 1141 TCCTTCGCTGGGCGCACAGGGGAGCACAGGCTTTCACAGTTCCTTTCGCTTTGGGCGAGCCT 1200
Db 1263 TCCTTCGCTGGGCGCACAGGGGAGCACAGGCTTTCACAGTTCCTTTCGCTTTGGGCGAGCCT 1322
Qy 1201 GACAACACCGGCTGTGTGCTGAGTGTGCCATGCGGTTTGGCACTGCGTGGAGCTG 1260
Db 1323 GACAACACCGGCTGTGTGCTGAGTGTGCCATGCGGTTTGGCACTGCGTGGAGCTG 1382
Qy 1261 CAGGCTTCAGCTGCCTTCAACTGGAACGACGAGCCTGCAAAACCCGAAACCGTTACATC 1320
Db 1383 CAGGCTTCAGCTGCCTTCAACTGGAACGACGAGCCTGCAAAACCCGAAACCGTTACATC 1442
Qy 1321 TGCAG 1326
Db 1443 TGCAG 1448
RESULT 2
AX80053
ID AAX80053 standard; cDNA; 1876 BP.
XX AAX80053;
AC AAX80053;
DT 12-AUG-1999 (first entry)
XX Human PRO347 nucleotide sequence.
DE Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
KW secreted protein; transmembrane protein; inflammation disorder; ss.
XX Homo sapiens.
XX OS
XX PN
XX WO928462-A2.

Db 1383 CAGGCTTCAGCTGCTTCAACTGGAACACACGAGCGCTGCAAAACCCGAAACCGTTTACATC 1442

QY 1321 TGCCAG 1326

Db 1443 TGCCAG 1448

RESULT 4

AAA49561

ID AAA49561 standard; cDNA; 1876 BP.

XX AC AAA49561;

XX 25-SEP-2000 (first entry)

XX Human PRO347 cDNA.

DE PRO; membrane bound protein; secreted protein; PRO357; PRO327;

KW PRO243; PRO715; PRO323; PRO299; PRO344; PRO347;

KW PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;

KW antibody; screening; detection; inhibition; probe; primer; human;

ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 123..1490

FT /*tag= a

FT /product= PRO347 polypeptide

XX WO200032776-A2.

XX 08-JUN-2000.

XX 01-DEC-1999; 99WO-US28301.

XX 01-DEC-1998; 98WO-US25108.

XX 16-DEC-1998; 98US-0112850.

XX 22-DEC-1998; 98US-0113296.

XX (GETH) GENENTECH INC.

XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;

PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;

PI Hallan KJ, Kijavini IJ, Napier MA, Roy MA, Tumas D, Wood WI;

XX WPT; 2000-412324/35.

DR P-PSDB; AAB01319.

XX New human nucleic acids encoding secreted and transmembrane

PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical

PT and diagnostic agents

XX Claim 2; Fig 19; 187pp; English.

XX New human nucleic acids encoding secreted and transmembrane

CC polypeptides which are designated as PRO polypeptides are described

CC The membrane-bound proteins have various industrial applications,

CC including as pharmaceutical and diagnostic agents. The membrane-bound

CC proteins can also be employed for screening of potential peptide or

CC small molecule inhibitors of the relevant receptor/ligand interaction.

CC Anti-PRO antibodies are useful for the affinity purification of PRO

CC from recombinant cell culture or natural sources.

XX Sequence 1876 BP; 387 A; 568 C; 574 G; 347 T; 0 other;

SQ

Query Match 100.0%; Score 1326; DB 21; Length 1876;

Best Local Similarity 100.0%; Pred. No. 7.8e-299;

Matches 1326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGCATCCAGACACCTCCCTGGCGGGGGCATCTCTGGCTGTCTCTGGCCCTC 60

Db 123 ATGCTGCATCCAGACACCTCCCTGGCGGGGGCATCTCTGGCTGTCTCTGGCCCTC 182

QY 61 CTTGGCACCACCTGGGCAGAGGTGTGCCACCCAGCTGCAGGACGAGCTCCGATGGCC 120
 Db 183 CTTGGCACCACCTGGGCAGAGGTGTGCCACCCAGCTGCAGGACGAGCTCCGATGGCC 242
 QY 121 GGAGCCCTGAACAGAGAGAGAGTTTCTTGTCTCTCTCCCTGCACAAACCGCTGGCGAGC 180
 Db 243 GGAGCCCTGAACAGAGAGAGAGTTTCTTGTCTCTCTCCCTGCACAAACCGCTGGCGAGC 302
 QY 181 TGGGTCCAGCCCTTCGGCTGACATGGGAGGCTTGGACTGGAGTGACAGCTGGCCCA 240
 Db 303 TGGGTCCAGCCCTTCGGCTGACATGGGAGGCTTGGACTGGAGTGACAGCTGGCCCA 362
 QY 241 CTGGCTCAAGCAGGCGAGCCCTCTGTGGAATCCAAACCCGAGCTGGCATCCGCGCTG 300
 Db 363 CTGGCTCAAGCAGGCGAGCCCTCTGTGGAATCCAAACCCGAGCTGGCATCCGCGCTG 422
 QY 301 TGGCGCACCTGCAAGTGGGTGGAACATGACAGTGTGCCCCGGGGTGGCTGCTCTTT 360
 Db 423 TGGCGCACCTGCAAGTGGGTGGAACATGACAGTGTGCCCCGGGGTGGCTGCTCTTT 482
 QY 361 GTTGAAGTGTGACCTATGTTTGCAGAGGGGAGCGGTACAGCCACGCGCAGGAGAG 420
 Db 483 GTTGAAGTGTGACCTATGTTTGCAGAGGGGAGCGGTACAGCCACGCGCAGGAGAG 542
 QY 421 TGTGCTCGCAACGCGACCTGCACCCACTACACGAGCTCGTGTGGGCCACCTCAAGCCAG 480
 Db 543 TGTGCTCGCAACGCGACCTGCACCCACTACACGAGCTCGTGTGGGCCACCTCAAGCCAG 602
 QY 481 CTGGCTGTGGGGGCGACCTGTGCTGTGAGGCCAGAGAGAGAGAGAGAGAGAGAG 540
 Db 603 CTGGCTGTGGGGGCGACCTGTGCTGTGAGGCCAGAGAGAGAGAGAGAGAGAGAG 662
 QY 541 GCCTACTCCCGGAGGCACTGGAGGTCAACGGAGAGAGAGAGAGAGAGAGAGAGAG 600
 Db 663 GCCTACTCCCGGAGGCACTGGAGGTCAACGGAGAGAGAGAGAGAGAGAGAGAGAG 722
 QY 601 GGTGCTGTGGTGTGCTGTGACAGCCAGTGTCTCAGGCTGTCTTCAAGAGCTGGGACCAT 660
 Db 723 GGTGCTGTGGTGTGCTGTGACAGCCAGTGTCTCAGGCTGTCTTCAAGAGCTGGGACCAT 782
 QY 661 GCAGGGGGCTGTGTGAGGTCCCGAGAGTCTTGTGCGATGAGTGCAGAGAGAGAGAGAG 720
 Db 783 GCAGGGGGCTGTGTGAGGTCCCGAGAGTCTTGTGCGATGAGTGCAGAGAGAGAGAGAG 842
 QY 721 CGTCTCAACATCAGACCTGCCACTGCCACTGTCCCTGTGCTACACGGGAGAGAGAGAG 780
 Db 843 CGTCTCAACATCAGACCTGCCACTGTCCCTGTGCTACACGGGAGAGAGAGAGAGAG 902
 QY 781 CAAGTGAAGTGCAGCTGTGTCAGCGCCCGTTCGGGGAGGAGAGAGTGTCTGTCCAC 840
 Db 903 CAAGTGAAGTGCAGCTGTGTCAGCGCCCGTTCGGGGAGGAGAGAGTGTCTGTCCAC 962
 QY 841 GTCTGTGACATCGGCTACGGGGAGGCCAGTGTGCCACCAAGTGCAATTTTCCCTTCCAC 900
 Db 963 GTCTGTGACATCGGCTACGGGGAGGCCAGTGTGCCACCAAGTGCAATTTTCCCTTCCAC 1022
 QY 901 ACCTGTGACCTGAGATCGACGAGAGTGTCTTCAAGTGTCTTTCAGAGGAGAGAGAGAG 960
 Db 1023 ACCTGTGACCTGAGATCGACGAGAGTGTCTTCAAGTGTCTTTCAGAGGAGAGAGAGAG 1082
 QY 961 TACAGGCCAGGATGAATGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 Db 1083 TACAGGCCAGGATGAATGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1142
 QY 1021 AAAGTGAAGGAGATCTCGCTTCTATCTGGGCCCGCTGGAGAGAGAGAGAGAGAGAGAG 1080
 Db 1143 AAAGTGAAGGAGATCTCGCTTCTATCTGGGCCCGCTGGAGAGAGAGAGAGAGAGAGAG 1202
 QY 1081 GACAGTGAAGTGAAGGAG 1140
 Db 1203 GACAGTGAAGTGAAGGAG 1262

Qy 1141 TCCTTCCGCTGGCCACAGGGGAGACACAGGCTTCACAGTTTTCCTTTGGGCGACCT 1200
Db 1263 TCCTTCCGCTGGCCACAGGGGAGACACAGGCTTCACAGTTTTCCTTTGGGCGACCT 1322
Qy 1201 GACACACAGGGCTGTGGCTGAGTGTGCATGGGCTTTGGCAACTGCGTGGAGCTG 1260
Db 1323 GACACACAGGGCTGTGGCTGAGTGTGCATGGGCTTTGGCAACTGCGTGGAGCTG 1382
Qy 1261 CAGGCTTCAGCTGCCCTTCAACTTGAACGACGAGCTGCAAAACCCGAAACCCCTTACATC 1320
Db 1393 CAGGCTTCAGCTGCCCTTCAACTTGAACGACGAGCTGCAAAACCCGAAACCCCTTACATC 1442
Qy 1321 TGCCAG 1326
Db 1443 TGCCAG 1448

RESULT 5

ID AA223300 standard; cDNA; 1338 BP.

XX AA223300;

XX 31-JAN-2000 (first entry)

XX Human T139 protein coding sequence.

XX Human: T139 polypeptide; immune system disorder; spermatogenesis; ss;
KW sperm-egg fusion; testicular disorder; testicular cancer; gene mapping.
XX Homo sapiens.

XX WO954343-A2.

XX 28-OCT-1999.

XX 23-APR-1999; 99WO-US08896.

XX 23-APR-1998; 98US-0065661.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX Holtzman D;

XX WPI; 1999-633969/54.

XX P-PSDB; AAY41266.

XX Human T139 nucleic acids and polypeptides, useful for treating
PT proliferative disorders associated with aberrant T139 expression or
PT activity -

XX Claim 2; Page 114; 115pp; English.

XX This represents the coding sequence of the human T139 polypeptide. The
CC T139 polypeptide can be expressed by standard recombinant methodology.
CC The T139 cDNA insert is deposited with ATCC under accession number
CC 98694. The T139 polypeptides and polynucleotides can be administered
CC therapeutically or prophylactically to treat/prevent disorders associated
CC with aberrant T139 expression or activity, especially proliferative or
CC differentiative disorders, e.g. of the immune system. They can be used to
CC modulate spermatogenesis, e.g. as a contraceptive to decrease
CC spermatogenesis or to treat disorders related to defects in sperm-egg
CC fusion. They may also be useful to treat testicular disorders e.g.
CC testicular cancer. The polypeptides may be used to identify selectively
CC binding compounds which may be useful for detecting the polypeptides in
CC samples; and identifying compounds modulating polypeptide activity. The
CC polynucleotides are useful for producing probes or primers that
CC selectively hybridize to the polynucleotides which may be useful for
CC detecting the polynucleotides in a sample, gene mapping; identifying
CC cells or tissues expressing aberrant T139 levels; determining if a gene
CC has been mutated or deleted to identify subjects at risk for or having a
CC disorder associated with T139 expression or activity and to monitor
CC therapeutic interventions; and for producing antisense sequences for

CC therapeutic administration to modulate/prevent T139 expression.
XX
SQ Sequence 1338 BP; 259 A; 420 C; 413 G; 246 T; 0 other;
Query Match 94.6%; Score 1254; DB 20; Length 1338;
Best Local Similarity 97.6%; Pred. No. 4e-282;
Matches 1294; Conservative 0; Mismatches 5; Indels 27; Gaps 1;
Qy 1 ATGCTGCATCCAGAGACCTCCCTGGCCGGGGGATCTCTCGCTGTGCTCTGCGCCCTC 60
Db 1 ATGCTGCATCCAGAGACCTCCCTGGCCGGGGGATCTCTCGCTGTGCTCTGCGCCCTC 60
Qy 61 CTTGGCACCCACTGGGCAGAGGTGTGGCCACCCAGCTGCGAGGAGAGGCTCCGATGGCC 120
Db 61 CTTGGCACCCGCTGGGCAGAGGTGTGGCCACCCAGCTGCGAGGAGAGGCTCCGATGGCC 120
Qy 121 GGAGCCCTGAACAGAGAGAGTTCCTTGTCTCCTTCACAAACCCGCTGCCGACG 180
Db 121 GGAGCCCTGAACAGAGAGAGTTCCTTGTCTCCTTCACAAACCCGCTGCCGACG 180
Qy 181 TGGTCCAGCCCCCTTGGCGCTGCATGCGAGGCTGAGTGGAGTGACAGCCTGGCCCCA 240
Db 181 TGGTCCAGCCCCCTTGGCGCTGCATGCGAGGCTGAGTGGAGTGACAGCCTGGCCCCA 240
Qy 241 CTGGCTCAAGCCAGGCGAGCCCTCTGTGGATCCCAACCCGAGCTGGCATCCGCGCTG 300
Db 241 CTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCGAGCTGGCGTCCGCGCTG 300
Qy 301 TGGCGCACCCCTGCAAGTGGCTGGAACATGCAGCTGTGCCCGCGGCTTGGCGTCTTT 360
Db 301 TGGCGCACCCCTGCAAGTGGCTGGAACATGCAGCTGTGCCCGCGGCTTGGCGTCTTT 360
Qy 361 GTTGAAGTGTGTCAGCCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACCGCGAGAGAG 420
Db 361 GTTGAAGTGTGTCAGCCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACCGCGAGAGAG 420
Qy 421 TGTGCTGCGACAGCCACCTGCACCCACTACAGCGAGCTGCTGGGCGACCTCAAGCCAG 480
Db 421 TGTGCTGCGACAGCCACCTGCACCCACTACAGCGAGCTGCTGGGCGACCTCAAGCCAG 480
Qy 481 CTGGGCTGTGGCGGCGACCTGTGCTCTGCAGGCGACAGCGATAGAAGCCTTTGTCTGT 540
Db 481 CTGGGCTGTGGCGGCGACCTGTGCTCTGCAGGCGACAGCGATAGAAGCCTTTGTCTGT 540
Qy 541 GCCTACTCCCCCGGAGGCAACTGGAGGTCAACGGGAGACAAATCATCCCCATATAAGAG 600
Db 541 GCCTACTCCCCCGGAGGCAACTGGAGGTCAACGGGAGACAAATCATCCCCATATAAGAG 600
Qy 601 GGTGCTGGTGTGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAGCCCTGGGACCAT 660
Db 601 GGTGCTGGTGTGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAGCCCTGGGACCAT 660
Qy 661 GCAGGGGGCTCTGTGAGTCCCCAGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGA 720
Db 661 GCAGGGGGCTCTGTGAGTCCCCAGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGA 720
Qy 721 CGTCTCAACATCAGACCTGCCACTGCCACTGTCCCTTGGCTTACACGGGAGATGCTGC 780
Db 721 CGTCTCAACATCAGACCTGCCACTGCCACTGTCCCTTGGCTTACACGGGAGATGCTGC 780
Qy 781 CAAGTGAGTGCAGCTCAGTGTGTGCACGGCGGTTCCGGGAGGAGGAGTGTCTGCTGC 840
Db 781 CAAGTGAGTGCAGCTCAGTGTGTGCACGGCGGTTCCGGGAGGAGGAGTGTCTGCTGC 840
Qy 841 GTCTGTGACATCGGCTACGGGGAGCCAGTGTGCCACCAAGTGCATTTTCCCTTCCAC 900
Db 841 GTCTGTGACATCGGCTACGGGGAGCCAGTGTGCCACCAAGTGCATTTTCCCTTCCAC 900
Qy 901 ACCTGTGACCTGAGGATGACGGAGACTGCTTCATGGTGTCTTCAGAGGAGACACCTAT 960
Db 901 ACCTGTGACCTGAGGATGACGGAGACTGCTTCATGGTGTCTTCAGAGGAGACACCTAT 960
Qy 961 TACAGAGCCAGGATGAATGTCTAGAGGAAAGCGGGGTGCTGGCCCCAGATCAAGAGCCAG 1020

Db 335 CTGGCTCAAGCCAGGCGAGCCCTCTGTGGAAATCCCAACCCGAGCCCTGGGCTCGGCGCTG 394
 QY 301 TGGCGCACCTGCAAGTGGGCTGGAACATGAGTGTGCGCGGGCTTGGCGTCTCTTT 360
 Db 395 TGGCGCACCTGCAAGTGGGCTGGAACATGAGTGTGCGCGGGCTTGGCGTCTCTTT 454
 QY 361 GTTGAAGTGGTCAAGCTATGTTGACAGAGGGGAGGCTACAGCCACGGCGGAGAGAG 420
 Db 455 GTTGAAGTGGTCAAGCTATGTTGACAGAGGGGAGGCTACAGCCACGGCGGAGAGAG 514
 QY 421 TGTGCTCGAAACCCACCTGCACCCACTACAGCAGCTGTGTGGGCACTCAAGCCAG 480
 Db 515 TGTGCTCGAAACCCACCTGCACCCACTACAGCAGCTGTGTGGGCACTCAAGCCAG 574
 QY 481 CTGGGCTGTGGGCGGACCTGTCTCTGAGGCGGAGAGGATAGAGGCTTGTCTGT 540
 Db 575 CTGGGCTGTGGGCGGACCTGTCTCTGAGGCGGAGAGGATAGAGGCTTGTCTGT 634
 QY 541 GCTACTCCCGGAGGCACTGGGAGGTCAACGGGAGAGCAATCATCCCTATAGAAG 600
 Db 635 GCTACTCCCGGAGGCACTGGGAGGTCAACGGGAGAGCAATCATCCCTATAGAAG 694
 QY 601 GGTGCTGTGTGCTGTCTGACAGCAGTGTCTCAGGCTGCTTCAAGGCTGGGACCAT 660
 Db 695 GGTGCTGTGTGCTGTCTGACAGCAGTGTCTCAGGCTGCTTCAAGGCTGGGACCAT 754
 QY 661 GCAGGGGGCTCTGTAGGTCCCGAGGAATCTTGTGCGATGAGTGCAGCAACCATGGA 720
 Db 755 GCAGGGGGCTCTGTAGGTCCCGAGGAATCTTGTGCGATGAGTGCAGCAACCATGGA 814
 QY 721 CGTCTCAACATCAGCAGCTGCCACTGCCACTGTCCCTGCTCAGCGGAGATACATGC 780
 Db 815 CGTCTCAACATCAGCAGCTGCCACTGCCACTGTCCCTGCTCAGCGGAGATACATGC 874
 QY 781 CAAGTGAAGTGCAGCTGTGTCAGCGGCGGTTCGGGAGGAGTGTCTGTGTC 840
 Db 875 CAAGTGAAGTGCAGCTGTGTCAGCGGCGGTTCGGGAGGAGTGTCTGTGTC 934
 QY 841 GTCTGACATCGGCTACGGGGAGCCAGTGTGCCAAGAGTGCATTTCCCTTCCAC 900
 Db 935 GTCTGTGACATCGGCTACGGGGAGCCAGTGTGCCAAGAGTGCATTTCCCTTCCAC 994
 QY 901 ACCTGTACCTGAGGATCGAGGAGTGTCTTATGTTGTTCTTACAGAGCAGACACCTAT 960
 Db 995 ACCTGTACCTGAGGATCGAGGAGTGTCTTATGTTGTTCTTACAGAGCAGACACCTAT 1054
 QY 961 TACAGAGCCAGGATGAATGTACAGAGGAAGCGGGTGTGCGCCAGATCAAGAGCCAG 1020
 Db 1055 TACAGAGCCAGGATGAATGTACAGAGGAAGCGGGTGTGCGCCAGATCAAGAGCCAG 1114
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 Db 1115 AAAGTGAAGGATCTCTGCGCTTCTATCTGGGCGGCTGTGAGACACCAACGAGGTGACT 1174
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 Db 1175 GACAGTGAAGTGAAGGATCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1234
 QY 1141 TCCCTTCCGCTGGGCGGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
 Db 1235 TCCCTTCCGCTGGGCGGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1294
 QY 1201 GACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
 Db 1295 GACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1327
 QY 1261 CAGGCTTCAAGTGTCAAGTGTCAAGTGTCAAGTGTCAAGTGTCAAGTGTCAAGTGTCAAGT 1320
 Db 1328 CAGGCTTCAAGTGTCAAGTGTCAAGTGTCAAGTGTCAAGTGTCAAGTGTCAAGTGTCAAGT 1387
 QY 1321 TGGCAG 1326
 | | | | |

Db 1388 TGCCAG 1393
 RESULT 8
 AAD33531
 ID AAD33531 standard; cDNA; 1856 BP.
 XX
 AC AAD33531;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE Human T139 (TANGO-139) cDNA.
 XX
 KW Human; haematopoiesis; clotting; kidney failure; wound healing; cancer;
 KW neoplasia; pancreatic disorder; pancreatitis; cerebrovascular disease;
 KW heart disorder; ischaemic heart disease; neuroprotective; vulnerary;
 KW cardiovascular disorder; ischaemic heart disease; immunosuppressive;
 KW glomerular disease; glomerulonephritis; uterine disorder; hyperplasia;
 KW fetal spleen; prostate disorder; inflammatory disease; Crohn's disease;
 KW proliferative disorder; gynaecological; haemostatic; antibacterial;
 KW systemic lupus erythematosus; immunodeficiency disorder; antiasthmatic;
 KW cystostatic; nephrotropic; antidiabetic; cerebroprotective; tranquilliser;
 KW hypotensive; tumour; injury; trauma; antianginal; vasotropic; antialler;
 KW apoptotic disorder; rheumatoid arthritis; cardiac; renal disorder;
 KW hepatotropic; antipsoriatic; antiallergic; dermatological; virucide;
 KW T139; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 95..1435
 FT /*tag= a
 FT /product= "Human T139 protein"
 FT sig_peptide 95..172
 FT mat_peptide 173..1432
 FT /*tag= c
 FT /product= "Human mature T139 protein"
 FT misc_feature 95..1432
 FT /*tag= d
 FT /note= "This region designated as SEQ.ID.NO.3 is specifically referred in claim 27"
 XX
 US2002028508-A1.
 XX
 PD 07-MAR-2002.
 XX
 PF 21-FEB-2001; 2001US-0790264.
 XX
 PR 23-APR-1998; 98US-0065363.
 PR 23-APR-1998; 98US-0065661.
 PR 22-JUN-1998; 98US-0102705.
 PR 29-JUL-1998; 98US-0124538.
 PR 23-APR-1999; 99US-0298531.
 PR 22-JUN-1999; 99US-0337930.
 PR 29-JUL-1999; 99US-0363630.
 XX
 PA (HOLT/) HOLTZMAN D A.
 PA (GOOD/) GOODEARL A D J.
 PA (MCCA/) MCCARTHY S A.
 XX
 PI Holtzman DA, Goodearl ADJ, McCarthy SA;
 XX
 DR WPI: 2002-303420/34.
 DR P-PSDB; AAE21077.
 XX
 PT Novel TANGO polypeptides and nucleic acid molecules useful as
 PT modulating agents in regulating cellular processes and for diagnosing
 PT and treating heart, liver, lung, kidney, inflammatory and cellular
 PT proliferative disorders
 XX
 PS Claim 26; Fig 1; 138pp; English.
 XX

CC The invention relates to nucleic acids encoding a variety of proteins
 CC human T139 (TANGO-139), T125 (TANGO-125), T110 (TANGO-110), murine T175
 CC (TANGO-175), human T175 or murine WDNM-2, having diagnostic, preventive,
 CC therapeutic and other uses. Polypeptide of the invention has the ability
 CC to inhibit a proteinase activity, to modulate cell-cell interactions,
 CC haematopoiesis and the ability to modulate clotting. Polypeptide and
 CC polynucleotide of the invention are useful for diagnosing and treating
 CC disorder characterised by their aberrant expression or activity. The
 CC antibodies are useful as modulating agents in regulating a variety of
 CC cellular processes e.g. cell proliferation and/or cell differentiation.
 CC TANGO-139 is useful for treating kidney defects such as kidney failure,
 CC TANGO-125 is useful in wound healing and for treating cancer, TANGO-110
 CC is useful for treating neoplasia, TANGO-177 or WDNM-2 is useful for
 CC treating cancer, are useful to treat pancreatic disorders, such as
 CC pancreatitis, cerebrovascular disease, and tumours, and injury or trauma
 CC to the brain. TANGO-125, 110, 175 molecules treat heart disorders, e.g.,
 CC ischaemic heart disease, cardiovascular disorders, such as ischaemic
 CC heart (kidney) disorders, 125, 110 and 175 molecules are useful to treat
 CC chronic glomerulonephritis), TANGO-175 is useful to treat uterine
 CC disorders, hyperplasia of the endometrium. TANGO-110 is useful to treat
 CC spleen, e.g., the fetal spleen, associated diseases and disorder. TANGO-
 CC 125 treats prostate disorders, such as inflammatory diseases, Crohn's
 CC disease and tumours. TANGO-139, 125, 110, 175 or WDNM-2 are useful for
 CC treating proliferative disorders, inflammatory disorders. TANGO-175, or
 CC WDNM-2 activity also include apoptotic disorders, rheumatoid arthritis,
 CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,
 CC immune-related disorders, e.g., immunodeficiency disorders, viral
 CC disorders, cell growth disorders, e.g., cancers and inflammatory
 CC disorders and apoptotic disorders. The nucleic acids of the invention
 CC are used in gene therapy. The present sequence is human T139 cDNA.
 CC
 XX
 SQ

Sequence 1856 BP; 402 A; 560 C; 564 G; 330 T; 0 other;

Query Match 94.6%; Score 1254; DB 24; Length 1856;
 Best Local Similarity 97.6%; Pred. No. 4.4e-282;
 Matches 1294; Conservative 0; Mismatches 5; Indels 27; Gaps 1;

QY 1 ATGCTGCATCCAGAGACCTCCCTGGCGGGGGGATCTCTGGCTGTGCTGGCCCTC 60
 DB 95 ATGCTGCATCCAGAGACCTCCCTGGCGGGGGGATCTCTGGCTGTGCTGGCCCTC 154
 QY 61 CTTGGCACCACCTGGGACAGGTTGTGGCCACCCAGCTGCAGGAGAGGCTCCGATGGCC 120
 DB 155 CTTGGCACCCTGGGACAGGTTGTGGCCACCCAGCTGCAGGAGAGGCTCCGATGGCC 214
 QY 121 GGAGCCCTGAACAGGAAGGAGAGTTTCTTGTCTCTCTCCCTGCACAAACCGCTCGCAGC 180
 DB 215 GGAGCCCTGAACAGGAAGGAGAGTTTCTTGTCTCTCTCCCTGCACAAACCGCTCGCAGC 274
 QY 181 TGGGTCAGCCCTCGCGCTGACATGCGGAGGCTGGACTGGAGTGACAGCTGGGCCAA 240
 DB 275 TGGGTCAGCCCTCGCGCTGACATGCGGAGGCTGGACTGGAGTGACAGCTGGGCCAA 334
 QY 241 CTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCGAGCTGGCATCCGCGCTG 300
 DB 335 CTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCGAGCTGGCGTCCGCGCTG 394
 QY 301 TGGCGCAGCTGCAAGTGGGCTGGAAATGACAGCTGCTGCCCGCGGCTTGGCGTCTTT 360
 DB 395 TGGCGCAGCTGCAAGTGGGCTGGAAATGACAGCTGCTGCCCGCGGCTTGGCGTCTTT 454
 QY 361 GTTGAAGTGGTCAGGCTATGGTTTCAGAGGGGCGAGCGGTACAGCCACGGCGAGAGAG 420
 DB 455 GTTGAAGTGGTCAGGCTATGGTTTCAGAGGGGCGAGCGGTACAGCCACGGCGAGAGAG 514
 QY 421 TGTGCTCGAAGCGCCACCTGCACCCACTACAGCAGCTGCTGTGGGCCACCTCAAGCCAG 480
 DB 515 TGTGCTCGAAGCGCCACCTGCACCCACTACAGCAGCTGCTGTGGGCCACCTCAAGCCAG 574
 QY 481 CTGGGCTGTGGCGGCGACCTGTGCTGTGAGGCCAGACAGCGATAGAGCCCTTTGTCTGT 540
 DB 575 CTGGGCTGTGGCGGCGACCTGTGCTGTGAGGCCAGGCGATAGAGCCCTTTGTCTGT 634

QY 541 GCTACTCCCGGAGGCACTGGAGGTCAACGGGAGAGCAATCATCCCTATAGAAG 600
 DB 635 GCTACTCCCGGAGGCACTGGAGGTCAACGGGAGAGCAATCATCCCTATAGAAG 694
 QY 601 GGTGCTGTGTTCGCTCTGCACAGGCAAGTGTCTCAGGCTGTCTCAAGGCTGGGACCAT 660
 DB 695 GGTGCTGTGTTCGCTCTGCACAGGCAAGTGTCTCAGGCTGTCTCAAGGCTGGGACCAT 754
 QY 661 GCAGGGGGGCTGTGAGGTCCCGAGAAATCCCTTGTGCGCATGAGCTGCCAGAACCATGGA 720
 DB 755 GCAGGGGGGCTGTGAGGTCCCGAGAAATCCCTTGTGCGCATGAGCTGCCAGAACCATGGA 814
 QY 721 CCTCTCAACATCAGCAGCTGCCACTGCCACTGTCTCCCTGGCTACACGGGAGATATGC 780
 DB 815 CCTCTCAACATCAGCAGCTGCCACTGCCACTGTCTCCCTGGCTACACGGGAGATATGC 874
 QY 781 CAAGTGAGGTGACGCTGCCACTGTGTGCAGGGCGGTTCCGGGAGGAGGTGCTCGTGC 840
 DB 875 CAAGTGAGGTGACGCTGCCACTGTGTGCAGGGCGGTTCCGGGAGGAGGTGCTCGTGC 934
 QY 841 GTCCTGACATCGGCTACGGGGGAGCCAGTGTGCCACCAAGTGATGCTTCCCTCCAC 900
 DB 935 GTCCTGACATCGGCTACGGGGGAGCCAGTGTGCCACCAAGTGATGCTTCCCTCCAC 994
 QY 901 ACCTGTGACCTGAGGATCCAGGAGACTGCTTCATGCTGTCTTCAGAGGCGAGACCAT 960
 DB 995 ACCTGTGACCTGAGGATCCAGGAGACTGCTTCATGCTGTCTTCAGAGGCGAGACCAT 1054
 QY 961 TACAGAGCCAGGATGAAATGTTCAGAGGAAAGCGGGGTGCTGGCCAGATCAAGAGCCAG 1020
 DB 1055 TACAGAGCCAGGATGAAATGTTCAGAGGAAAGCGGGGTGCTGGCCAGATCAAGAGCCAG 1114
 QY 1021 AAAGTGACGACATCCTCGCCTTCTATCTGGGCGGCTGGAGACCAACAGAGGTGACT 1080
 DB 1115 AAAGTGACGACATCCTCGCCTTCTATCTGGGCGGCTGGAGACCAACAGAGGTGACT 1174
 QY 1081 GACAGTGTACTTCGAGACCAAGGAATCTTGGATCGGCTCACCTTACAGAGCCGCAAGGAC 1140
 DB 1175 GACAGTGTACTTCGAGACCAAGGAATCTTGGATCGGCTCACCTTACAGAGCCGCAAGGAC 1234
 QY 1141 TCCCTCCGCTGGGCGACAGGGGAGACCAAGGCTTACACAGTTTGGCTTTGGGCGAGCT 1200
 DB 1235 TCCCTCCGCTGGGCGACAGGGGAGACCAAGGCTTACACAGTTTGGCTTTGGGCGAGCT 1294
 QY 1201 GACAACCAAGGCTGTGCTGGCTGAGTGTGCTGATGGGTTGGCAACTGCGTGGAGCTG 1260
 DB 1295 GACAACCAAGGCTGTGCTGGCTGAGTGTGCTGATGGGTTGGCAACTGCGTGGAGCTG 1327
 QY 1261 CAGGCTTCAGTGTGCTTCAACTGGAAACGACCGCTGCAAAACCCGAAACCGTTTACATC 1320
 DB 1328 CAGGCTTCAGTGTGCTTCAACTGGAAACGACCGCTGCAAAACCCGAAACCGTTTACATC 1387
 QY 1321 TGCCAG 1326
 DB 1388 TGCCAG 1393

RESULT 9

AAF24152
 ID AAF24152 standard; DNA; 1923 BP.

AC AAF24152;

XX 23-MAR-2001 (first entry)

XX Human secreted protein DNA #2.

XX Secreted protein; gene therapy; vaccine; cancer; leukemia;
 KW autoimmune disease; allergy; inflammation; graft rejection;
 KW hyperproliferation; cardiovascular; infection; ds.
 XX Homo sapiens.
 OS

EP1130094-A2.
05-SEP-2001.
07-JUL-2000; 2000EP-0114089.
08-JUL-1999; 99JP-0194486.
11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
(HELI-) HELIX RES INST.
Ota T, Nishikawa T, Isogai T, Hayaashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
WPI; 2001-524255/58.
P-PSDB; AAM93326.
830 Primers useful for synthesizing full length cDNA clones and their
use in genetic manipulation -
Claim 8: SEQ ID NO 2850; 1380bp + sequence listing; English.
The invention relates to primers for synthesizing full length cDNA
clones. 830 cDNA molecules encoding a human protein have been
isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
molecules have been determined. Primers for synthesizing the full length
cDNA are useful for clarifying the function of the protein encoded by
the cDNA. The full length clones were obtained by construction of full
length enriched cDNA libraries that were synthesized by the oligo-capping
method. The primers enable the production of the full length cDNA easily
without any special methods. The present sequence is a full length
human cDNA of the invention.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in CD-ROM format directly from EPO.
Sequence 1786 BP; 361 A; 548 C; 553 G; 324 T; 0 other;
Query Match 94.0%; Score 1246; DB 22; Length 1786;
Best Local Similarity 97.2%; Pred. No. 3.1e-280;
Matches 1289; Conservative 0; Mismatches 10; Indels 27; Gaps 1;
QY 1 ATGCTGCATCCAGAGACCTCCCTGGCGGGGCGCATCTCTGGCTGCTGCTGGCCCTC 60
DB 73 ATGCTGCATCCAGAGACCTCCCTGGCGGGGCGCATCTCTGGCTGCTGCTGGCCCTC 132
QY 61 CTGGCACCACCTGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCC 120
DB 133 CTGGCAGCGCTGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCC 192
QY 121 GGAGCCCTGACAGGAGAGAGATTCTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
DB 193 GGAGCCCTGACAGGAGAGAGATTCTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 252
QY 181 TGGGTCCAGCCCTCGGCTGCATGCGGAGGCTGGAGTGGAGTGCACGCTGGCCCAA 240
DB 253 TGGGTCCAGCCCTCGGCTGCATGCGGAGGCTGGAGTGGAGTGCACGCTGGCCCAA 312
QY 241 CTGGCTCAAGCAGGCGACGCTCTCTGGAATCCCAACCCAGCCTGGCATCCGGCCTG 300
DB 313 CTGGCTCAAGCAGGCGACGCTCTCTGGAATCCCAACCCAGCCTGGCGTCCGGCCG 372
QY 301 TGGCGCACCTGCAAGTGGGCTGGACATGCAGCTGCTGCCCGGGCTTGGGCTCCTTT 360
DB 373 TGGCGCACCTGCAAGTGGGCTGGACATGCAGCTGCTGCCCGGGCTTGGGCTCCTTT 432
QY 361 GTGAAGTGGTCAGGCTATGGTTTGCAGAGGGGACGCGGTACAGCACGCGGAGGAG 420
DB 433 GTGAAGTGGTCAGGCTATGGTTTGCAGAGGGGACGCGGTACAGCACGCGGAGGAG 492
QY 421 TGTGCTCGCAAGCCACCTGCACCCACTACAGCAGCTGTTGGGCGACCTCAAGCCAG 480
DB 493 TGTGCTCGCAAGCCACCTGCACCCACTACAGCAGCTGTTGGGCGACCTCAAGCCAG 552

QY 481 CTGGGCTGTGGCGGCACCTGTGCTCTGCAGCCAGCAGCAGATAGAGCCTTTGTCTGT 540
DB 553 CTGGGCTGTGGCGGCACCTGTGCTCTGCAGCCAGCAGCAGATAGAGCCTTTGTCTGT 612
QY 541 GCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCTCCCTATAAAG 600
DB 613 GCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCTCCCTATAAAG 672
QY 601 GGTGCTGTGTCTGCTCTGCACAGCAGTGTCTCAGGCTGTCTCAAGCCTGGAGCAT 660
DB 673 GGTGCTGTGTCTGCTCTGCACAGCAGTGTCTCAGGCTGTCTCAAGCCTGGAGCAT 732
QY 661 GCAGGGGGGCTCTGTGAGGTGCCAGCAATCTTGTGCGCATGAGTGCAGAACCATGGA 720
DB 733 GCAGGGGGGCTCTGTGAGGTGCCAGCAATCTTGTGCGCATGAGTGCAGAACCATGGA 792
QY 721 CTTCTCAACATCAGCAGCCTGCCACTGCCACTGTCCCTCTGCTACACGGGAGAGTGTGC 780
DB 793 CGTCTCAACATCAGCAGCCTGCCACTGCCACTGTCCCTCTGCTACACGGGAGAGTGTGC 852
QY 781 CAAAGTCAAGTGCAGCCTGCAGTGTGTGCACGGCGGTTCCGGGAGGAGTGTCTGTGC 840
DB 853 CAAAGTCAAGTGCAGCCTGCAGTGTGTGCACGGCGGTTCCGGGAGGAGTGTCTGTGC 912
QY 841 GTCTGTGACATCGGCTACCGGGGAGGCCAGTGTGCCACCAAGTGTCAATTTCCCTTCCAC 900
DB 913 GTCTGTGACATCGGCTACCGGGGAGGCCAGTGTGCCACCAAGTGTCAATTTCCCTTCCAC 972
QY 901 ACCTGTGACCTGAGGATCAGGAGTGTGCCACTGTCTCATGGTGTCTTTCAGAGGAGAGTGT 960
DB 973 ACCTGTGACCTGAGGATCAGGAGTGTGCCACTGTCTCATGGTGTCTTTCAGAGGAGAGTGT 1032
QY 961 TACAGAGCCAGGATGAATGTTCAGAGGAAGCGGGGTGCTGCCCGCAGATCAAGAGCCAG 1020
DB 1033 TACAGAGCCAGGATGAATGTTCAGAGGAAGCGGGGTGCTGCCCGCAGATCAAGAGCCAG 1092
QY 1021 AAGTGCAGGACATCTCGCTTCTATCTGGCGCGCTTGAGACCCACCAACGAGGTGACT 1080
DB 1093 AAGTGCAGGACATCTCGCTTCTATCTGGCGCGCTTGAGACCCACCAACGAGGTGACT 1152
QY 1081 GACAGTGTGACATCAGACAGGAACTTCTGTGATCGGCTCACCTACAGAGCCGCAAGGAC 1140
DB 1153 GACAGTGTGACATCAGACAGGAACTTCTGTGATCGGCTCACCTACAGAGCCGCAAGGAC 1212
QY 1141 TCCTTCCGCTGGGCCACAGGGGAGCAGGCTTCCACAGTGTTCGCTTTGGGCGAGCCT 1200
DB 1213 TCCTTCCGCTGGGCCACAGGGGAGCAGGCTTCCACAGTGTTCGCTTTGGGCGAGCCT 1272
QY 1201 GACAAACAGGGCTGTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1260
DB 1273 GACAAACAGGGCTGTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1305
QY 1261 CAGGCTTCCAGTGTGCTTCACTGGAAACAGCAGGCTGCAAAACCCGAAACCCGTTACATC 1320
DB 1306 CAGGCTTCCAGTGTGCTTCACTGGAAACAGCAGGCTGCAAAACCCGAAACCCGTTACATC 1365
QY 1321 TGCCAG 1326
DB 1366 TGCCAG 1371

RESULT 11
AAS91790
ID AAS91790 standard; cDNA: 1934 BP.

XX AAS91790;

XX AC

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #27594.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW

XX Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
KW tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.
XX Homo sapiens.
XX WO200036107-A2.
XX 22-JUN-2000.
XX 17-DEC-1999; 99WO-US30270.
XX 17-DEC-1998; 98US-0215681.
XX 17-DEC-1998; 98US-0216003.
XX 23-JUN-1999; 99US-0338933.
XX 24-SEP-1999; 99US-0404879.
XX (CORI-) CORIXA CORP.
XX Mitcham JL, King GE, Algate PA, Frudakis TN;
XX WPI; 2000-431589/37.
XX Immunogenic portion of an ovarian carcinoma protein and the nucleic
PT acid encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer -
XX Claim 1; Page 177; 299pp; English.
XX The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants).
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytostatic activity and can be used in gene therapy and vaccines.
CC Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines
CC are useful for the prevention, diagnosis and treatment of cancer,
CC preferably ovarian cancer. AAA69691 to AA70077 and AAB12552 to AAB12557
CC represent human ovarian carcinoma polynucleotides and proteins used in
CC the exemplification of the present invention.
XX Sequence 690 BP; 148 A; 197 C; 212 G; 131 T; 2 other;
Query Match 50.7%; Score 672.8; DB 21; Length 690;
Best Local Similarity 99.3%; Pred. No. 5.4e-147;
Matches 685; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 482 TGGGCTGTGGGGCCACCTGTCTCTGCAGCCAGACAGAGGATGAGAGCTTTGTCTGTG 541
DB 1 TGGGCTGTGGGGCCACCTGTCTCTGCAGCCAGACAGAGGATGAGAGCTTTGTCTGTG 60
QY 542 CCTACTCCCCGGAGCACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAAAG 601
DB 61 CCTACTCCCCGGAGCACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAAAG 120
QY 602 GTGCTGTGTCTGTCTGCAGCCAGGCTCTCAGGCTGCTCAAGGCTGGGACCATG 661
DB 121 GTGCTGTGTCTGTCTGCAGCCAGGCTCTCAGGCTGCTCAAGGCTGGGACCATG 180
QY 662 CAGGGGGCTGTGTGAGTCTCCAGGAATCTTGTGCGCATGAGCTGCCAGAACCATGGAC 721
DB 181 CAGGGGGCTGTGTGAGTCTCCAGGAATCTTGTGCGCATGAGCTGCCAGAACCATGGAC 240
QY 722 GTCTCAACATCAGCACTGCCACTGCCACTGTCCCTGGCTACAGGGGAGATCTGCC 781
DB 241 GTCTCAACATCAGCACTGCCACTGCCACTGTCCCTGGCTACAGGGGAGATCTGCC 300
QY 782 AAGTGAAGTGCAGCTGTGAGTGTGTGTCAGCGCGGCTCCGGAGGAGGAGTCTCGTGG 841
DB 301 AAGTGAAGTGCAGCTGTGAGTGTGTGTCAGCGCGGCTCCGGAGGAGGAGTCTCGTGG 360
QY 842 TCTGTGACATCGGCTACGGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTCCACA 901
DB 361 TCTGTGACATCGGCTACGGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTCCACA 420

QY 902 CCTGTGACCTGAGGATCGAGCGGAGACTGCTTCTATGGTGTCTTTCAGAGCGAGACCTATT 961
DB 421 CCTGTGACCTGAGGATCGAGCGGAGACTGCTTCTATGGTGTCTTTCAGAGCGAGACCTATT 480
QY 962 ACAG-AGCCAGGATGAATGTTCAGAGGAAAGCGGGGTGCTGGCCAGATCAAGAGCCAG 1020
DB 481 ACAGAGCCAGGATGAATGTTCAGAGGAAAGCGGGGTGCTGGCCAGATCAAGAGCCAG 540
QY 1021 AAAGTGCAGGACATCCCTCGCCTTCTATCTGGGCGCCCTGGAGACACCAAGAGGTGACT 1080
DB 541 AAAGTGCAGGACATCCCTCGCCTTCTATCTGGGCGCCCTGGAGACACCAAGAGGTGACT 600
QY 1081 GACAGTGAATTCGAGAGCCAGGAACTTCTGATCGGGCTCACCTACAGACCGCCAGGAC 1140
DB 601 GACAGTGAATTCGAGAGCCAGGAACTTCTGATCGGGCTCACCTACAGACCGCCAGGAC 660
QY 1141 TCCTTCCGCTGGGCCACAGGGGAGCACCAG 1170
DB 661 TCCTTCCGCTGGGCCACAGGGGAGCACCAG 690

RESULT 14

ABN72904

ID ABN72904 standard; DNA; 690 BP.

XX AC ABN72904;

XX DT 02-JUL-2002 (first entry)

XX DE Ovarian carcinoma antigen polynucleotide #9.

XX KW Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; ds.

XX OS Homo sapiens.

XX PN WO200206317-A2.

XX PD 24-JAN-2002.

XX PF 17-JUL-2001; 2001WO-US22635.

XX PR 17-JUL-2000; 2000US-0617747.

XX PR 10-AUG-2000; 2000US-0636801.

XX PR 20-SEP-2000; 2000US-0667857.

XX PR 04-APR-2001; 2001US-0827271.

XX PR 18-JUN-2001; 2001US-0884441.

XX PA (CORI-) CORIXA CORP.

XX PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;

XX PI Read SG, Vedrick TS, Carter D, Hill P, Albone E;

XX PS WPI; 2002-164781/21.

XX Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer -
XX Example 2; Page 296; 408pp; English.
XX This invention relates to polypeptides comprising an immunogenic
CC portion of an ovarian carcinoma protein which acts as an
CC immunostimulant and is cytostatic. The polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells that express the polypeptides are useful for stimulating an
CC immune response in a patient and treating ovarian cancer. This
CC sequence represents DNA related to the invention.

SQ Sequence 690 BP; 148 A; 197 C; 212 G; 131 T; 2 other;

Query Match 50.7%; Score 672.8; DB 24; Length 690;

Best Local Similarity 99.3%; Pred. No. 5.4e-147;

Matches 685; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

XX (HYSE-) HYSEQ INC.
 XX PA
 XX
 XX Drmanac RT, Liu C, Tang YT;
 XX
 XX WPI; 2001-639362/73.
 DR DR P-PSDB; ABG12156.
 DR

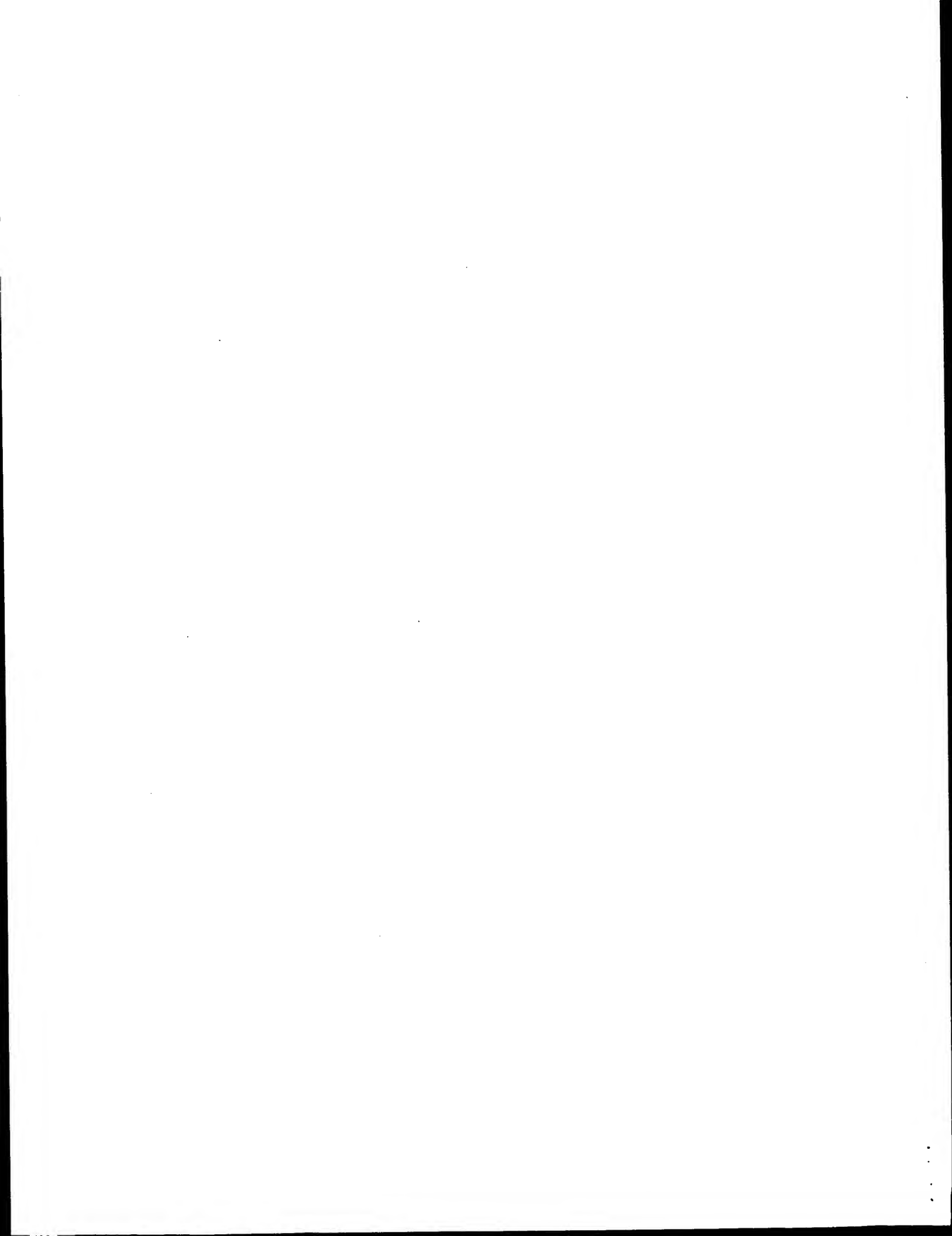
Query Match	49.6%	Score 657.2;	DB 23;	Length 906;
Best Local Similarity	95.3%;			
Matches 688;	Conservative 0;	Mismatches 33;	Indels 1;	Gaps 1;

QY	1	ATGCTGCATCCAGAGACCTCCCTGGCCGGGGGCGATCTCTCGGTGTGCTCTCGGCCCTC	60
bb	127	ATGCTGCATCCAGACCTCCCTGGCCGGGGGCGATCTCTCGGTGTGCTCTCGGCCCTC	186

QY	121	GGAGCCCTGAACAGGAGGAGGTTCTTGCTCCTCTCCCTGCACAACCGCTGCGCAGC	180
Db	247	GGAGCCCTGAACAGGAGGAGGTTCTTGCTCCTCTCCCTGCACAACCGCTGCGCAGC	306
QY	181	TGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGCCCAA	240
Db	307	TGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGCCCAA	366
QY	241	CTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCCTG	300
Db	367	CTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCCTG	426
QY	301	TGGCGCACCCCTGCAGTGGCTGGAACTGCAGCTGCTCCCGCGGCTTGCGCTCCTTT	360
Db	427	TGGCGCACCCCTGCAGTGGCTGGAACTGCAGCTGCTACCCCGCGGCTTGCGCTCCTTT	486
QY	361	GTGGAAGTGGTCAGCCTATGTTTTCAGAGGGGACCGGTACAGCCACGCGCAGAGAG	420
Db	487	GTGGAAGTGGTCAGCCTATGTTTTCAGAGGGGACCGGTACAGACACGCGCAGAGAG	546
QY	421	TGTGCTGGAAGCCACCTGCACCCACTACAGCGAGCTGTGTGGCCACCTCAAGCCAG	480

Db 547 TGAGCTCGAAGCCACCTGACCCCACTACATGACAGCTCGTGTGGCCACCTCAAGCCAG 606
 QY 481 CTGGGCTGTGGCGGCACCTGTGCTCTGAGGCGCAGACAGCGATAGAAGCCTTTGCTGTGT 540
 Db 607 CTGGGCTGTGGCGGCACCTGTGCTCTGAGGCGCAGCGATAGAAGCCTTTGCTGTGT 666
 QY 541 GCCTACTCCCCCGGAGGCAACTGGGAGGTCAAGGGGAAGACAATCATCCCTATAGAAG 600
 Db 667 GCCTACTCCCCCGAGAGGCAACTGGGAGGTCAAGGGGAAGACAATCGTCCCTATAAAG 726
 QY 601 GGTGCTGTGTGCTCTGACAGCCAGTGTCTCAGGCTGTCTCAAGCCTGGGACCAT 660
 Db 727 GGGGCTGTGGGCTGCTCTGACAGCCAGTGTCTCAAGCCTGTCTAAAGCCTGGGACCAT 786
 QY 661 GCAGGGGGCT-CTGTGAGGTCCCGAGGAATCTTGTGCTGATGAGTGCAGAACCATGG 719
 Db 787 GCCAGGGGGCTACTGGGGGGCCCCCGGGAACCTTGGGGAAGAGCCGACAGAACCCCTGG 846
 QY 720 AC 721
 Db 847 AC 848

Search completed: December 28, 2002, 17:01:44
 Job time : 271.586 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 15:40:17 ; Search time 48.913 Seconds
(without alignments)
11372.097 Million cell updates/sec

Title: US-09-944-896-49_COPY_201_447

Perfect score: 247

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	247	100.0	1876	20	AAH87260
2	247	100.0	1876	20	AAH80053
3	247	100.0	1876	21	AAH46918
4	247	100.0	1876	21	AAH49561
5	245.4	99.4	855	21	AAH45026
6	245.4	99.4	906	23	AAH50926
7	245.4	99.4	1338	20	AAH76343
8	245.4	99.4	1775	22	AAH23300
9	245.4	99.4	1856	20	AAH23299

10	245.4	99.4	1856	24	AAH33531
11	245.4	99.4	1923	22	AAH24152
12	243.8	98.7	517	22	AAH98469
13	242.2	98.1	512	22	AAH91830
14	242.2	98.1	512	22	AAH92323
15	242.2	98.1	1786	22	AAH94246
16	242.2	98.1	1934	23	AAH91790
17	110.6	44.8	1519	23	AAH76344
18	106.6	43.2	792	23	AAH76345
19	46.6	18.9	759	24	ABL57727
20	46.6	18.9	840	22	AAH05058
21	46.6	18.9	939	22	AAH98687
22	46.6	18.9	1491	22	AAH77686
23	46.6	18.9	1494	24	ABL57728
24	46.6	18.9	1669	22	AAH17765
25	46.6	18.9	1690	22	AAH15690
26	46.6	18.9	1824	24	ABK33563
27	46.6	18.9	2272	22	AAH77687
28	46.6	18.9	2400	22	AAH17764
29	46.6	18.9	2403	22	AAH17766
30	46.6	18.9	2412	22	AAH17767
31	46.6	18.9	3483	24	AAH38692
32	46.6	18.9	3836	24	AAH39682
33	46.6	18.9	4877	22	AAH60871
34	46.6	18.9	4877	22	AAH60872
35	46.6	18.9	4877	22	AAH60883
36	45.6	18.5	2305	22	AAH17763
37	37.8	15.3	3183	22	AAH60833
38	37.6	15.2	720	22	AAH94034
39	37.6	15.2	1288	23	AAH83963
40	37.6	15.2	1877	22	AAH93835
41	36.6	14.8	2818	23	AAH94552
42	36.2	14.7	7047	23	AAH75116
43	36	14.6	970	19	AAH2646
44	36	14.6	1803	22	AAH60658
45	36	14.6	1875	20	AAH52263

ALIGNMENTS

RESULT 1

AAH87260

ID AAX87260 standard; cDNA; 1876 Bp.

AC AAX87260;

DT 27-SEP-1999 (first entry)

DE cDNA clone encoding human PRO347, amplified in tumour cells.

KW PRO347; UNQ306; cancer; tumour; diagnosis; therapy; human; ss.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX CDS

XX /*tag= a

XX sig_peptide

XX /*tag= b

XX mat_peptide

XX /*tag= c

XX WO9935170-A2.

XX 15-JUL-1999.

XX 05-JAN-1999;

XX 95WO-US00106.

XX 20-NOV-1998;

XX 98US-0109304.

XX 05-JAN-1998;

XX 98US-0070440.

XX 29-APR-1998;

XX 98US-0083500.

XX 22-MAY-1998;

XX 98US-0086414.

Mon Dec 30 09:16:19 2002

PR 10-JUN-1998; 98US-0088742.
 PR 10-NOV-1998; 98US-0107783.
 XX (GETH) GENENTECH INC.
 XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
 PI Roy MA, Wood WI;
 XX WPI; 1999-430385/36.
 DR P-PSDB; AAY06483.
 XX Antibody against proteins expressed in neoplastic cells, useful for
 PT tumor diagnosis and treatment
 XX Example 1; Fig 13; 162pp; English.
 XX This is the nucleotide sequence of cDNA clone DNA44176 (ATCC 209532)
 CC coding for human PRO347 (UHQ306) (see AAY06482). The clone was
 CC isolated from a foetal kidney library. Amplification of DNA44176
 CC occurs in various tumours, suggesting an association with tumour
 CC formation or growth. Antagonists (e.g. antibodies) directed against
 CC PRO347 may have use in cancer therapy. The invention identifies 14
 CC genes (see AAX87254-67) that are amplified in the genome of tumour
 CC cells. Such amplification is expected to be associated with
 CC overexpression of the gene product and to contribute to
 CC tumorigenesis. The encoded proteins (see AAY06477-90) may be useful
 CC targets for the diagnosis and/or treatment (including prevention) of
 CC of certain cancers, and may act as predictors of the prognosis of
 CC tumour treatment.
 XX Sequence 1876 BP; 387 A; 568 C; 574 G; 347 T; 0 other;

Query Match 100.0%; Score 247; DB 20; Length 1876;
 Best Local Similarity 100.0%; Pred. No. 7.1e-51;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAGGTGTGCGCCACCCAGCTGCAGGAGCAGGCTCCGATGCGCGGAGCCCTGAACAGGAAG 60
 Db 201 GAGGTGTGCGCCACCCAGCTGCAGGAGCAGGCTCCGATGCGCGGAGCCCTGAACAGGAAG 260
 QY 61 GAGAGTTTCTTGTCTCTCTCCCTGACACACCGCTGCGGAGCTGGTCCAGCCCTCGG 120
 Db 261 GAGAGTTTCTTGTCTCTCTCCCTGACACACCGCTGCGGAGCTGGTCCAGCCCTCGG 320
 QY 121 GCTGACATGCGGAGGCTGGACTGGAGTGACAGCTGCGCCCAACTGGCTCAAGCCAGGGA 180
 Db 321 GCTGACATGCGGAGGCTGGACTGGAGTGACAGCTGCGCCCAACTGGCTCAAGCCAGGGA 380
 QY 181 GCCCTCTGTGGAATCCCAACCCGAGCTGSCATCCGCGCTGTGGCGCACCCTGCAAGTG 240
 Db 381 GCCCTCTGTGGAATCCCAACCCGAGCTGSCATCCGCGCTGTGGCGCACCCTGCAAGTG 440
 QY 241 GGCTGGA 247
 Db 441 GGCTGGA 447

RESULT 2
 AAX80053
 ID AAX80053 standard; cDNA; 1876 BP.
 XX AAX80053;
 XX 12-AUG-1999 (first entry)
 DT Human PRO347 nucleotide sequence.
 DE Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
 KW secreted protein; transmembrane protein; inflammation disorder; ss.
 XX Homo sapiens.
 XX W0928462-A2.
 PN

XX 10-JUN-1999.
 PD 01-DEC-1998; 98WO-US25108.
 XX 25-FEB-1998; 98US-0075945.
 PR 03-DEC-1997; 97US-0067411.
 PR 11-DEC-1997; 97US-0069278.
 PR 11-DEC-1997; 97US-0069334.
 PR 11-DEC-1997; 97US-0069335.
 PR 12-DEC-1997; 97US-0069425.
 PR 16-DEC-1997; 97US-0069694.
 PR 16-DEC-1997; 97US-0069702.
 PR 17-DEC-1997; 97US-0069870.
 PR 17-DEC-1997; 97US-0069873.
 PR 18-DEC-1997; 97US-0068017.
 PR 05-JAN-1998; 98US-0070440.
 PR 09-FEB-1998; 98US-0074086.
 PR 09-FEB-1998; 98US-0074092.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;
 XX Yuan J;
 PI WPI; 1999-371118/31.
 DR P-PSDB; AAY17828.
 XX Nucleic acids encoding PRO secreted and transmembrane proteins
 PT Claim 2; Fig 22; 123pp; English.
 XX The present invention describes nucleic acids encoding PRO secreted and
 CC transmembrane proteins used therapeutically. The PRO proteins have
 CC cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive
 CC activity. The proteins and polynucleotides can be used in therapy,
 CC identification of homologues, raising antibodies and design of probes
 CC and primers. They can be used in a range of diseases related to proteins
 CC that they have homology with, e.g. a PRO protein having homology to
 CC complement proteins may be used in inflammatory responses.
 XX Sequence 1876 BP; 387 A; 568 C; 574 G; 347 T; 0 other;

Query Match 100.0%; Score 247; DB 20; Length 1876;
 Best Local Similarity 100.0%; Pred. No. 7.1e-51;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAGGTGTGCGCCACCCAGCTGCAGGAGCAGGCTCCGATGCGCGGAGCCCTGAACAGGAAG 60
 Db 201 GAGGTGTGCGCCACCCAGCTGCAGGAGCAGGCTCCGATGCGCGGAGCCCTGAACAGGAAG 260
 QY 61 GAGAGTTTCTTGTCTCTCTCCCTGACACACCGCTGCGGAGCTGGTCCAGCCCTCGG 120
 Db 261 GAGAGTTTCTTGTCTCTCTCCCTGACACACCGCTGCGGAGCTGGTCCAGCCCTCGG 320
 QY 121 GCTGACATGCGGAGGCTGGACTGGAGTGACAGCTGCGCCCAACTGGCTCAAGCCAGGGA 180
 Db 321 GCTGACATGCGGAGGCTGGACTGGAGTGACAGCTGCGCCCAACTGGCTCAAGCCAGGGA 380
 QY 181 GCCCTCTGTGGAATCCCAACCCGAGCTGSCATCCGCGCTGTGGCGCACCCTGCAAGTG 240
 Db 381 GCCCTCTGTGGAATCCCAACCCGAGCTGSCATCCGCGCTGTGGCGCACCCTGCAAGTG 440
 QY 241 GGCTGGA 247
 Db 441 GGCTGGA 447

RESULT 3
 AAA46918
 ID AAA46918 standard; cDNA; 1876 BP.
 XX

QY 1 GAGGTGTGGCCACCCAGCTGCAGAGCAGGCTCCGATGGCGGAGCCCTGAACAGGAAG 60
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 201 GAGGTGTGGCCACCCAGCTGCAGAGCAGGCTCCGATGGCGGAGCCCTGAACAGGAAG 260
 QY 61 GAGAGTTTCTTGTCTCTCCCTGCACAAACCGCTGCGAGCTGGGTCCAGCCCCCTGGG 120
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 261 GAGAGTTTCTTGTCTCTCCCTGCACAAACCGCTGCGAGCTGGGTCCAGCCCCCTGGG 320
 QY 121 GCTGACATGGCGGAGCTGGAGTGCAGTGCAGAGCTGGCCCACTGGCTCAAGCCAGGGCA 180
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 321 GCTGACATGGCGGAGCTGGAGTGCAGTGCAGAGCTGGCCCACTGGCTCAAGCCAGGGCA 380
 QY 181 GCCTCTGTGGAATCCCAACCCGAGCTGGCATCCGGCTGTGGCGCAACCTGCAAGTG 240
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 381 GCCTCTGTGGAATCCCAACCCGAGCTGGCATCCGGCTGTGGCGCAACCTGCAAGTG 440
 QY 241 GGCTGGA 247
 Db | | | | |
 441 GGCTGGA 447

RESULT 5

AAZ50926
 ID AAZ50926 standard; cDNA; 855 BP.

AC AAZ50926;

DT 05-JUN-2000 (first entry)

XX Human Protease and associated protein-9 (PPRG-9) encoding cDNA.

XX Protease and associated protein-9; PPRG-9; anti-PPRG antibody;
 KW diagnosis; treatment; cell proliferative disorder; cancer; cirrhosis;
 KW arteriosclerosis; atherosclerosis; bursitis; hepatitis; immune disorder;
 KW AIDS; Addison's disease; adult respiratory distress syndrome; allergy;
 KW ankylosing spondylitis; amyloidosis; cytostatic; antiarteriosclerotic;
 KW hepatotropic; antiinflammatory; virucide; antipsoriatic; anti-HIV;
 KW antiallergic; immunosuppressive; antidiabetic; antianaemic;
 XX neuroprotective; human; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH 233..733
 FT CDS /tag= a
 FT /product= "Human PPRG-9"
 FT sig_peptide 233..310
 FT /tag= b
 FT mat_peptide 311..730
 FT /tag= c
 FT /product= "Mature PPRG-9"
 FT misc_binding 326..370
 FT /tag= d
 FT /bound_moiety= "Probe or Primer"

XX WO200009709-A2.

XX 24-FEB-2000.

XX 06-AUG-1999; 99WO-US17818.

XX 10-AUG-1998; 98US-0096114.

XX 11-FEB-1999; 99US-0119768.

XX (INCY-) INCYTE PHARM INC.

XX Bandman O, Hillman JL, Baughn MR, Azimzai Y, Guegler KJ;

XX Corley NC, Yue H, Tang YT, Reddy R, Patterson C, Au-Young J;

XX Shih LL, Lu DM;

XX WPI; 2000-224346/19.

XX P-PSDB; AAY70015.

PT New human proteases, useful for diagnosis, treatment and prevention of
 XX cell proliferative disorders such as atherosclerosis -
 XX Claim 9; Page 105; 114pp; English.

XX The present sequence is a cDNA identified in Incyte clone 998626
 CC derived from KIDNUT01 cDNA library. It encodes human protease and
 CC associated protein-9 (PPRG-9), which is expressed in urologic
 CC and musculoskeletal tissues. Anti-PPRG antibodies can be used
 CC as therapeutic antagonists, reagents for diagnosis and monitoring
 CC diseases and for isolating PPRG. PPRG nucleotide sequence can be used
 CC as probe or primer for diagnosis and monitoring of PPRG-related
 CC diseases and gene mapping. PPRG can be used in the treatment of cell
 CC proliferative disorders like cancer, arteriosclerosis, atherosclerosis,
 CC bursitis, cirrhosis and hepatitis, and immune disorders like AIDS,
 CC Addison's disease, adult respiratory distress syndrome, allergies,
 CC ankylosing spondylitis and amyloidosis.

XX Sequence 855 BP; 152 A; 283 C; 257 G; 162 T; 1 other;

Query Match 99.4%; Score 245.4; DB 21; Length 855;
 Best Local Similarity 99.6%; Pred. No. 1.6e-50;
 Matches 246; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGTGTGGCCACCCAGCTGCAGAGCAGGCTCCGATGGCGGAGCCCTGAACAGGAAG 60
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 311 GAGGTGTGGCCACCCAGCTGCAGAGCAGGCTCCGATGGCGGAGCCCTGAACAGGAAG 370
 QY 61 GAGAGTTTCTTGTCTCTCCCTGCACAAACCGCTGCGAGCTGGGTCCAGCCCCCTGGG 120
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 371 GAGAGTTTCTTGTCTCTCCCTGCACAAACCGCTGCGAGCTGGGTCCAGCCCCCTGGG 430
 QY 121 GCTGACATGGCGGAGCTGGAGTGCAGTGCAGAGCTGGCCCACTGGCTCAAGCCAGGGCA 180
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 431 GCTGACATGGCGGAGCTGGAGTGCAGTGCAGAGCTGGCCCACTGGCTCAAGCCAGGGCA 490
 QY 181 GCCTCTGTGGAATCCCAACCCGAGCTGGCATCCGGCTGTGGCGCAACCTGCAAGTG 240
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 491 GCCTCTGTGGAATCCCAACCCGAGCTGGCATCCGGCTGTGGCGCAACCTGCAAGTG 550
 QY 241 GGCTGGA 247
 Db | | | | |
 551 GGCTGGA 557

RESULT 6

AAZ76343
 ID AAZ76343 standard; cDNA; 906 BP.

AC AAZ76343;

DT 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #12147.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.
XX P-PSDB; ABG12156.
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX
PS Claim 1; SEQ ID No 12147; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC imaging of sites expressing (II). (I) and (II) are useful in medical
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 906 BP; 175 A; 294 C; 286 G; 151 T; 0 other;
Query Match 99.4%; Score 245.4; DB 23; Length 906;
Best Local Similarity 99.6%; Pred. No. 1.6e-50;
Matches 246; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAGGTGGCCACCCAGCTGCAGGAGCAGCTCCGATGCGCGGAGCCCTGAACAGGAAG 60
Db 205 GAGGTGGCCACCCAGCTGCAGGAGCAGCTCCGATGCGCGGAGCCCTGAACAGGAAG 264
QY 61 GAGAGTTTCTTGCTCCCTCTCCCTGCACACCGCTGCGAGCTGGTCCAGCCCTCGC 120
Db 265 GAGAGTTTCTTGCTCCCTCTCCCTGCACACCGCTGCGAGCTGGTCCAGCCCTCGC 324
QY 121 GCTGACATCGGAGGCTGGAGTGCAGAGCTGGCCCAACTGGCTCAAGCCAGGCA 180
Db 325 GCTGACATCGGAGGCTGGAGTGCAGAGCTGGCCCAACTGGCTCAAGCCAGGCA 384
QY 181 GCCTCTGTGGATCCCAACCCGAGCTGGCATCCGGCTGTGGCGACCCCTCAAGTG 240
Db 385 GCCTCTGTGGATCCCAACCCGAGCTGGCATCCGGCTGTGGCGACCCCTCAAGTG 444
QY 241 GGCTGGA 247
Db 445 GGCTGGA 451
RESULT 7
AAZ23300
ID AAZ23300 standard; cDNA; 1338 BP.
XX
AC AAZ23300;
XX
XX 31-JAN-2000 (first entry)
DE Human T139 protein coding sequence.
KW Human; T139 polypeptide; immune system disorder; spermatogenesis; ss;
KW sperm-egg fusion; testicular disorder; testicular cancer; gene mapping.
XX
OS Homo sapiens.

XX PN WO954343-A2.
XX XX
PD 28-OCT-1999.
XX XX
PF 23-APR-1999; 99WO-US08896.
XX XX
PR 23-APR-1998; 98US-0065661.
XX XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX Holtzman D;
XX WPI; 1999-633969/54.
XX P-PSDB; AAY41266.
PT Human T139 nucleic acids and polypeptides, useful for treating
PT proliferative disorders associated with aberrant T139 expression or
PT activity -
XX
PS Claim 2; Page 114; 115pp; English.
XX
CC This represents the coding sequence of the human T139 polypeptide. The
CC T139 polypeptide can be expressed by standard recombinant methodology.
CC The T139 cDNA insert is deposited with ATCC under accession number
CC 98694. The T139 polypeptides and polynucleotides can be administered
CC therapeutically or prophylactically to treat/prevent disorders associated
CC with aberrant T139 expression or activity, especially proliferative or
CC differentiative disorders, e.g. of the immune system. They can be used to
CC modulate spermatogenesis, e.g. as a contraceptive to decrease
CC spermatogenesis or to treat disorders related to defects in sperm-egg
CC fusion. They may also be useful to treat testicular disorders e.g.
CC testicular cancer. The polypeptides may be used to identify selectively
CC binding compounds which may be useful for detecting the polypeptides in
CC samples; and identifying compounds modulating polypeptide activity. The
CC polynucleotides are useful for producing probes or primers that
CC selectively hybridize to the polynucleotides which may be useful for
CC detecting the polynucleotides in a sample, gene mapping, identifying
CC cells or tissues expressing aberrant T139 levels; determining if a gene
CC has been mutated or deleted to identify subjects at risk for or having a
CC disorder associated with T139 expression or activity and to monitor
CC therapeutic interventions; and for producing antisense sequences for
CC therapeutic administration to modulate/prevent T139 expression.
XX
SQ Sequence 1338 BP; 259 A; 420 C; 413 G; 246 T; 0 other;
Query Match 99.4%; Score 245.4; DB 20; Length 1338;
Best Local Similarity 99.6%; Pred. No. 1.7e-50;
Matches 246; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAGGTGGCCACCCAGCTGCAGGAGCAGCTCCGATGCGCGGAGCCCTGAACAGGAAG 60
Db 79 GAGGTGGCCACCCAGCTGCAGGAGCAGCTCCGATGCGCGGAGCCCTGAACAGGAAG 138
QY 61 GAGAGTTTCTTGCTCCCTCTCCCTGCACACCGCTGCGAGCTGGTCCAGCCCTCGC 120
Db 139 GAGAGTTTCTTGCTCCCTCTCCCTGCACACCGCTGCGAGCTGGTCCAGCCCTCGC 198
QY 121 GCTGACATCGGAGGCTGGAGTGCAGAGCTGGCCCAACTGGCTCAAGCCAGGCA 180
Db 199 GCTGACATCGGAGGCTGGAGTGCAGAGCTGGCCCAACTGGCTCAAGCCAGGCA 258
QY 181 GCCTCTGTGGATCCCAACCCGAGCTGGCATCCGGCTGTGGCGACCCCTCAAGTG 240
Db 259 GCCTCTGTGGATCCCAACCCGAGCTGGCATCCGGCTGTGGCGACCCCTCAAGTG 318
QY 241 GGCTGGA 247
Db 319 GGCTGGA 325
RESULT 8
AAD12570

ID	AA12570 standard; cDNA; 1775 BP.
XX	AA12570:
XX	
XX	25-SEP-2001 (first entry)
XX	
XX	Human protein having hydrophobic domain encoding cDNA clone HPI0760.
XX	
KW	Human; hydrophobic domain; gene therapy; nutritional supplement;
KW	cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
KW	multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
KW	haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
KW	Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
KW	haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
KW	contraceptive; antiinfertility; antiinflammatory; ss.
XX	
XX	Homo sapiens.
XX	
XX	Key Location/Qualifiers
XX	CDS 62..1402
XX	/*tag= a
XX	/product= "Human protein having hydrophobic domain"
XX	/note= "CDS is specifically is claimed in claim 3"
XX	62..142
XX	sig_peptide
XX	/*tag= b
XX	143..1399
XX	mat_peptide
XX	/*tag= c
XX	/product= "Mature human protein with hydrophobic domain"
XX	
XX	WO200149728-A2.
XX	
XX	12-JUL-2001.
XX	
XX	28-DEC-2000; 2000WO-JP09359.
XX	
XX	06-JAN-2000; 2000JP-0000585.
XX	06-JAN-2000; 2000JP-0000588.
XX	11-JAN-2000; 2000JP-0002299.
XX	03-FEB-2000; 2000JP-0026862.
XX	03-MAR-2000; 2000JP-0058367.
XX	
XX	(PROT-) PROTEGENE INC.
XX	(SAGA) SAGAMI CHEM RES CENT.
XX	
XX	Kato S, Kimura T;
XX	
XX	WPI; 2001-418355/44.
XX	P-PSDB; AAE06575.
XX	
XX	Human proteins with hydrophobic domains and the nucleic acids encoding
XX	them, useful for preventing diagnosing and treating e.g. cancer,
XX	Alzheimer's and inflammation
XX	
XX	Claim 4; Page 271-275; 563pp; English.
XX	
XX	The present sequence is human protein with hydrophobic domain encoding
XX	cDNA clone Hpi0760. The polynucleotide and polypeptide of the invention
XX	may be used in the prevention, diagnosis and treatment of diseases
XX	associated with inappropriate polypeptide expression. The polynucleotides
XX	may be used to produce the polypeptide, by inserting the nucleic acids
XX	into a host cell and culturing the cell to express the protein. The
XX	polynucleotides and its complementary sequences may also be used as DNA
XX	probes in diagnostic assays and also used in gene therapy. The
XX	polypeptides may also be used as antigens in the production of antibodies
XX	and in assays to identify modulators of polypeptide expression and
XX	activity. The polypeptides and nucleic acids may be used as nutritional
XX	supplements, to modulate cytokine and cell proliferation activity, to
XX	modulate immune stimulation or suppression (e.g. for the treatment of
XX	microbial infections and autoimmune disorders such as multiple sclerosis,
XX	rheumatoid arthritis and insulin-dependent diabetes), to modulate
XX	haematopoiesis, to modulate tissue growth activity (e.g. for the
XX	treatment of Parkinson's disease, Huntington's disease and Alzheimer's
XX	disease), to modulate activin and inhibin activity (e.g. for controlling

expressed by standard recombinant methodology. The T139 cDNA insert is deposited with ATCC under accession number 98694. The T139 polypeptides and polynucleotides can be administered therapeutically or prophylactically to treat/prevent disorders associated with aberrant T139 expression or activity, especially proliferative or differentiative disorders, e.g. of the immune system. They can be used to modulate spermatogenesis, e.g. as a contraceptive to decrease spermatogenesis or to treat disorders related to defects in sperm-egg fusion. They may also be useful to treat testicular disorders e.g. testicular cancer. The polypeptides may be used to identify selectively binding compounds which may be useful for detecting the polypeptides in samples; and identifying compounds modulating polypeptide activity. The polynucleotides are useful for producing probes or primers that selectively hybridize to the polynucleotides which may be useful for detecting the polynucleotides in a sample, gene mapping; identifying cells or tissues expressing aberrant T139 levels; determining if a gene has been mutated or deleted to identify subjects at risk for or having a disorder associated with T139 expression or activity and to monitor therapeutic interventions; and for producing antisense sequences for therapeutic administration to modulate /prevent T139 expression.

XX Sequence 1856 BP; 402 A; 560 C; 564 G; 330 T; 0 other;

Query Match 99.43; Score 245.4; DB 20; Length 1856;
 Best Local Similarity 99.63; Pred. No. 1.7e-50;
 Matches 246; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCGGAGCCCTGAACAGGAAG 60
 |||||||
 Db 173 GAGGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCGGAGCCCTGAACAGGAAG 232
 |||||||

QY 61 GAGAGTTCTTGTCTCTCTCCCTGCACAAACCGCTGCGAGCTGGGTCCAGCCCTCGG 120
 |||||||
 Db 233 GAGAGTTCTTGTCTCTCTCTCCCTGCACAAACCGCTGCGAGCTGGGTCCAGCCCTCGG 292
 |||||||

QY 121 GCTGACATCGGAGGCTGGACTGAGTGACAGCTGCGCCCAACTGGCTCAAGCCAGGCA 180
 |||||||
 Db 293 GCTGACATCGGAGGCTGGACTGAGTGACAGCTGCGCCCAACTGGCTCAAGCCAGGCA 352
 |||||||

QY 181 GCCTCTGTGGAATCCCAACCCGAGCTGGCATCCGCGCTGGCGACCCCTCAAGT 240
 |||||||
 Db 353 GCCTCTGTGGAATCCCAACCCGAGCTGGCGTCCGCGCTGGCGACCCCTCAAGT 412
 |||||||

QY 241 GGCTGA 247
 |||||||
 Db 413 GGCTGA 419

RESULT 10

AAD33531

XX AAD33531 standard; cDNA; 1856 BP.

XX AC AAD33531;

XX 01-JUL-2002 (first entry)

XX Human T139 (TANGO-139) cDNA.

XX Human; haematopoiesis; clotting; kidney failure; wound healing; cancer;
 KW neoplasia; pancreatic disorder; pancreatitis; cerebrovascular disease;
 KW heart disorder; ischaemic heart disease; neuroprotective; vulnary;
 KW cardiovascular disorder; ischaemic heart disease; immunosuppressive;
 KW glomerular disease; glomerulonephritis; uterine disorder; hyperplasia;
 KW fetal spleen; prostate disorder; inflammatory disease; Crohn's disease;
 KW proliferative disorder; gynaecological; haemostatic; antibacterial;
 KW cystic; nephrotropic; immunodeficiency disorder; antiasthmatic;
 KW hypotensive; tumour; injury; trauma; antidiabetic; cerebroprotective; tranquiliser;
 KW hepatotropic; rheumatoid arthritis; cardiatic; renal disorder;
 KW T139; gene; ss.
 XX Homo sapiens.

XX FH Location/Qualifiers
 FT CDS 95..1435
 FT /*tag= a
 FT /product= "Human T139 protein"
 FT sig_peptide 95..172
 FT /*tag= b
 FT mat_peptide 173..1432
 FT /*tag= c
 FT misc_feature 95..1432
 FT /*tag= d
 FT /note= "This region designated as SEQ.ID.NO.3 is specifically referred in claim 27"

XX US2002028508-A1.

XX 07-MAR-2002.

XX 21-FEB-2001; 2001US-0790264.

XX 23-APR-1998; 98US-0065363.

XX 23-APR-1998; 98US-0065661.

XX 22-JUN-1998; 98US-0102705.

XX 29-JUL-1998; 98US-0124538.

XX 23-APR-1999; 99US-0298531.

XX 22-JUN-1999; 99US-0337930.

XX 29-JUL-1999; 99US-0363630.

XX (HOLT/) HOLTZMAN D A.

XX (GOOD/) GOODEARL A D J.

XX (MCCA/) MCCARTHY S A.

XX Holtzman DA, Goodearl ADJ, McCarthy SA;

XX WPI; 2002-303420/34.

XX P-PSDB; AAE21077.

XX Novel TANGO polypeptides and nucleic acid molecules useful as

modulating agents in regulating cellular processes and for diagnosing

and treating heart, liver, lung, kidney, inflammatory and cellular

proliferative disorders

XX Claim 26; Fig 1; 138pp; English.

XX The invention relates to nucleic acids encoding a variety of proteins
 CC human T139 (TANGO-139), T125 (TANGO-125), T110 (TANGO-110), murine T175
 CC (TANGO-175), human T175 or murine WDNM-2, having diagnostic, preventive,
 CC therapeutic and other uses. Polypeptide of the invention has the ability
 CC to inhibit a proteinase activity, to modulate cell-cell interactions,
 CC haematopoiesis and the ability to modulate clotting. Polypeptide and
 CC polynucleotide of the invention are useful for diagnosing and treating
 CC disorders characterised by their aberrant expression or activity. The
 CC cellular processes e.g. cell proliferation and/or cell differentiation.
 CC TANGO-139 is useful for treating kidney defects such as kidney failure,
 CC TANGO-125 is useful in wound healing and for treating cancer, TANGO-110
 CC is useful for treating neoplasia, TANGO-177 or WDNM-2 is useful for
 CC treating cancer, are useful to treat pancreatic disorders, such as
 CC pancreatitis, cerebrovascular disease, and tumours, and injury or trauma
 CC to the brain. TANGO-125, 110, 175 molecules treat heart disorders, e.g.,
 CC ischaemic heart disease, cardiovascular disorders, such as ischaemic
 CC renal (kidney) disorders, such as glomerular disease (e.g., acute and
 CC chronic glomerulonephritis), TANGO-175 is useful to treat uterine
 CC disorders, hyperplasia of the endometrium. TANGO-110 is useful to treat
 CC spleen, e.g., the fetal spleen, associated diseases and disorder. TANGO-
 CC 125 treats prostate disorders, such as inflammatory diseases, Crohn's
 CC disease and tumours. TANGO-139, 125, 110, 175 or WDNM-2 are useful for
 CC treating proliferative disorders, such as inflammatory diseases, Crohn's
 CC disease and tumours. TANGO-139, 125, 110, 175 or WDNM-2 are useful for
 CC WDNM-2 activity also include apoptotic disorders, rheumatoid arthritis,
 CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,
 CC immune-related disorders, e.g., immunodeficiency disorders, viral


```
XX Example 11; SEQ ID NO 1693; 1380pp + sequence listing; English.
XX
XX The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesizing the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence was used as the
CC representative sequence from a human clone which was used in
CC homology searches to identify the clone.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
XX Sequence 512 BP; 94 A; 166 C; 167 G; 82 T; 3 other;
SQ
Query Match 98.1%; Score 242.2; DB 22; Length 512;
Best Local Similarity 98.8%; Pred. NO. 8.8e-50;
Matches 244; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GAGGTGTGGCCACCCAGCTGCAGAGCAGGCTCCGATGCCGGAGCCCTGAACAGGAAG 60
DB 152 GAGGTGTGGCCACCCAGCTGCAGAGCAGGCTCCGATGCCGGAGCCCTGAACAGGAAG 211
QY 61 GAGAGTTTCTTGCTCTCCCTGCACAAACCGCTCGCGAGCTGGGTCCAGCCCTCGCG 120
DB 212 GAGAGTTTCTTGCTCTCCCTGCACAAACCGCTCGCGAGCTGGGTCCAGCCCTCGCG 271
QY 121 GCTGACATGGCGAGGCTGGAGTGCAGAGCTGGGCTGGGCTCAAGCCAGGGCA 180
DB 272 GCTGACATGGCGAGGCTGGAGTGCAGAGCTGGGCTGGGCTCAAGCCAGGGCA 331
QY 181 GCCTCTGTGGAAATCCCAACCCCGAGCTGGCATCCGGCCTGTGGCCACCCCTGCAAGTG 240
DB 332 GCCTCTGTGGAAATCCCAACCCCGAGCTGGCATCCGGCCTGTGGCCACCCCTGCAAGTG 391
QY 241 GGCTGGA 247
DB 391 GGCTGGA 398
RESULT 15
AAK94246
ID AAK94246 standard; cDNA; 1786 BP.
XX
XX AAK94246;
AC
XX
XX 06-NOV-2001 (first entry)
XX Human full-length cDNA, SEQ ID NO: 2850.
XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX Homo sapiens.
XX
XX EP1130094-A2.
XX
XX 05-SEP-2001.
XX
XX 07-JUL-2000; 2000EP-0114089.
XX
XX 08-JUL-1999; 99JP-0194486.
XX
XX 11-JAN-2000; 2000JP-0118774.
XX
XX 02-MAY-2000; 2000JP-0183765.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
```

```
DR WPI; 2001-524255/58.
XX P-PSDB; AAM93326.
XX
XX 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
XX Claim 8; SEQ ID NO 2850; 1380pp + sequence listing; English.
XX
XX The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesizing the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a full length
CC human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
XX Sequence 1786 BP; 361 A; 548 C; 553 G; 324 T; 0 other;
SQ
Query Match 98.1%; Score 242.2; DB 22; Length 1786;
Best Local Similarity 98.8%; Pred. NO. 1e-49;
Matches 244; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GAGGTGTGGCCACCCAGCTGCAGAGCAGGCTCCGATGCCGGAGCCCTGAACAGGAAG 60
DB 151 GAGGTGTGGCCACCCAGCTGCAGAGCAGGCTCCGATGCCGGAGCCCTGAACAGGAAG 210
QY 61 GAGAGTTTCTTGCTCTCCCTGCACAAACCGCTCGCGAGCTGGGTCCAGCCCTCGCG 120
DB 211 GAGAGTTTCTTGCTCTCCCTGCACAAACCGCTCGCGAGCTGGGTCCAGCCCTCGCG 270
QY 121 GCTGACATGGCGAGGCTGGAGTGCAGAGCTGGGCTGGGCTCAAGCCAGGGCA 180
DB 271 GCTGACATGGCGAGGCTGGAGTGCAGAGCTGGGCTGGGCTCAAGCCAGGGCA 330
QY 181 GCCTCTGTGGAAATCCCAACCCCGAGCTGGCATCCGGCCTGTGGCCACCCCTGCAAGTG 240
DB 331 GCCTCTGTGGAAATCCCAACCCCGAGCTGGCATCCGGCCTGTGGCCACCCCTGCAAGTG 390
QY 241 GGCTGGA 247
DB 391 GGCTGGA 397
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Search completed: December 28, 2002, 17:01:50
Job time : 54.913 secs

Mon Dec 30 09:16:17 2002

[illegible]

QY 241 CTGGCTCAAGCGGACAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCCTG 300
Db 363 CTGGCTCAAGCGGACAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCCTG 422
QY 301 TGGCGCACCTTCAAGTGGCTGGACATGCAGCTGCTGCCCGGGCTTGGGCTCCTTT 360
Db 423 TGGCGCACCTTCAAGTGGCTGGACATGCAGCTGCTGCCCGGGCTTGGGCTCCTTT 482
QY 361 GTTGAAGTGGTCAGCCTATGTTTTCAGAGGGGACGCGGTACAGCCACGCGGACGAGAG 420
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QY 421 TGTGCTCGAAGCGCACCTTGCACCCACTACACGACGCTGCTGTGGGCCACCTCAAGCCAG 480
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QY 481 CTGGCTGTGGCGGACCTGTGCTCTGAGGGCCAGACGCGATAGAGCCTTTGTCTGT 540
Db 603 CTGGCTGTGGCGGACCTGTGCTCTGAGGGCCAGACGCGATAGAGCCTTTGTCTGT 662
QY 541 GCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAAG 600
Db 663 GCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAAG 722
QY 601 GGTGCTGTGTGCTGTGCACAGCCAGTGTCTCAGGCTGCTTCAAGCCTGGGACCAT 660
Db 723 GGTGCTGTGTGCTGTGCACAGCCAGTGTCTCAGGCTGCTTCAAGCCTGGGACCAT 782
QY 661 GCAGGGGGCTGTGTGAGTCCCGAGATCCCTGTGCGATGAGCTGCCAAGCAATGGA 720
Db 783 GCAGGGGGCTGTGTGAGTCCCGAGATCCCTGTGCGATGAGCTGCCAAGCAATGGA 842
QY 721 CGCTCAACATCAGACCTGCCACTGCCACTGTCCCTCGCTACAGGGGACAGATACCTGC 780
Db 843 CGCTCAACATCAGACCTGCCACTGCCACTGTCCCTCGCTACAGGGGACAGATACCTGC 902
QY 781 CAAGTGAAGTGCAGCCTGCAGTGTGTGCAGCGCGGTTCGGGAGGAGAGTGTCTGTGC 840
Db 903 CAAGTGAAGTGCAGCCTGCAGTGTGTGCAGCGCGGTTCGGGAGGAGAGTGTCTGTGC 962
QY 841 GTCGTGACATCGCTTACGGGGAGCCCGAGTGTGCCACCAAGGTGCATTTCCCTTCCAC 900
Db 963 GTCGTGACATCGCTTACGGGGAGCCCGAGTGTGCCACCAAGGTGCATTTCCCTTCCAC 1022
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Db 1023 ACCTGTGACTGAGGATCGACGAGAGTGTCTTATGTGTCTTTCAGAGGACAGACCTTAT 1082
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Db 1083 TACAGAGCAGGATGAATGTTCAGAGAAAGCGGGGTGTGGCCCGAGATCAAGAGCCAG 1142
QY 1021 AAAGTGCAGGACATCTCGCCTTCTATCTGGCGGCTTGAGACCAACCAAGAGTGTACT 1080
Db 1143 AAAGTGCAGGACATCTCGCCTTCTATCTGGCGGCTTGAGACCAACCAAGAGTGTACT 1202
QY 1081 GACAGTGAATTCGAGACCAAGAACTTCTGGATCGGGCTCACCTACAGACCGCCCAAGGAC 1140
Db 1203 GACAGTGAATTCGAGACCAAGAACTTCTGGATCGGGCTCACCTACAGACCGCCCAAGGAC 1262
QY 1141 TCGTTCGGCTGGCCACAGAGGAGCAGCGCTTACAGTGTTCCTTTGGGAGCGCT 1200
Db 1263 TCGTTCGGCTGGCCACAGAGGAGCAGCGCTTACAGTGTTCCTTTGGGAGCGCT 1322
QY 1201 GACAAACAGGGCTGTGTGCTGTGAGTGTGCCATGGGTTTGGCAACTGGTGGAGCTG 1260
Db 1323 GACAAACAGGGCTGTGTGCTGTGAGTGTGCCATGGGTTTGGCAACTGGTGGAGCTG 1382
QY 1261 CAGGCTTCAGCTGCCTTCAACTGGAAGCAGCAGCGCTGCAAAACCCGAAACCGTTACATC 1320
Db 1383 CAGGCTTCAGCTGCCTTCAACTGGAAGCAGCAGCGCTGCAAAACCCGAAACCGTTACATC 1442

QY 1321 TGCCAG 1326
Db 1443 TGCCAG 1448

RESULT 3
US-09-944-896-49
; Sequence 49, Application US/09944896
; Patent No. US20020168715A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,896
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998

APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944, 944
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067, 411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069, 334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 694
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PRIOR FILING DATE: December 17, 1997
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PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070, 440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075, 945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112, 850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146, 222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218, 517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254, 311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301

PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 49
LENGTH: 1876
TYPE: DNA
ORGANISM: Homo Sapien
US-09-944-944-49

Query Match 100.0%; Score 1326; DB 9; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGCATCCAGAGACCTCCCTGGCGGGGGGCATCTCTGGCTGTCTCTGGCGCCCTC 60
Db 123 ATGCTGCATCCAGAGACCTCCCTGGCGGGGGGCATCTCTGGCTGTCTCTGGCGCCCTC 182
Qy 61 CTTGGCACACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGGCTCCGATGGCC 120
Db 183 CTTGGCACACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGGCTCCGATGGCC 242
Qy 121 GGACCCCTGAACAGAGAGAGTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Db 243 GGACCCCTGAACAGAGAGAGTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 302
Qy 181 TGGGTCCAGCCCTCGCGCTGACATGGGAGGCTGGAGTGCAGAGCTGGCCCAA 240
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Qy 241 CTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCCGAGCTGGCATCCGCGCTG 300
Db 363 CTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCCGAGCTGGCATCCGCGCTG 422
Qy 301 TGGCGCACCTGCAAGTGGCTGGAACATGCAGCTGCTGCCCGGGCTTGGCGTCTTT 360
Db 423 TGGCGCACCTGCAAGTGGCTGGAACATGCAGCTGCTGCCCGGGCTTGGCGTCTTT 482
Qy 361 GTTAAAGTGTGTCAGCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACGCGCAGAGAG 420
Db 483 GTTAAAGTGTGTCAGCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACGCGCAGAGAG 542
Qy 421 TGTGCTGCAACAGCCACCTGCACCCACTACAGCGAGCTGCTGTGGGCCACCTCAAGCCAG 480
Db 543 TGTGCTGCAACAGCCACCTGCACCCACTACAGCGAGCTGCTGTGGGCCACCTCAAGCCAG 602
Qy 481 CTGGGCTGTGGGCGGCACTGTGCTCTGCAGGCCAGACAGCGATAGAAGCTTTGTCTGT 540
Db 603 CTGGGCTGTGGGCGGCACTGTGCTCTGCAGGCCAGACAGCGATAGAAGCTTTGTCTGT 662
Qy 541 GCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTTATAGAAG 600
Db 663 GCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTTATAGAAG 722
Qy 601 GGTGCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGTCTCAAGCCCTGGGACCAT 660
Db 723 GGTGCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGTCTCAAGCCCTGGGACCAT 782

QY	661	GCAGGGGGGCTCTGTGAGSTCCCAGGAATCCTTGTGCGATGAGCTGCAGAACCATGGA	720
Db	783	GCAGGGGGGCTCTGTGAGSTCCCAGGAATCCTTGTGCGATGAGCTGCAGAACCATGGA	842
QY	721	CGTCTCAACATCAGCACTGCCACTGCCACTGTCCCCCTGGCTACAGGGCAGATACTGC	780
Db	843	CGTCTCAACATCAGCACTGCCACTGCCACTGTCCCCCTGGCTACAGGGCAGATACTGC	902
QY	781	CAAGTGAGTGCAGCCTGCAGTGTGTGCAGCGCCGGTTCGGGAGGAGGAGTGCCTGCTGC	840
Db	903	CAAGTGAGTGCAGCCTGCAGTGTGTGCAGCGCCGGTTCGGGAGGAGGAGTGCCTGCTGC	962
QY	841	GNCTGTGACATCGGCTACGGGGAGCCCAAGTGTGCACCAAGTGCATTTTCCCTTCCAC	900
Db	963	GNCTGTGACATCGGCTACGGGGAGCCCAAGTGTGCACCAAGTGCATTTTCCCTTCCAC	1022
QY	901	ACCTGTGACCTGAGGATCGACGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCTAT	960
Db	1023	ACCTGTGACCTGAGGATCGACGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCTAT	1082
QY	961	TACAGAGCCAGATCAATGTGCAGAGGAAGGCGGGTGTCTGGCCCGAGATCAAGAGCCAG	1020
Db	1083	TACAGAGCCAGATCAATGTGCAGAGGAAGGCGGGTGTCTGGCCCGAGATCAAGAGCCAG	1142
QY	1021	AAAGTGCAGGACATCCTCGCCTTCTATCTGGCGCGCTGGAGACCAACACGAGGTGACT	1080
Db	1143	AAAGTGCAGGACATCCTCGCCTTCTATCTGGCGCGCTGGAGACCAACACGAGGTGACT	1202
QY	1081	GACAGTGACTTCGAGACGAGGAACCTCTGGATCGGGCTCACCTACAAGACCGCAAGGAC	1140
Db	1203	GACAGTGACTTCGAGACGAGGAACCTCTGGATCGGGCTCACCTACAAGACCGCAAGGAC	1262
QY	1141	TCCTTCGCTGGGCCACAGGGGAGCACAGGCCTTACCAAGTTTGGCCTTTGGCGAGCCT	1200
Db	1263	TCCTTCGCTGGGCCACAGGGGAGCACAGGCCTTACCAAGTTTGGCCTTTGGCGAGCCT	1322
QY	1201	GACAACACCGGGCTGGTGTGGCTGAGTCTGCGATGGGTTTGGCAACTGCGTGGAGCTG	1260
Db	1323	GACAACACCGGGCTGGTGTGGCTGAGTCTGCGATGGGTTTGGCAACTGCGTGGAGCTG	1382
QY	1261	CAGGCTTCAGTGCCTTCACTGGAACACAGCGCTGAAACCCGAAACCGTTACATC	1320
Db	1383	CAGGCTTCAGTGCCTTCACTGGAACACAGCGCTGAAACCCGAAACCGTTACATC	1442
QY	1321	TGCCAG	1326
Db	1443	TGCCAG	1448

RESULT 5
US-09-866-028-49
; Sequence 49, Application US/098666028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P2548P1C1									
; CURRENT APPLICATION NUMBER: US/09/866,028									
; CURRENT FILING DATE: 2001-05-25									
; Prior application data removed - consult PALM or file wrapper									
; NUMBER OF SEQ ID NOS: 120									
; SEQ ID NO 49									
; LENGTH: 1876									
; TYPE: DNA									
; ORGANISM: Homo Sapien									
US-09-866-028-49									
Query Match 100.0%; Score 1326; DB 10; Length 1876;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1326; Conservative 0; Mismatches 0; Indels 0; Gaps									
QY	1	ATGCTGATCCAGAGACCTCCCTGCGCGGGGGGCATCTCCTGGCTGTGCTCTGGCCCTC	182						
Db	123	ATGCTGATCCAGAGACCTCCCTGCGCGGGGGGCATCTCCTGGCTGTGCTCTGGCCCTC	182						
QY	61	CTTGGCACCACTGGCAGAGGTGTGGCCACCCAGCTGCGAGGAGAGCTCCGATGGCC	120						
Db	183	CTTGGCACCACTGGCAGAGGTGTGGCCACCCAGCTGCGAGGAGAGCTCCGATGGCC	242						
QY	121	GGAGCCCTGAACAGGAAGAGAGATTCTTGCTCTCTCCCTGTCACAAACGCTGCGCAGC	180						
Db	243	GGAGCCCTGAACAGGAAGAGAGATTCTTGCTCTCTCCCTGTCACAAACGCTGCGCAGC	302						
QY	181	TGGGTCAGCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCTTGSCCAA	240						
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QY	241	CTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCTG	300						
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QY	301	TGGCGCACCTGCAAGTGGGCTGGAACATGCAGCTGTGCCCGGGGCTTGGCGTCTTT	360						
Db	423	TGGCGCACCTGCAAGTGGGCTGGAACATGCAGCTGTGCCCGGGGCTTGGCGTCTTT	482						
QY	361	GTTGAAGTGTGAGCCTATGTTTGCAGAGGGCAGCGGTACAGCCAGCGCGCAGGAGAG	420						
Db	483	GTTGAAGTGTGAGCCTATGTTTGCAGAGGGCAGCGGTACAGCCAGCGCGCAGGAGAG	542						
QY	421	TGTGCTGCGAACGCCACCTGCACCCACTACACGAGCTCGTGTGGGCCACCTCAAGCCAG	480						
Db	543	TGTGCTGCGAACGCCACCTGCACCCACTACACGAGCTCGTGTGGGCCACCTCAAGCCAG	602						
QY	481	CTGGGCTGTGGGGGCACCTGTGCTCTGCAGGCCAGACGGATAGAGGCTTTGTCTGT	540						
Db	603	CTGGGCTGTGGGGGCACCTGTGCTCTGCAGGCCAGACGGATAGAGGCTTTGTCTGT	662						
QY	541	GCTTACTCCCGGGAGCACTGGGAGGTCAACGGGAAGACAATCATCCCTATACGAAG	600						
Db	663	GCTTACTCCCGGGAGCACTGGGAGGTCAACGGGAAGACAATCATCCCTATACGAAG	722						
QY	601	GGTGGCTGTGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAGCCCTGGGACCAT	660						
Db	723	GGTGGCTGTGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAGCCCTGGGACCAT	782						
QY	661	GCAGGGGGGCTGTGAGGTGCCCCAGGAATCTTGTGCGATGAGCTGCCAGAACCATGGA	720						
Db	783	GCAGGGGGGCTGTGAGGTGCCCCAGGAATCTTGTGCGATGAGCTGCCAGAACCATGGA	842						
QY	721	CGTCTCAACATCAGACCTGCCACTGCCACTGTCCCTTGGGTACAGGGCAGACTGTC	780						
Db	843	CGTCTCAACATCAGACCTGCCACTGCCACTGTCCCTTGGGTACAGGGCAGACTGTC	902						
QY	781	CAAGTGAAGTGCAGCTGTGTGCACAGCCGGTTCGCGGAGGAGGAGTCTCGTGC	840						
Db	903	CAAGTGAAGTGCAGCTGTGTGCACAGCCGGTTCGCGGAGGAGGAGTCTCGTGC	962						
QY	841	GTCTGTGACATCGGCTACGGGGAGCCCAAGTGTGCCACCAAGGTGATTTTCCCTTCCAC	900						

Mon Dec 30 09:16:17 2002

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Db 963 GTCTGTGACATCGGCTACGGGGGAGCCACAGTGTGCCACCAAGAGTGCAATTTCCCTTCAC 1022
Qy 901 ACCTGTGACTGAGGATCGACGAGACTGCTTCTATGTTGTCTTCAGAGGCGACACACCTAT 960
Db 1023 ACCTGTGACTGAGGATCGACGAGACTGCTTCTATGTTGTCTTCAGAGGCGACACACCTAT 1082
Qy 961 TACAGAGCCAGGATGAATGTCAGAGAAAGCGGGGTGCTGGCCAGATCAAGAGCCAG 1020
Db 1083 TACAGAGCCAGGATGAATGTCAGAGAAAGCGGGGTGCTGGCCAGATCAAGAGCCAG 1142
Qy 1021 AAAGTCAGACATCTCGCTTCTATCTGGCCGCTGGAGACACCAACGAGGTGACT 1080
Db 1143 AAAGTCAGACATCTCGCTTCTATCTGGCCGCTGGAGACACCAACGAGGTGACT 1202
Qy 1081 GACAGTCACTTCGAGACCAAGAACTTCTGGATCGGGCTCACCTACAAGACCCGCAAGGAC 1140
Db 1203 GACAGTCACTTCGAGACCAAGAACTTCTGGATCGGGCTCACCTACAAGACCCGCAAGGAC 1262
Qy 1141 TCCTTCGCTGGGCCACAGGGGAGACACAGGCTTCACAGTTTGGCTTGGGCGAGCCT 1200
Db 1263 TCCTTCGCTGGGCCACAGGGGAGACACAGGCTTCACAGTTTGGCTTGGGCGAGCCT 1322
Qy 1201 GACAAACACGGCTGGTGTGCTGAGTGTGCTGATGGGCTTGGCAACTGCGTGGAGCTG 1260
Db 1323 GACAAACACGGCTGGTGTGCTGAGTGTGCTGATGGGCTTGGCAACTGCGTGGAGCTG 1382
Qy 1261 CAGGCTTCAGCTGCTTCAACTGGAACGACGAGCGGTGCAAAACCCGCAACCGTTTACATC 1320
Db 1383 CAGGCTTCAGCTGCTTCAACTGGAACGACGAGCGGTGCAAAACCCGCAACCGTTTACATC 1442
Qy 1321 TGCCAG 1326
Db 1443 TGCCAG 1448

RESULT 6
US-09-944-449-49
; Sequence 49, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944, 449
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866, 028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067, 411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069, 334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 425
; PRIOR FILING DATE: December 12, 1997
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; PRIOR APPLICATION NUMBER: 60/069, 696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069, 873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068, 017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070, 440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074, 086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074, 092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075, 945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112, 850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113, 296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146, 222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216, 021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218, 517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254, 311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-449-49

Query Match 100.0%; Score 1326; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
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Matches 1326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 183 CTTGGCACCACCTGGCAGAGTGTGGCCACCCACAGCTGAGAGAGAGGCTCCGATGGCC 242
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Db 243 GGAGCCCTGAACAGGAAGAGAGATTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 302
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QY 241 CTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCNACCAGCTGAGCTGAGCCCTG 300
Db 363 CTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCNACCAGCTGAGCTGAGCCCTG 422
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QY 361 GTTGAAGTGTGAGCCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACCGCGCAGGAG 420
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QY 541 GCCTACTCCCGCGAGGCACTGGAGGTCAACGGGAAGACAATCATCCCTTAAAGAG 600
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QY 1201 GACAACACCGGCTGGTGTGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
Db 1323 GACAACACCGGCTGGTGTGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1382
QY 1261 CAGGCTTCAGCTGCTTCACTGGAACGACGAGCTGCAAAACCGGAAACCGTTTACATC 1320
Db 1383 CAGGCTTCAGCTGCTTCACTGGAACGACGAGCTGCAAAACCGGAAACCGTTTACATC 1442
QY 1321 TGCCAG 1326
Db 1443 TGCCAG 1448
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RESULT 7

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US-09-944-457-49
; Sequence 49, Application US/09944457
; Patent No. US20020110859A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/09/944,457
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
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1 PRIOR FILING DATE: January 5, 1998
2 PRIOR APPLICATION NUMBER: 60/074,086
3 PRIOR FILING DATE: February 9, 1998
4 PRIOR APPLICATION NUMBER: 60/074,092
5 PRIOR FILING DATE: February 9, 1998
6 PRIOR APPLICATION NUMBER: 60/075,945
7 PRIOR FILING DATE: February 25, 1998
8 PRIOR APPLICATION NUMBER: 60/112,850
9 PRIOR FILING DATE: December 16, 1998
10 PRIOR APPLICATION NUMBER: 60/113,296
11 PRIOR FILING DATE: December 22, 1998
12 PRIOR APPLICATION NUMBER: 60/146,222
13 PRIOR FILING DATE: July 28, 1999
14 PRIOR APPLICATION NUMBER: PCT/US98/19330
15 PRIOR FILING DATE: September 16, 1998
16 PRIOR APPLICATION NUMBER: PCT/US98/25108
17 PRIOR FILING DATE: December 1, 1998
18 PRIOR APPLICATION NUMBER: 09/216,021
19 PRIOR FILING DATE: December 16, 1998
20 PRIOR APPLICATION NUMBER: 09/218,517
21 PRIOR FILING DATE: December 22, 1998
22 PRIOR APPLICATION NUMBER: 09/254,311
23 PRIOR FILING DATE: March 3, 1999
24 PRIOR APPLICATION NUMBER: PCT/US99/12252
25 PRIOR FILING DATE: June 22, 1999
26 PRIOR APPLICATION NUMBER: PCT/US99/21090
27 PRIOR FILING DATE: September 15, 1999
28 PRIOR APPLICATION NUMBER: PCT/US99/28409
29 PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
30 PRIOR APPLICATION NUMBER: PCT/US99/28313
31 PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
32 PRIOR APPLICATION NUMBER: PCT/US99/28301
33 PRIOR FILING DATE: December1, 1999
34 PRIOR APPLICATION NUMBER: PCT/US99/30095
35 PRIOR FILING DATE: December 16, 1999
36 PRIOR APPLICATION NUMBER: PCT/US00/03565
37 PRIOR FILING DATE: February 11, 2000
38 PRIOR APPLICATION NUMBER: PCT/US00/04414
39 PRIOR FILING DATE: February 22, 2000
40 PRIOR APPLICATION NUMBER: PCT/US00/05841
41 PRIOR FILING DATE: March 2, 2000
42 PRIOR APPLICATION NUMBER: PCT/US00/08439
43 PRIOR FILING DATE: March 30, 2000
44 PRIOR APPLICATION NUMBER: PCT/US00/14042
45 PRIOR FILING DATE: May 22, 2000
46 PRIOR APPLICATION NUMBER: PCT/US00/20710
47 PRIOR FILING DATE: July 28, 2000
48 PRIOR APPLICATION NUMBER: PCT/US00/32678
49 PRIOR FILING DATE: December 1, 2000
50 PRIOR APPLICATION NUMBER: PCT/US01/06520
51 PRIOR FILING DATE: February 28, 2001
52 NUMBER OF SEQ ID NOS: 120
53 SEQ ID NO 49
54 LENGTH: 1876
55 TYPE: DNA
56 ORGANISM: Homo Sapien
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Qy	121	GGAGCCCTGAACAGAGGAGAGTTCTTGCTCTCTCCCTGCACAAACCGGCTGGGCAGC	180		
Db	243	GGAGCCCTGAACAGAGGAGAGTTCTTGCTCTCTCCCTGCACAAACCGGCTGGGCAGC	302		

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QY	241	CTGGCTCAAGCCAGGCGAGCCCTCTGTGGAAATCCAAACCCGAGGCTGGCATCCGGCCTG	300
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QY	301	TGGCGCACCCCTGCAAGTGGGCTGGAACATGACGTGCTGCCCGCGGGCTTGGCGTCCTTT	360
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QY	361	GTTGAAGTGTGTAGCCTATGGTTTTCAGAGGGCGAGCGGTACAGCCAGCGGCAGAGAG	420
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QY	421	TGTGCTCGCAAGCGCACCTGCAACCACTACACGCAAGCTCGTGTGGGCCACCTCAAGCCAG	480
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QY	481	CTGGGCTGTGGGGGCACTGTGCTCTCAGGCCAGACAGCATAGAAAGCCTTTGTCTGT	540
Db	603	CTGGGCTGTGGGGGCACTGTGCTCTCAGGCCAGACAGCATAGAAAGCCTTTGTCTGT	662
QY	541	GCCTACTCCCGGAGGCAACTGGGAGTCTACGGGAAGACAAATCATCCCTATAAGAAG	600
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QY	601	GGTGCCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGTGCTTCAAAGCCTGGGACAT	660
Db	723	GGTGCCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGTGCTTCAAAGCCTGGGACAT	782
QY	661	GCAGGGGGGCTCTGTGAGGTCCCAAGGAATCCTGTCTGCATGAGCTGCCAGAACCATGGA	720
Db	783	GCAGGGGGGCTCTGTGAGGTCCCAAGGAATCCTGTCTGCATGAGCTGCCAGAACCATGGA	842
QY	721	CGTCTCAACATCAGCACCTGCCACTGTCCCACTGTCCCCCTGGCTACAGGGGAGATATGTC	780
Db	843	CGTCTCAACATCAGCACCTGCCACTGTCCCACTGTCCCCCTGGCTACAGGGGAGATATGTC	902
QY	781	CAAGTGAGGTGAGGCTGAGTGTGTGCACGCGCGGTTCGGGAGGAGGAGTGTCTGTGC	840
Db	903	CAAGTGAGGTGAGGCTGAGTGTGTGCACGCGCGGTTCGGGAGGAGGAGTGTCTGTGTG	962
QY	841	GTCGTGACATCGGTACGGGGAGCCCAAGTGTGCCACCAAGGTGCATTTTCCCTTCCAC	900
Db	963	GTCGTGACATCGGTACGGGGAGCCCAAGTGTGCCACCAAGGTGCATTTTCCCTTCCAC	1022
QY	901	ACCTGTGACCTGAGGATCGACGGAGCTGCTTCATGGTGTCTCAGAGGCAGACACCTAT	960
Db	1023	ACCTGTGACCTGAGGATCGACGGAGCTGCTTCATGGTGTCTCAGAGGCAGACACCTAT	1082
QY	961	TACAGAGCCAGGATCAATGTCCAGGAAGGCGGGTGTGGCCCAAGTCAAGAGCCAG	1020
Db	1083	TACAGAGCCAGGATCAATGTCCAGGAAGGCGGGTGTGGCCCAAGTCAAGAGCCAG	1142
QY	1021	AAAGTGCAAGGACATCCTCGCCCTTCTATCTGGGCGGCTGGAGACCAACAGAGTGACT	1080
Db	1143	AAAGTGCAAGGACATCCTCGCCCTTCTATCTGGGCGGCTGGAGACCAACAGAGTGACT	1202
QY	1081	GACAGTGACTTCGAGACACAGGAACCTTCTGGATCGGGCTCACTACAGACCGCCAAAGAC	1140
Db	1203	GACAGTGACTTCGAGACACAGGAACCTTCTGGATCGGGCTCACTACAGACCGCCAAAGAC	1262
QY	1141	TCCTTTCGGCTGGCCACAGGGGAGCACAGGCGCTTCACCACTTTTGGCAGCCT	1200
Db	1263	TCCTTTCGGCTGGCCACAGGGGAGCACAGGCGCTTCACCACTTTTGGCAGCCT	1322
QY	1201	GACACCAAGGCTGTGTGGCTGAGTGCTGCCATGGGTTTGGCAACTCGGTGGAGCTG	1260
Db	1323	GACACCAAGGCTGTGTGGCTGAGTGCTGCCATGGGTTTGGCAACTCGGTGGAGCTG	1382

Qy 1261 CAGGCTTCAGCTGCCTTCAACTGGAACGACGCGCTGCAAAACCCGAAACCGTTACATC 1320
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Db 1393 CAGGCTTCAGCTGCCTTCAACTGGAACGACGCGCTGCAAAACCCGAAACCGTTACATC 1442
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Qy 1321 TGCCAG 1326
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Db 1443 TGCCAG 1448

RESULT 8

US-09-945-587-49
; Sequence 49, Application US/09945587
; Patent No. US20020127643A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Bolstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999

; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-09-945-587-49

Query Match 100.0%; Score 1326; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGCATCCAGAGACCTCCCTGGCGGGGGCATCTCCTGGCTGTGCTTCCTGGCCCTC 60
|||||
Db 123 ATGCTGCATCCAGAGACCTCCCTGGCGGGGGCATCTCCTGGCTGTGCTTCCTGGCCCTC 182
Qy 61 CTTGGCACACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGAGGCTCCGATGGCC 120
|||||
Db 183 CTTGGCACACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGAGGCTCCGATGGCC 242
Qy 121 GGAGCCCTCAACAGAGGAGAGTTCCTCCTCCTCCCTGCACACCCCTGGCGAGC 180
|||||
Db 243 GGAGCCCTCAACAGAGGAGAGTTCCTCCTCCTCCCTGCACACCCCTGGCGAGC 302
Qy 181 TGGGTCACAGCCCTCGCGCTGACATGCGGAGGCTGGAGTGGAGTGAAGCTGGCCCAA 240
|||||
Db 303 TGGGTCACAGCCCTCGCGCTGACATGCGGAGGCTGGAGTGAAGTGAAGCTGGCCCAA 362
Qy 241 CTTGGTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCGAGCTGGGATCCGGCTG 300
Db 363 CTTGGTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCGAGCTGGGATCCGGCTG 422
Qy 301 TGGCGCACCTGCAAGTGGGCTGGAACATGACAGTGTGCTGCGCGGCTGGCGCTCTTT 360
|||||
Db 423 TGGCGCACCTGCAAGTGGGCTGGAACATGACAGTGTGCTGCGCGGCTGGCGCTCTTT 482

QY	361	GTGTAAGTGGTGACGCTATGGTTGTGAGAGGGCAGCGGTACAGCCACGGCGAGAGAG	420
DB	483	GTGTAAGTGGTGACGCTATGGTTGTGAGAGGGCAGCGGTACAGCCACGGCGAGAGAG	542
QY	421	TCGTGCTCGCAAGCCACCTGCAACCCACTACACGACGCTCGTGTGGGCCACTCAAGCCAG	480
DB	543	TGTGCTCGCAAGCCACCTGCAACCCACTACACGACGCTCGTGTGGGCCACTCAAGCCAG	602
QY	481	CTGGGCTGTGGCGGCAACTGTGCTCTGCAAGGCCACAGCGATAGAAGCCTTTGCTGT	540
DB	603	CTGGGCTGTGGCGGCAACTGTGCTCTGCAAGGCCACAGCGATAGAAGCCTTTGCTGT	662
QY	541	GCTACTCTCCCGGAGGCAACTGGGAGGTCAACGGGAAGCAATCATCCTCCCTATAAGAAG	600
DB	663	GCCTACTCCCGGAGGCAACTGGGAGGTCAACGGGAAGCAATCATCCTCCCTATAAGAAG	722
QY	601	GGTGCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTTCAAAGCCTGGGACCAT	666
DB	723	GGTGCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTTCAAAGCCTGGGACCAT	782
QY	661	GCAGGGGGCTCTGTGAGTCCCCAGGAATCTTGTGCGATGAGCTGCACAGACCATGGA	720
DB	783	GCAGGGGGCTCTGTGAGTCCCCAGGAATCTTGTGCGATGAGCTGCACAGACCATGGA	842
QY	721	CGTCTCAACATCAGCACACCTGCCACTGCCACTGTCCCCCTGGCTTACAGGGCAGATACTGC	780
DB	843	CGTCTCAACATCAGCACACCTGCCACTGCCACTGTCCCCCTGGCTTACAGGGCAGATACTGC	902
QY	781	CAAGTGAGGTGCAGCTCGAGTGTGTCAGCGCCGGTTCGGGAGAGAGAGTGCTCGTGC	840
DB	903	CAAGTGAGGTGCAGCTCGAGTGTGTCAGCGCCGGTTCGGGAGAGAGAGTGCTCGTGC	962
QY	841	GCTGTGACATGGCTACGGGGAGCCCAAGTGTGCCACCAAGTGCTATTTCCCTTTCCAC	900
DB	963	GCTGTGACATGGCTACGGGGAGCCCAAGTGTGCCACCAAGTGCTATTTCCCTTTCCAC	1022
QY	901	ACCTGTGACCTGAGGATCGACGGAGCTCTTCATGGTGTCTTCAGAGGCGAGACCTTAT	960
DB	1023	ACCTGTGACCTGAGGATCGACGGAGCTCTTCATGGTGTCTTCAGAGGCGAGACCTTAT	1082
QY	961	TACAGAGCCAGGATGAATGTACAGGAAAGCGGGGTGCTGGCCAGATCAAGAGCCAG	1020
DB	1083	TACAGAGCCAGGATGAATGTACAGGAAAGCGGGGTGCTGGCCAGATCAAGAGCCAG	1142
QY	1021	AAAGTGCAGGACATCTCGCTTCTATCTGGCCGCTTGGAGCCACCAACGAGTGTACT	1080
DB	1143	AAAGTGCAGGACATCTCGCTTCTATCTGGCCGCTTGGAGCCACCAACGAGTGTACT	1202
QY	1081	GACAGTGACTTCGAGACCAAGGAATCTTGGATCGGGCTCACCTACAAGACCGCAAGGAC	1140
DB	1203	GACAGTGACTTCGAGACCAAGGAATCTTGGATCGGGCTCACCTACAAGACCGCAAGGAC	1262
QY	1141	TCCTTCCGCTGGGCCACAGGGAGCACAGGCTTTCACCAAGTTTTCCTTTGGGACGCT	1200
DB	1263	TCCTTCCGCTGGGCCACAGGGAGCACAGGCTTTCACCAAGTTTTCCTTTGGGACGCT	1322
QY	1201	GACAACCAAGGCTGGTGTGCTGAGTGTCTGCCATGGGTTTGGCAACTTCGCTGGAGCTG	1260
DB	1323	GACAACCAAGGCTGGTGTGCTGAGTGTCTGCCATGGGTTTGGCAACTTCGCTGGAGCTG	1382
QY	1261	CAGGCTTCAGTGCTCTCAACTGGACACAGCGCTGCANACCGGAACCGTTTACATC	1320
DB	1383	CAGGCTTCAGTGCTCTCAACTGGACACAGCGCTGCANACCGGAACCGTTTACATC	1442
QY	1321	TGCCAG	1326
DB	1443	TGCCAG	1448

RESULT 9
US-09-945-015-49 : Sequence 49, Application US/09945015
: Patent No. US20020132768A1

: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12352
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-09-945-015-49

Query Match 100.0%; Score 1326; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGCATCCAGAGACCTCCCTCGCCGGGGGCGATCTCTGGGTGTCCTCGCCCTC 60
Db 123 ATGCTGCATCCAGAGACCTCCCTCGCCGGGGGCGATCTCTGGGTGTCCTCGCCCTC 182

QY 61 CTGGCCACCACTGGGCGAGAGGTTGGCCACCCAGCTGCAGGAGAGGCTCCGATGCC 120
Db 183 CTGGCCACCACTGGGCGAGAGGTTGGCCACCCAGCTGCAGGAGAGGCTCCGATGCC 242

QY 121 GGAGCCCTGAACAGGAGAGGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Db 243 GGAGCCCTGAACAGGAGAGGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 302

QY 181 TGGGTCCAGCCCTCGGCTGACATGCGAGGCTGGAGTGGAGTGCAGAGCTGGCCCAA 240
Db 303 TGGGTCCAGCCCTCGGCTGACATGCGAGGCTGGAGTGGAGTGCAGAGCTGGCCCAA 362

QY 241 CTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCTG 300
Db 363 CTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCTG 422

QY 301 TGGCGCACCTTGAAGTGGGCTGGAACATGCAGTGTCTGCGCGGGCTTGGCGTCTCTTT 360
Db 423 TGGCGCACCTTGAAGTGGGCTGGAACATGCAGTGTCTGCGCGGGCTTGGCGTCTCTTT 482

QY 361 GTTGAAGTGGTACGCTATGTTTGCAGAGGCGGAGCGGTACAGCCACGGGCGAGAGAG 420
Db 483 GTTGAAGTGGTACGCTATGTTTGCAGAGGCGGAGCGGTACAGCCACGGGCGAGAGAG 542

QY 421 TGTGCTCGAAGCCACCTCTGACCCACTACACGAGCTGCTGTGGGCGACCTCAAGCCAG 480
Db 543 TGTGCTCGAAGCCACCTCTGACCCACTACACGAGCTGCTGTGTGGGCGACCTCAAGCCAG 602

QY 481 CTGGGCTGTGGGCGGACCTGTCTCTGAGGCGCAGACGATAGAGAGCTTTGTCTGT 540
Db 603 CTGGGCTGTGGGCGGACCTGTCTCTGAGGCGCAGACGATAGAGAGCTTTGTCTGT 662

QY 541 GCTACTCCCCGGAGGCAACTGGAGGTCAACGGGAAGACAATCATCCCTCATAGAAG 600

Db 663 GCTTACTCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTCATAGAAG 722
QY 601 GTTGCTGTGTGTGCTGTGCACAGCCAGTGTCTCAGGCTGCTTCAAGGCTGGGACCAT 660
Db 723 GGTGCTGTGTGTGCTGTGCACAGCCAGTGTCTCAGGCTGCTTCAAGGCTGGGACCAT 782
QY 661 GCAGGGGGGCTCTGTGAGGTCCCGAGGAATCCCTTGTGCGATGAGTGCAGGCGCAGATGGA 720
Db 783 GCAGGGGGGCTCTGTGAGGTCCCGAGGAATCCCTTGTGCGATGAGTGCAGGCGCAGATGGA 842
QY 721 CGTCTCAACATCAGCACCTGCTCCACTGCTCCCTGCTCCCTGCTACAGGCGCAGATGTC 780
Db 843 CGTCTCAACATCAGCACCTGCTCCACTGCTCCCTGCTCCCTGCTACAGGCGCAGATGTC 902
QY 781 CAAGTGTGAGTGTGAGTGTGTCAGGCGGCTGTCAGGCGGCTTCCGGGAGGAGTGTCTGTC 840
Db 903 CAAGTGTGAGTGTGAGTGTGTCAGGCGGCTTCCGGGAGGAGTGTCTGTCGTCGTC 962
QY 841 GTCTGTGATCATCGGCTACGGGGAGCCAGTGTGCCACCAAGGTGCAATTTTCCCTTCCAC 900
Db 963 GTCTGTGATCATCGGCTACGGGGAGCCAGTGTGCCACCAAGGTGCAATTTTCCCTTCCAC 1022
QY 901 ACCTGTGACCTGAGGATCGACGAGAGTGTCTTCAATGCTGTCTTCAAGGCGCAGACCTAT 960
Db 1023 ACCTGTGACCTGAGGATCGACGAGAGTGTCTTCAATGCTGTCTTCAAGGCGCAGACCTAT 1082
QY 961 TACAGAGCCAGGATGAATGTGAGAGGAAGGCGGGGTGCTGCCCGAGATCAAGAGCCAG 1020
Db 1083 TACAGAGCCAGGATGAATGTGAGAGGAAGGCGGGGTGCTGCCCGAGATCAAGAGCCAG 1142
QY 1021 AAAGTGCAGGACATCTCGCCTTCTATCTGGGCGGCTGGAGACCACCAACGAGGTGACT 1080
Db 1143 AAAGTGCAGGACATCTCGCCTTCTATCTGGGCGGCTGGAGACCACCAACGAGGTGACT 1202
QY 1081 GACAGTGTCTCGAGACCAGGAACCTTCTTGATCGGGCTACCTTACAGAGCCGCGCAAGGAC 1140
Db 1203 GACAGTGTCTCGAGACCAGGAACCTTCTTGATCGGGCTACCTTACAGAGCCGCGCAAGGAC 1262
QY 1141 TCCTTCCGCTGGCCACAGGGGAGCAGGCGCTTCAACAGTGTGCTTGGGCGAGCCT 1200
Db 1263 TCCTTCCGCTGGCCACAGGGGAGCAGGCGCTTCAACAGTGTGCTTGGGCGAGCCT 1322
QY 1201 GACAAACCGGCTGGTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
Db 1323 GACAAACCGGCTGGTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1382
QY 1261 CAGGCTTACGCTGCTTCAACTTGAACGAGCAGGCGCTGCAAAACCCGAAACCGTTACATC 1320
Db 1383 CAGGCTTACGCTGCTTCAACTTGAACGAGCAGGCGCTGCAAAACCCGAAACCGTTACATC 1442
QY 1321 TGCCAG 1326
Db 1443 TGCCAG 1448

RESULT 10
US-09-944-396-49
; Sequence 49, Application US/09944396
; Patent No. US20020132981A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar

Db 1263 TCCTTCGGCTGGGCCACACAGGGGAGCAGCGCTTACCAGCTTTTGCCTTTGGGAGCCT 1322
QY 1201 GACAACACAGGGCTGGTGTGGCTGAGTGTGCTGCCATGGGTTTGGCAACTGCGTGGAGCTG 1260
Db 1323 GACAACACAGGGCTGGTGTGGCTGAGTGTGCTGCCATGGGTTTGGCAACTGCGTGGAGCTG 1382
QY 1261 CAGGCTTCAGCTGCTTCACTGAACAGCAGCGCTGCAAAACCCGAAACCGTTACATC 1320
Db 1383 CAGGCTTCAGCTGCTTCACTGAACAGCAGCGCTGCAAAACCCGAAACCGTTACATC 1442
QY 1321 TGCCAG 1326
Db 1443 TGCCAG 1448

RESULT 13
US-09-943-762-49
; Sequence 49, Application US/09943762
; Patent No. US20020142958A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Flivauroff, Ellen
; APPLICANT: Gerriksen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/943,762
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
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; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998

; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
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; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
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; PRIOR APPLICATION NUMBER: 09/218,517
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; PRIOR FILING DATE: June 22, 1999
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; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
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; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
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; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-943-762-49
Query Match 100.0%; Score 1326; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGTCATCCAGAGACCTCCCTGGCGGGGGGATCTCTGGCTGTCTCTCTGGCCCTC 60
Db 123 ATGCTGTCATCCAGAGACCTCCCTGGCGGGGGGATCTCTGGCTGTCTCTCTGGCCCTC 182
QY 61 CTGTGGCACCACTGGGACAGAGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCC 120
Db 183 CTGTGGCACCACTGGGACAGAGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCC 242
QY 121 GGAGCCCTGAACAGAGAGAGTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Db 243 GGAGCCCTGAACAGAGAGAGTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 302
QY 181 TGGTCTCAGCCCTCCCTGGCGGCTGACATGGGAGCTGGACTGGAGTGCACACCTGGCCAA 240
Db 303 TGGTCTCAGCCCTCCCTGGCGGCTGACATGGGAGCTGGAGTGCACACCTGGCCAA 362
QY 241 CTGCTCAAGCAGGAGGAGCCCTCTGTGGAATCCCAACCCGAGCTGGATCCGGCTG 300

Db	363	CTGCTCAAGCCAGGGAGGCCCTCTGTGGAATCCCAACCCGAGAGCTGGCATCCGCGCTG	429
QY	301	TGGCGCACCTCTGCAAGTGGGCTGAAACATGACAGCTGTGTGCCCGGGGCTTGGCGTCCCTTT	360
Db	423	TGGCGCACCTCTGCAAGTGGGCTGAAACATGACAGCTGTGTGCCCGGGGCTTGGCGTCCCTTT	482
QY	361	GTTGAAGTGTGAGCCTATGGTTTGCAGAGGGGACAGGGTACAGCCACCGCGCAGGAGAG	420
Db	483	GTTGAAGTGTGAGCCTATGGTTTGCAGAGGGGACAGGGTACAGCCACCGCGCAGGAGAG	542
QY	421	TGTGCTCGCAACGCCACCTCGACCCACTACAGCAGCTCGTGTGGGGCACTCAAGCCAG	480
Db	543	TGTGCTCGCAACGCCACCTCGACCCACTACAGCAGCTCGTGTGGGGCACTCAAGCCAG	602
QY	481	CTGGGCTGTGGGCGGACCTGTGCTCTGCAGGCGCAGACAGCATAGAAAGCCTTTGTCTGT	540
Db	603	CTGGGCTGTGGGCGGACCTGTGCTCTGCAGGCGCAGACAGCATAGAAAGCCTTTGTCTGT	662
QY	541	GCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTATATAAGAG	600
Db	663	GCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTATATAAGAG	722
QY	601	GGTGCTGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAGCCTGGGACCAT	660
Db	723	GGTGCTGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAGCCTGGGACCAT	782
QY	661	GCAGGGGGCTCTGTGAGTGTCCCGAGGAATCCTTGTGCATGAGCTGCCAGAACCATGGA	720
Db	783	GCAGGGGGCTCTGTGAGTGTCCCGAGGAATCCTTGTGCATGAGCTGCCAGAACCATGGA	842
QY	721	CGCTTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTTGGCTTACAGGSCAGATACTGC	780
Db	843	CGCTTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTTGGCTTACAGGSCAGATACTGC	902
QY	781	CAAGTGAGGTGCAGCGCTGCAGTGTGTGCACGGCCGGTTCGGGAGAGGAGTCTCGTGC	840
Db	903	CAAGTGAGGTGCAGCGCTGCAGTGTGTGCACGGCCGGTTCGGGAGAGGAGTCTCGTGC	962
QY	841	GTCCTGTACATCGGCTACGGGGAGCCCACTGTGCCACCAAGGTGCTATTTCCCTTCCAC	900
Db	963	GTCCTGTACATCGGCTACGGGGAGCCCACTGTGCCACCAAGGTGCTATTTCCCTTCCAC	1022
QY	901	ACCTGTGACCTGAGGATCGACGGAGCTGCTTCATGGTCTTTCAGAGGCGACACCTAT	960
Db	1023	ACCTGTGACCTGAGGATCGACGGAGCTGCTTCATGGTCTTTCAGAGGCGACACCTAT	1082
QY	961	TACAGAGCCAGATGAATGTTCAGAGGAAGGCGGGGCTGTGCCCCAGATCAAGAGCCAG	1020
Db	1083	TACAGAGCCAGATGAATGTTCAGAGGAAGGCGGGGCTGTGCCCCAGATCAAGAGCCAG	1142
QY	1021	AAAGTGCAGGACATCTCGCCTTCTATCTGGGCCGCTGGAGACCAACAGAGTGACT	1080
Db	1143	AAAGTGCAGGACATCTCGCCTTCTATCTGGGCCGCTGGAGACCAACAGAGTGACT	1202
QY	1081	GACAGTGACTTCGAGACCCAGGAATTCCTGGATCGGGCTCACTCAAGACCCCAAGGAC	1140
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QY	1141	TCCTTCGCTGGGCCACAGGGGACGACAGGCTTCACAGTTTTTGCCTTTGGGAGGCT	1200
Db	1263	TCCTTCGCTGGGCCACAGGGGACGACAGGCTTCACAGTTTTTGCCTTTGGGAGGCT	1322
QY	1201	GACAACCAACGGCTGTGTGTGCTGAGTGTGCCATGGGTTTGGCACTGGTGGAGGTG	1260
Db	1323	GACAACCAACGGCTGTGTGTGCTGAGTGTGCCATGGGTTTGGCACTGGTGGAGGTG	1382
QY	1261	CAGGCTTCACTGCCCTTCAACTGGAAGACACAGCGCTGCAAAACCCGAAACCGTTACATC	1320
Db	1383	CAGGCTTCACTGCCCTTCAACTGGAAGACACAGCGCTGCAAAACCCGAAACCGTTACATC	1442
QY	1321	TGCCAG	1326
Db	1443	TGCCAG	1448

		PRIORITY FILING DATE: December 22, 1998			
		PRIORITY APPLICATION NUMBER: 09/254,311			
		PRIORITY FILING DATE: March 3, 1999			
		PRIORITY APPLICATION NUMBER: PCT/US99/12252			
		PRIORITY FILING DATE: June 22, 1999			
		PRIORITY APPLICATION NUMBER: PCT/US99/21090			
		PRIORITY FILING DATE: September 15, 1999			
		PRIORITY APPLICATION NUMBER: PCT/US99/28409			
		PRIORITY FILING DATE: No. US20020142959A1ember 30, 1999			
		PRIORITY APPLICATION NUMBER: PCT/US99/28313			
		PRIORITY FILING DATE: No. US20020142959A1ember 30, 1999			
		PRIORITY APPLICATION NUMBER: PCT/US99/28301			
		PRIORITY FILING DATE: December 1, 1999			
		PRIORITY APPLICATION NUMBER: PCT/US99/30095			
		PRIORITY FILING DATE: December 16, 1999			
		PRIORITY APPLICATION NUMBER: PCT/US00/03565			
		PRIORITY FILING DATE: February 11, 2000			
		PRIORITY APPLICATION NUMBER: PCT/US00/04414			
		PRIORITY FILING DATE: February 22, 2000			
		PRIORITY APPLICATION NUMBER: PCT/US00/05841			
		PRIORITY FILING DATE: March 2, 2000			
		PRIORITY APPLICATION NUMBER: PCT/US00/08439			
		PRIORITY FILING DATE: March 30, 2000			
		PRIORITY APPLICATION NUMBER: PCT/US00/14042			
		PRIORITY FILING DATE: May 22, 2000			
		PRIORITY APPLICATION NUMBER: PCT/US00/20710			
		PRIORITY FILING DATE: July 28, 2000			
		PRIORITY APPLICATION NUMBER: PCT/US00/32678			
		PRIORITY FILING DATE: December 1, 2000			
		PRIORITY APPLICATION NUMBER: PCT/US01/06520			
		PRIORITY FILING DATE: February 28, 2001			
		NUMBER OF SEQ ID NOS: 120			
		SEQ ID NO 49			
		LENGTH: 1876			
		TYPE: DNA			
		ORGANISM: Homo Sapien			
		US-09-944-654-49			
		Query Match 100.08; Score 1326; DB 10; Length 1876;			
		Best Local Similarity 100.08; Pred. No. 0;			
		Matches 1326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGTCGATCCAGAGACCTCCCTGGCGGGGGGCACTCTCTGGCTGTGTCTCTGGCCCTC	60		
DB	123	ATGTCGATCCAGAGACCTCCCTGGCGGGGGGCACTCTCTGGCTGTGTCTCTGGCCCTC	182		
QY	61	CTTGACACACCTGGCGAGAGTGTGGCCACCCAGCTGACGAGCAGGCTCCGATGCC	120		
DB	183	CTTGACACACCTGGCGAGAGTGTGGCCACCCAGCTGACGAGCAGGCTCCGATGCC	242		
QY	121	GGAGCCCTGAACAGGAGAGAGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	180		
DB	243	GGAGCCCTGAACAGGAGAGAGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	302		
QY	181	TGGGTCCAGCCCTCGGCTGACATCGGAGGCTGAGCTGAGTGTGACAGCTGGCCCAA	240		
DB	303	TGGGTCCAGCCCTCGGCTGACATCGGAGGCTGAGCTGAGTGTGACAGCTGGCCCAA	362		
QY	241	CTGGCTCAAGCAGGAGCCCTCTGTGGAATCCCAACCCGAGCTGGCATCCGGCCCTG	300		
DB	363	CTGGCTCAAGCAGGAGCCCTCTGTGGAATCCCAACCCGAGCTGGCATCCGGCCCTG	422		
QY	301	TGGCGCACCCTGCAAGTGGGCTGGAACATGACATGCTGTGCTGCTGCTGCTGCTGCTG	360		
DB	423	TGGCGCACCCTGCAAGTGGGCTGGAACATGACATGCTGTGCTGCTGCTGCTGCTGCTG	482		
QY	361	GTTGAAGTGTGACCTATGTTTGGAGAGGCGGAGCTGACAGCAGCGCAGAGAG	420		
DB	483	GTTGAAGTGTGACCTATGTTTGGAGAGGCGGAGCTGACAGCAGCGCAGAGAG	542		
QY	421	TGTGCTCGCAACGCCACTCTGACCCACTTACAGCAGCTGTGTGTGGGCCACCTCAAGCC	480		
DB	543	TGTGCTCGCAACGCCACTCTGACCCACTTACAGCAGCTGTGTGTGGGCCACCTCAAGCC	602		

RESULT 15

US-09-943-851A-49
; Sequence 49, Application US/09943851A
; Patent No. US20020150976A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary

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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 16:48:37 ; Search time 9.88286 Seconds
(without alignments)
7664.597 Million cell updates/sec

Title: US-09-944-896-49_COPY_201_447

Perfect score: 247

Sequence: 1 gaggtgtggcaccacagct.....cacctgcgaagtggctgga 247

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA:*

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- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	36	14.6	970	2	US-08-773-368-2
2	36	14.6	970	3	US-09-199-887-2
3	33.8	13.7	13842	4	US-09-105-537-30
4	33.8	13.7	36778	4	US-09-105-537-5
5	33.8	13.7	38506	3	US-09-320-878-19
6	32.6	13.2	3186	1	US-08-761-258-8
7	32.6	13.2	3186	2	US-08-977-306-8
8	32.4	13.1	2808	3	US-08-870-126-7
9	32.4	13.1	2808	4	US-09-445-247-7
10	32.4	13.1	30001	1	US-08-125-468-1
11	32.4	13.1	30001	2	US-08-474-933-1
12	32.2	13.0	465	4	US-09-370-838-229
13	32.2	13.0	6854	4	US-09-194-905-7
14	32.2	13.0	20235	1	US-07-642-734C-3
15	32.2	13.0	20235	3	US-08-439-009A-3
16	32	13.0	1642	1	US-08-232-015-2
17	31.2	12.6	753	4	US-08-998-416-567
18	31.2	12.6	1281	4	US-09-082-092-8
19	31.2	12.6	1876	4	US-09-082-092-5
20	31.2	12.6	3103	3	US-08-826-246-3
21	31.2	12.6	3103	3	US-08-944-495-3
22	31.2	12.6	3103	3	US-09-126-640-2
23	31.2	12.6	3103	4	US-08-925-588-3
24	31.2	12.6	3103	4	US-09-288-292A-2
25	31.2	12.6	3111	3	US-09-487-444-3
26	31	12.6	3624	1	US-07-951-715A-6
27	31	12.6	3624	2	US-08-459-448A-6

28	31	12.6	3624	3	US-08-459-595A-6
29	31	12.6	3624	3	US-08-459-504B-6
30	31	12.6	3624	3	US-08-459-444-6
31	31	12.6	3624	3	US-09-053-549-7
32	31	12.6	3624	4	US-09-547-422-6
33	31	12.6	8854	3	US-09-053-549-1
34	31	12.6	36519	3	US-08-923-137-2
35	30.8	12.5	2456	3	US-08-813-150-5
36	30.8	12.5	3855	4	US-08-974-549A-4
37	30.8	12.5	4015	3	US-08-851-843A-224
38	30.8	12.5	4015	4	US-08-974-549A-1
39	30.8	12.5	4015	4	US-08-854-050-224
40	30.8	12.5	4015	4	US-09-430-323-224
41	30.8	12.5	4015	4	US-09-572-423B-3
42	30.8	12.5	4015	4	US-09-128-354-1
43	30.8	12.5	4015	4	US-09-675-321-1
44	30.8	12.5	4015	4	US-09-052-919-1
45	30.8	12.5	4037	4	US-08-974-549A-343

ALIGNMENTS

RESULT 1
US-08-773-368-2
; Sequence 2, Application US/08773368
; Patent No. 5856130
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goll, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/773,368
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy RJ
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0186 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 1599164
US-08-773-368-2

Query Match 14.6%; Score 36; DB 2; Length 970;
Best Local Similarity 52.3%; Pred. No. 0.81; Indels 0;
Matches 78; Conservative 0; Mismatches 71; Caps 0;

Qy	163	CTGGCTCAAGCCAGGGCAGCCCTCTGTGG	191
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Db	207	TTCGCCCAAGGCCCTACGCACGGCAGTNTCG	235

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RESULT 3
US-09-105-537-30
; Sequence 30, Application US/09105537A
; Patent NO. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D. H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105.537A
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 13842
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-30

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Query Match	13.7%	Score 33.8	DB 4	Length 13842
Best Local Similarity	54.4%	Pred. No. 4.6		
Matches 68	Conservative 0	Mismatches 57	Indels 0	Gaps 0
QY 24	GGAGGAGGCTCCGATGCCGGAGCCCTGACACAGGAAGGAGATTCTTGCTCTCTCCCT	83		
Db 3288	GGAGCGGCTCCGGTGGCGCGCGCGGTGCGTGCAGAGCGCGGTGGCGATCGCTCGCAT	3347		
QY 84	GCACAACCGCCTCGGAGCTGGGTCCAGCCCCCTGCGGCTGACATGGGAGGCTGGACTG	143		
Db 3348	GGCCTGCCGCTCCCGGTGGGTGCGCTCGCCGGAGGACCTGTGGCGGTGTGTGGCCGG	3407		
QY 144	GAGTG 148			
Db 3408	CGGCG 3412			

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RESULT 4
US-09-105-537-5
; Sequence 5, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 36778
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-5

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53	TGGTTCAGACCCCTCGCGCTGCACATCGCGAGGCTGGACTGGAGTGACAGCTTGCCCA	162
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						Gaps 0;
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84	GCACAAACCCCTTCGCAGCTGGGTGCAGCCCTCGCGGTGCATCGGAGGCTGGACTG	143				

Db 5089 GGCCTGCGCTCCGCGTGGGTGCGCTCGCGGAGGACCTGTGGCGCTGGTGGCGG 5148
QY 144 GAGTG 148
Db 5149 CGGCG 5153

RESULT 5

US-09-320-878-19
; Sequence 19, Application US/09320878A
; Patent No. 6117659
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 300622002120
; CURRENT APPLICATION NUMBER: US/09/320,878A
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: 60/119,139
; EARLIER FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: 60/100,880
; EARLIER FILING DATE: 1998-09-22
; EARLIER APPLICATION NUMBER: 60/087,080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19
; LENGTH: 38506
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-320-878-19

Query Match 13.7%; Score 33.8; DB 3; Length 38506;
Best Local Similarity 54.4%; Pred. No. 5.5;
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 24 GGAGCAGGCTCCGATGCGCGGAGCCCTGAACAGGAAGAGAGTTCTGTCTCTCCCT 83
Db 3171 GGAGCGGCTCCGATGCGCGGAGCCCTGAACAGGAAGAGAGTTCTGTCTCTCCCT 83
QY 84 GCACAAACCGCTCGCGAGCTGGGTCCAGCCCTCGCGCTGACATGCGGAGGCTGGAGTG 143
Db 3231 GGCCTGCGGCTGCGCGGTGGGTGCGCTGCGCGGAGGAGCTGTGGCGGCTGGTGGCGG 3290
QY 144 GAGTG 148
Db 3291 CGGCG 3295

RESULT 6

US-08-977-306-8
; Sequence 8, Application US/08761258
; Patent No. 5756087
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Lam, Stephen T.
; APPLICANT: Gaffney, Thomas D.
; APPLICANT: Torkewitz, Nancy
; TITLE OF INVENTION: Genetically Modified Pseudomonas Strains
; TITLE OF INVENTION: with Enhanced Biocontrol Activity
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,258
; FILING DATE:

; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3186 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas fluorescens
; STRAIN: CGA267356 (aka MOCG134 and aka BL915)
; IMMEDIATE SOURCE:
; CLONE: PCIR146
; FEATURE:

; NAME/KEY: RBS
; LOCATION: 245..251
; OTHER INFORMATION: /note= "potential ribosome binding
; OTHER INFORMATION: site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 256..3006
; OTHER INFORMATION: /product= "LemA"
; OTHER INFORMATION: /note= "LemA coding sequence."
US-08-761-258-8

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Best Local Similarity 52.6%; Pred. No. 7.3;
Matches 71; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 22 CAGGACGAGCTCCGATGCGCGGAGCCCTGAACAGGAAGAGAGTTCTGTCTCTCTCC 81
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QY 82 CTGCACACCGCTCGCGAGCTGGGTCCAGCCCTCGCGCTGACATGCGGAGGCTGGAC 141
Db 982 CAGGAAGAACTGCAGCACAGCATCGACCCAGGCCACCGAGGAGCTCGGCAAAACCTGGAG 1041
QY 142 TGGAGTGACAGCTG 156
Db 1042 ACCATCGAGATCCAG 1056

RESULT 7

US-08-977-306-8
; Sequence 8, Application US/08977306
; Patent No. 5955348
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Gaffney, Thomas D.
; APPLICANT: Torkewitz, Nancy

APPLICANT: Stafford, Jill M.
TITLE OF INVENTION: Genetically Modified Pseudomonas Strains
TITLE OF INVENTION: with Enhanced Biocontrol Activity
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 595348artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,306
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3186 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Pseudomonas fluorescens
STRAIN: CGA267356 (aka MCG134 and aka BL915)
IMMEDIATE SOURCE:
CLONE: pCIB146
FEATURE:
NAME/KEY: RBS
LOCATION: 245..251
OTHER INFORMATION: /note= "potential ribosome binding
OTHER INFORMATION: site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 256..3006
OTHER INFORMATION: /product= "Lema"
OTHER INFORMATION: /note= "Lema coding sequence."

US-08-977-306-8
Query Match 13.28; Score 32.6; DB 2; Length 3186;
Best Local Similarity 52.68; Pred. No. 7.3;
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DB 922 CAGGAAGTGGACGAGCTGGCCCTCGGCAATCAACCGATGGCCGACCTGCAGATGCC 981
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QY 82 CTCACAAACCCCTCGCAGCTGGGTCCAGCCCTCGCGCTGACATGCGGAGGCTGGAC 141
||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
DB 982 CAGGAAGAACTGCAGCAGCATCGAACCGGACCGAGGAGCTCGCGGAAAACCTGGAG 1041
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QY 142 TGGAGTCAGACCTTG 156
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DB 1042 ACCATCGAGATCCAG 1056
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RESULT 8
US-08-870-126-7
; Sequence 7, Application US/08870126
; Patent No. 6048702

GENERAL INFORMATION:
APPLICANT: Prendergast, George C.
APPLICANT: Sakamuro, Daitoku
TITLE OF INVENTION: Murine and Human Box-Dependent
TITLE OF INVENTION: MYC-Interacting Protein (Bin1) and Uses Therefor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,126
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,454
FILING DATE: 05-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,972
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kodroff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: WST60CUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2808 base pairs
TYPE: nucleic acid
STRAINEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: exon
LOCATION: 2051..2294
OTHER INFORMATION: /note= "exon 1"
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NAME/KEY: CDS
LOCATION: 2211..2213
OTHER INFORMATION: /note= "start site for translation
OTHER INFORMATION: Initiation"
US-08-870-126-7
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Best Local Similarity 46.48; Pred. No. 8;
Matches 102; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
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DB 2449 CAGGCTGGCTTCCCGGCGCTCTGGGTGCCCTCTTAGTTGGCTCTCTCTCTCTCCAC 2508
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QY 88 AACCCCTCGCAGCTGGGTCCAGCCCTCGCGCTGACATGCGGAGGCTGGAGT 147
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DB 2509 ACCCGCGGCGGAGGAGGCGGCGCTTTCACCTTCGTGGCTCGGCTGCACAGCAGT 2568
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DB 2569 GCGCGGCGCTGCTCCAGGCTCTTCTCAGCGGCGGCTCCAAAGCTACCCCTTTGGAAGC 2628
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QY 208 CTGGCATCGGCTGTGGCGCACCCCTGCAAGTGGGCTGGA 247
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RESULT 9

US-09-445-247-7
 ; Sequence 7, Application US/09445247
 ; Patent No. 6410238
 ; GENERAL INFORMATION:
 ; APPLICANT: Wistar Institute of Anatomy & Biology
 ; Prendergast, George C.
 ; Sakamuro, Daitoku
 ; TITLE OF INVENTION: Box-Dependent MYC-Interacting Protein
 ; (Bin1) Compositions and Uses Therefor
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howson and Howson
 ; STREET: Spring House Corporate Cntr, P O Box 457
 ; CITY: Spring House
 ; STATE: Pennsylvania
 ; COUNTRY: USA
 ; ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/445,247
 FILING DATE: 03-Dec-1999
 CLASSIFICATION: <Unknown>

PRIORITY INFORMATION:

APPLICATION NUMBER: US 08/870,126
 FILING DATE: 06-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.
 REGISTRATION NUMBER: 31,215
 REFERENCE/DOCKET NUMBER: WST60DPCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200
 TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2808 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

FEATURE:
 NAME/KEY: exon
 LOCATION: 2051..2294
 OTHER INFORMATION: /note= "exon 1"

FEATURE:

NAME/KEY: CDS
 LOCATION: 2211..2213
 OTHER INFORMATION: /note= "start site for translation
 initiation"

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-445-247-7

Query Match

Best Local Similarity 13.1%; Score 32.4; DB 4; Length 2808;
 Matches 102; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

Qy 28 CAGGCTCCGATCGCGAGCCCTGAACAGAGAGAGAGTTCTTGTCTCTCTCCCTGCAC 87

Db 2449 CAGGCTGGTTCCTCCCGGCTCTGGTGGCCCTTTAGGTTTGGCTCTCTCTCCCTGCAC 87

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Db 2509 AACCCGCTGGGAGCTGGGTTCAGGCCCCCTGGCGCTGACATGGGAGGCTGGACTGGAGT 147

Qy 148 GACAGCTGGCCCAACTGGCTCAAGCAGGAGGAGCCCTCTGTGGAAATCCCAACCCGAGC 207

Db 2569 GCGCGGCTGCTCAGGCTCTTCTCAGGCGCGGCTCCAAAGCTACCCCTTTTGAAGC 2628

Qy 208 CTGGCATCGGCTCTGTGGCGCACCTCTGCAAGTGGGCTGGA 247
 Db 2629 CAAGGGCCNGGAAGCTTGGGAAGCCAGTTGGTGACCTCNA 2668

RESULT 10

US-08-125-468-1

; Sequence 1, Application US/08125468

; Patent No. 5589385

; GENERAL INFORMATION:

; APPLICANT: Ryan, Michael J.

; APPLICANT: Lotvin, Jason A.

; APPLICANT: Strathy, Nancy

; APPLICANT: Fantini, Susan E.

; TITLE OF INVENTION: Cloning of the biosynthetic pathway for

; chlorotetracycline and tetracycline formation and cosmid

; TITLE OF INVENTION: useful therein

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Cyanamid Plaza

; CITY: Wayne

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07470

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/125,468

; FILING DATE: 22-SEP-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Tsevdos, Estelle J

; REGISTRATION NUMBER: 31,145

; REFERENCE/DOCKET NUMBER: 31,255-02

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (201)831-3241

; TELEFAX: (201)831-3305

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 30001 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-125-468-1

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; Matches 102; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

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Qy 137 TGGAGTGCAGTGCAGGCTGGCCCACTGCTCAAGCAGGAGGAGCCCTCTGTGTGGAATCC 196

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RESULT 11

US-08-474-933-1

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; Sequence 1, Application US/08474933
; Patent No. 5866410
; GENERAL INFORMATION:
; APPLICANT: Ryan, Michael J.
; APPLICANT: Lotvin, Jason A.
; APPLICANT: Strathy, Nancy
; APPLICANT: Fantini, Susan E.
; TITLE OF INVENTION: Cloning of the biosynthetic pathway for
; TITLE OF INVENTION: chlortetracycline and tetracycline formation and cosmids
; TITLE OF INVENTION: useful therein
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07470
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,933
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,468
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsevdos, Estelle J.
; REGISTRATION NUMBER: 31,145
; REFERENCE/DOCKET NUMBER: 31,255-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3241
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30001 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-474-933-1

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QY 77 TCTCCTGACACACCGCCCTGCGAGCTGGGTCCAGCCCCCTGGCGGTGACATGGCGAGGC 136
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QY 137 TCGACTGGAGTACACCGCTGGCCCACTGCTCAAGCCAGGCGAGCCCTGTGTGGAATCC 196
Db 17637 TCGGGGCAAGCGCATCCCTCAAGCACTGACACAGGACCAAGGAGACCGGCGACACACCC 17696

QY 197 CAACCCCGAGCCTGGCATCGGCGCTGTGGCGCACCCCTG 234
Db 17697 ACTGCCAGGCGTGGAGACACACCCGTACCCGGSCCTG 17734

RESULT 12
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; Sequence 229, Application US/09370838
; Patent No. 644425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.

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; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Roadoh
; APPLICANT: Secretist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
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; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-370-838-229

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Best Local Similarity 50.3%; Pred. No. 6.7;
Matches 79; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

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QY 68 TCTTGCTCTCTCCCTGCACACCGCTGCGAGCTGGGTCCAGCCCTCGGCTGACA 127
Db 279 AGTTCTCCAGCATTGATGAGTGCATCTGCAGTTGCCCTCCCGCTTCATACCACTGCCA 220

QY 128 TCGGAGGCTGAGTGGAGTGACAGCCTGGCCCCAAT 164
Db 219 TCATCATACTGCAAGTTTGGCACAACTCTCTGCATCT 183

RESULT 13
US-09-194-905-7/c
; Sequence 7, Application US/09194905
; Patent No. 6306627
; GENERAL INFORMATION:
; APPLICANT: DECKER, Heinrich
; TITLE OF INVENTION: ISOLATION OF THE BIOSYNTHESIS GENES FOR
; TITLE OF INVENTION: PSEUDO-OLIGOSACCHARIDES FROM STREPTOMYCES GLAUCESCENS
; TITLE OF INVENTION: GLA.O AND THEIR USE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/194,905
; FILING DATE: 29-JUL-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/02826
; FILING DATE: 30-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19622783.6
; FILING DATE: 07-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 026083/0193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300

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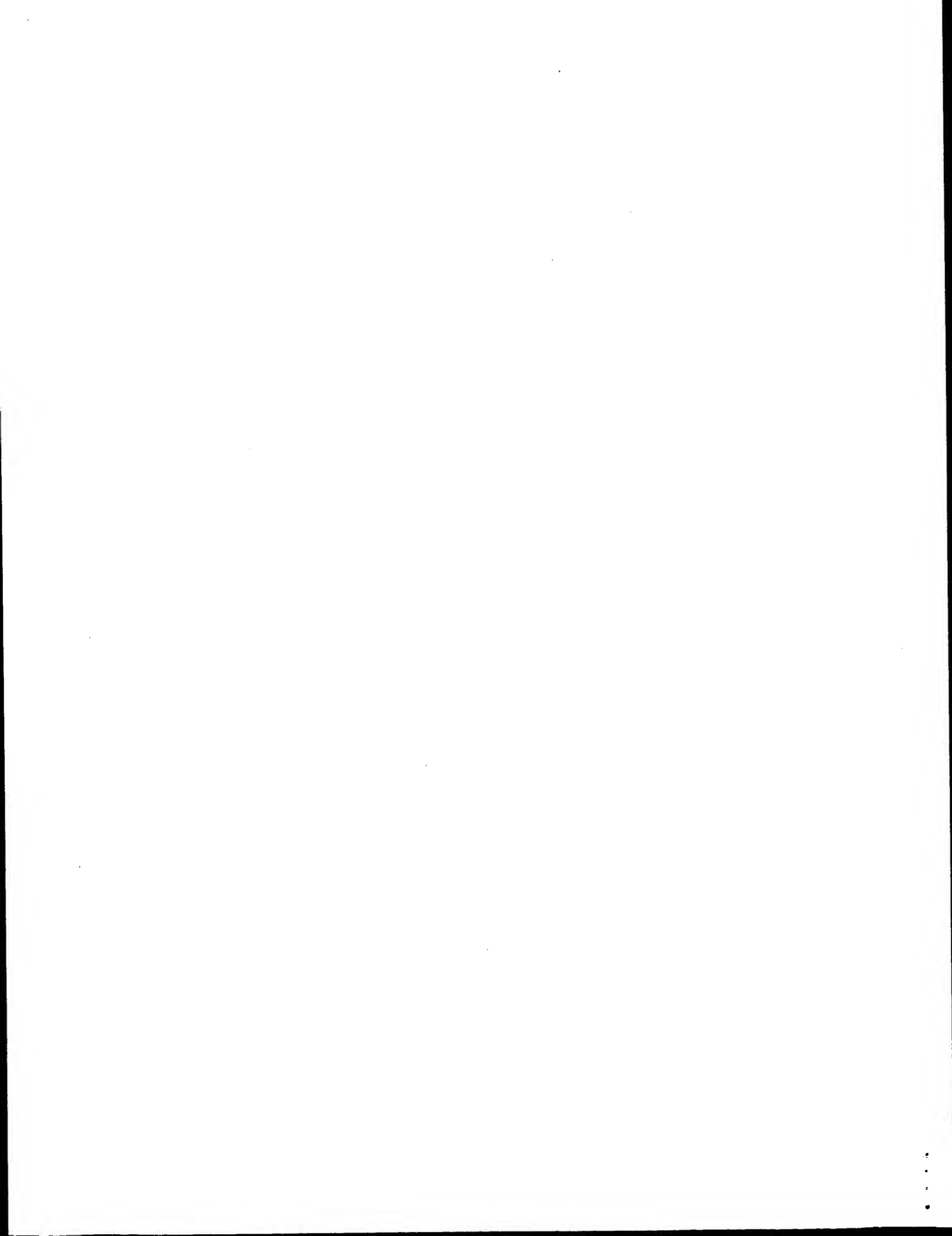
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; Qy 76 CTCCTCCCTGCACAAACCGCTCGCGACGTGGTCCAGCCCTCGGCTGACATCGCGGAG 135
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; Qy 136 CTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGCGCCCTCTGTGGAAATC 195
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; RESULT 15
; US-08-439-009A-3
; Sequence 3, Application US/08439009A
; Patent No. 6004787
; GENERAL INFORMATION:
; APPLICANT: Donadio, S
; APPLICANT: Katz, L
; APPLICANT: McAlpine, J B
; TITLE OF INVENTION: Method of Directing Biosynthesis of
; TITLE OF INVENTION: Specific Polyketides
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven F. Weinstock
; STREET: Abbott Laboratories D377/AP6D-2 One Abbott
; STREET: Park Rd
; CITY: Abbott Park
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,009A
; FILING DATE: 11-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Casuto, Dianne
; REGISTRATION NUMBER: 40,943
; REFERENCE/DOCKET NUMBER: 4952.US.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-938-3137
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
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; OTHER INFORMATION: /product= "eryA ORF2 encoding modules 3 & 4 for
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; OTHER INFORMATION: beta-ketoacyl ACP synthase of module 3"
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; OTHER INFORMATION: beta-ketoacylACPSynthase domain of modul"
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; OTHER INFORMATION: acyl carrier domain of module 6"
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; Query Match 13.0%; Score 32.2; DB 3; Length 20235;
; Best Local Similarity 52.6%; Pred. No. 13;
; Matches 70; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
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; QY 76 CTCTCCCTGCACACCGCGCTGCGCAGTGGTGCAGCCCCCTGGCGGCTGCATGCGGAGG 135
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; Db 11238 CACCGCCTCCAGCGTCCGCTCCGCGCGGCTGCGCTACTGCTGGGCTTGAAGGCCCGGC 11297
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; QY 136 CTGGACTGGAGTGACAGCGCTGGCCCAACTGGCTCAAGCCAGGCGAGCCCTCTGTGGATC 195
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; Db 11298 GATGACCGTCGACACCGCCCTGTTCTCCGGGCTCACCGCCCTGCACCTGGCGATGGATC 11357
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Listing first 45 summaries

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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	247	100.0	1876	9	US-09-944-403-49
3	247	100.0	1876	9	US-09-944-896-49
4	247	100.0	1876	9	US-09-944-944-49
5	247	100.0	1876	10	US-09-866-028-49
6	247	100.0	1876	10	US-09-944-449-49
7	247	100.0	1876	10	US-09-944-457-49
8	247	100.0	1876	10	US-09-945-587-49
9	247	100.0	1876	10	US-09-945-015-49
10	247	100.0	1876	10	US-09-944-396-49
11	247	100.0	1876	10	US-09-944-097-49
12	247	100.0	1876	10	US-09-944-432-49
13	247	100.0	1876	10	US-09-943-762-49
14	247	100.0	1876	10	US-09-944-654-49
15	247	100.0	1876	10	US-09-943-851A-49
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17	245.4	99.4	1856	10	US-09-790-264-1
18	245.4	99.4	1923	9	US-10-042-141-12
19	245.4	99.4	1923	10	US-09-726-643-12

c	20	46.6	18.9	4877	10	US-09-834-975-872	Sequence 872, App
c	21	46.6	18.9	4877	10	US-09-834-975-873	Sequence 873, App
c	22	46.6	18.9	4877	10	US-09-834-975-884	Sequence 884, App
c	23	36	14.6	1875	9	US-09-905-291A-284	Sequence 284, App
c	24	36	14.6	1875	9	US-09-902-853-284	Sequence 284, App
c	25	36	14.6	1875	10	US-09-909-320-284	Sequence 284, App
c	26	36	14.6	1875	10	US-09-909-088B-284	Sequence 284, App
c	27	35.4	14.3	1738	9	US-09-992-598-360	Sequence 360, App
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c	30	35.4	14.3	1738	9	US-09-990-444-360	Sequence 360, App
c	31	35.4	14.3	1738	10	US-09-989-722-360	Sequence 360, App
c	32	35.4	14.3	1738	10	US-09-989-723-360	Sequence 360, App
c	33	35.4	14.3	1738	10	US-09-989-279-360	Sequence 360, App
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c	35	35.4	14.3	1738	10	US-09-989-731-360	Sequence 360, App
c	36	35.4	14.3	1738	10	US-09-989-732-360	Sequence 360, App
c	37	35.4	14.3	1738	10	US-09-991-073-360	Sequence 360, App
c	38	35.4	14.3	1738	10	US-09-990-442-360	Sequence 360, App
c	39	35.4	14.3	1738	10	US-09-991-163-360	Sequence 360, App
c	40	35.4	14.3	1738	10	US-09-993-604-360	Sequence 360, App
c	41	35.4	14.3	1738	10	US-09-990-456-360	Sequence 360, App
c	42	35.4	14.3	1738	10	US-09-989-721-360	Sequence 360, App
c	43	35.4	14.3	1738	12	US-10-052-586-239	Sequence 239, App
c	44	35.2	14.3	10144	10	US-09-880-107-2168	Sequence 2168, App
c	45	35	14.2	404	10	US-09-960-352-9210	Sequence 9210, App

ALIGNMENTS

RESULT 1

US-09-944-413-49

; Sequence 49, Application US/099444413

; Patent No. US20020156004A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P2548PIC1

; CURRENT APPLICATION NUMBER: US/09/944,413

; CURRENT FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: 09/866,028

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/067,411

; PRIOR FILING DATE: December 3, 1997

; PRIOR APPLICATION NUMBER: 60/069,334

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,335

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,278

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,425

; PRIOR FILING DATE: December 12, 1997

; PRIOR APPLICATION NUMBER: 60/069,696

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,694

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,694

; PRIOR FILING DATE: December 16, 1997


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; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020156004A,ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020156004A,ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-413-49

Query Match 100.0%; Score 247; DB 9; Length 1876;
Best Local Similarity 100.0%; Pred. No. 1.2e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGTGTGCCACCCAGCTGCAGGAGCAGCTCCGATGCCGAGCCCTGCAACAGGAAG 60
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RESULT 2

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US-09-944-403-49
; Sequence 49, Application US/09944403
; Patent No. US20020163143A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,403
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
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; PRIOR APPLICATION NUMBER: 60/069,873
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; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998

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Db 381 GCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGCGCTGTGGCGCACCTGCAAGTG 444
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 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin
 ; APPLICANT: Botstein, David
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerriksen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Kljavin, Ivar
 ; APPLICANT: Napier, Mary
 ; APPLICANT: Roy, Margaret
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P2548P1C1
 ; CURRENT APPLICATION NUMBER: US/09/944,896
 ; CURRENT FILING DATE: 2001-08-31
 ; PRIOR APPLICATION NUMBER: 09/866,028
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/069,334
 ; PRIOR FILING DATE: December 11, 1997
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 ; PRIOR FILING DATE: January 5, 1998
 ; PRIOR APPLICATION NUMBER: 60/074,086
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/074,092
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/075,945
 ; PRIOR FILING DATE: February 25, 1998
 ; PRIOR APPLICATION NUMBER: 60/112,850
 ; PRIOR FILING DATE: December 16, 1998
 ; PRIOR APPLICATION NUMBER: 60/113,296
 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 60/146,222
 ; PRIOR FILING DATE: July 28, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US98/19330
 ; PRIOR FILING DATE: September 16, 1998
 ; PRIOR APPLICATION NUMBER: PCT/US98/25108
 ; PRIOR FILING DATE: December 1, 1998

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; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-896-49

Query Match      100.0%; Score 247; DB 9; Length 1876;
Best Local Similarity 100.0%; Pred. No. 1.2e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGTGTGGCCACCCAGCTGCAGAGCAGGCTCCGATGGCCGAGCCCTGAACAGGAAG 60
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Db 201 GAGGTGTGGCCACCCAGCTGCAGAGCAGGCTCCGATGGCCGAGCCCTGAACAGGAAG 260

QY 61 GAGAGTTTCTTGTCTCTCTCCCTGCACAAACCCCTGCGCAGCTGGTCCAGCCCCCTGCG 120
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Db 261 GAGAGTTTCTTGTCTCTCTCCCTGCACAAACCCCTGCGCAGCTGGTCCAGCCCCCTGCG 320

QY 121 GCTGACATGGCGAGGCTGAGTGCAGTGCACAGCCCTGGCCCACTGGCTCAAGCCAGGCA 180
   |||||||
Db 321 GCTGACATGGCGAGGCTGAGTGCAGTGCACAGCCCTGGCCCACTGGCTCAAGCCAGGCA 380

QY 181 GCCCTCTGTGGAATCCCAACCCAGCCTGGCATCCGGCCCTGTGGCGCACCCCTGCAAGTG 240
   |||||||
Db 381 GCCCTCTGTGGAATCCCAACCCAGCCTGGCATCCGGCCCTGTGGCGCACCCCTGCAAGTG 440

QY 241 GGCTGGA 247
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Db 441 GGCTGGA 447

RESULT 4
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; Sequence 49, Application US/09944944
; Patent No. US20020173463A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
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; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,944
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
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; PRIOR FILING DATE: December 18, 1997
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; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
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; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
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; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
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; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-944-49

Query Match 100.0%; Score 247; DB 9; Length 1876;
Best Local Similarity 100.0%; Pred. No. 1.2e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGTGTGGCCACCCAGCTGCAGGAGGCTCCGATGCGCGGAGCCCTGACAGGAAG 60
|||||
Db 201 GAGGTGTGGCCACCCAGCTGCAGGAGGCTCCGATGCGCGGAGCCCTGACAGGAAG 260
QY 61 GAGAGTTTCTTGTCTCTCCCTGCACACCCCTGCGCAGCTGGGTCCAGCCCCCTGGG 120
|||||
Db 261 GAGAGTTTCTTGTCTCTCCCTGCACACCCCTGCGCAGCTGGGTCCAGCCCCCTGGG 320
QY 121 GCTGACATGCGGAGGCTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGGCA 180
|||||
Db 321 GCTGACATGCGGAGGCTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGGCA 380
QY 181 GCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTGCAAGTG 240
|||||
Db 381 GCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTGCAAGTG 440
QY 241 GGCTGGA 247
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Db 441 GGCTGGA 447

RESULT 5
US-09-866-028-49
; Sequence 49, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-866-028-49

Query Match 100.0%; Score 247; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 1.2e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGTGTGGCCACCCAGCTGCAGGAGGCTCCGATGCGCGGAGCCCTGACAGGAAG 60
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Db 201 GAGGTGTGGCCACCCAGCTGCAGGAGGCTCCGATGCGCGGAGCCCTGACAGGAAG 260
QY 61 GAGAGTTTCTTGTCTCTCCCTGCACACCCCTGCGCAGCTGGGTCCAGCCCCCTGGG 120
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Db 261 GAGAGTTTCTTGTCTCTCCCTGCACACCCCTGCGCAGCTGGGTCCAGCCCCCTGGG 320
QY 121 GCTGACATGCGGAGGCTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGGCA 180
|||||
Db 321 GCTGACATGCGGAGGCTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGGCA 380
QY 181 GCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTGCAAGTG 240
|||||
Db 381 GCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTGCAAGTG 440
QY 241 GGCTGGA 247
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Db 441 GGCTGGA 447

RESULT 6
US-09-944-449-49
; Sequence 49, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,449
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335

PRIOR FILING DATE: December 11, 1997	
PRIOR APPLICATION NUMBER: 60/069,278	
PRIOR FILING DATE: December 11, 1997	
PRIOR APPLICATION NUMBER: 60/069,425	
PRIOR FILING DATE: December 12, 1997	
PRIOR APPLICATION NUMBER: 60/069,696	
PRIOR FILING DATE: December 16, 1997	
PRIOR APPLICATION NUMBER: 60/069,694	
PRIOR FILING DATE: December 16, 1997	
PRIOR APPLICATION NUMBER: 60/069,702	
PRIOR FILING DATE: December 16, 1997	
PRIOR APPLICATION NUMBER: 60/069,870	
PRIOR FILING DATE: December 17, 1997	
PRIOR APPLICATION NUMBER: 60/069,873	
PRIOR FILING DATE: December 17, 1997	
PRIOR APPLICATION NUMBER: 60/068,017	
PRIOR FILING DATE: December 18, 1997	
PRIOR APPLICATION NUMBER: 60/070,440	
PRIOR FILING DATE: January 5, 1998	
PRIOR APPLICATION NUMBER: 60/074,086	
PRIOR FILING DATE: February 9, 1998	
PRIOR APPLICATION NUMBER: 60/074,092	
PRIOR FILING DATE: February 9, 1998	
PRIOR APPLICATION NUMBER: 60/075,945	
PRIOR FILING DATE: February 25, 1998	
PRIOR APPLICATION NUMBER: 60/112,850	
PRIOR FILING DATE: December 16, 1998	
PRIOR APPLICATION NUMBER: 60/113,296	
PRIOR FILING DATE: December 22, 1998	
PRIOR APPLICATION NUMBER: 60/146,222	
PRIOR FILING DATE: July 28, 1999	
PRIOR APPLICATION NUMBER: PCT/US98/19330	
PRIOR FILING DATE: September 16, 1998	
PRIOR APPLICATION NUMBER: PCT/US98/25108	
PRIOR FILING DATE: December 1, 1998	
PRIOR APPLICATION NUMBER: 09/216,021	
PRIOR FILING DATE: December 16, 1998	
PRIOR APPLICATION NUMBER: 09/218,517	
PRIOR FILING DATE: December 22, 1998	
PRIOR APPLICATION NUMBER: 09/254,311	
PRIOR FILING DATE: March 3, 1999	
PRIOR APPLICATION NUMBER: PCT/US99/12252	
PRIOR FILING DATE: June 22, 1999	
PRIOR APPLICATION NUMBER: PCT/US99/21090	
PRIOR FILING DATE: September 15, 1999	
PRIOR APPLICATION NUMBER: PCT/US99/28409	
PRIOR FILING DATE: No. US20020102647a1ember 30, 1999	
PRIOR APPLICATION NUMBER: PCT/US99/28313	
PRIOR FILING DATE: No. US20020102647a1ember 30, 1999	
PRIOR APPLICATION NUMBER: PCT/US99/28301	
PRIOR FILING DATE: December 1, 1999	
PRIOR APPLICATION NUMBER: PCT/US99/30095	
PRIOR FILING DATE: December 16, 1999	
PRIOR APPLICATION NUMBER: PCT/US00/03565	
PRIOR FILING DATE: February 11, 2000	
PRIOR APPLICATION NUMBER: PCT/US00/04414	
PRIOR FILING DATE: February 22, 2000	
PRIOR APPLICATION NUMBER: PCT/US00/05841	
PRIOR FILING DATE: March 2, 2000	
PRIOR APPLICATION NUMBER: PCT/US00/08439	
PRIOR FILING DATE: March 30, 2000	
PRIOR APPLICATION NUMBER: PCT/US00/14042	
PRIOR FILING DATE: May 22, 2000	
PRIOR APPLICATION NUMBER: PCT/US00/20710	
PRIOR FILING DATE: July 28, 2000	
PRIOR APPLICATION NUMBER: PCT/US00/32678	
PRIOR FILING DATE: December 1, 2000	
PRIOR APPLICATION NUMBER: PCT/US01/06520	
PRIOR FILING DATE: February 28, 2001	
NUMBER OF SEQ ID NOS: 120	
SEQ ID NO 49	
LENGTH: 1876	
HYDROPHOBIC	

[illegible]

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; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
; ORGANISM: Homo Sapien
US-09-945-587-49

Query Match 100.0% Score 247; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 1.2e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGTGTGCGCCACCCAGCTGCAGGAGCAGGCTCCGATGCCCGAGCCCTGAACAGGAAG 60
DB 201 GAGGTGTGCGCCACCCAGCTGCAGGAGCAGGCTCCGATGCCCGAGCCCTGAACAGGAAG 260

QY 61 GAGAGTTTCTTGTCTCTCTCCCTGCACACCCGCTGCGGAGCTGGGTCCAGCCCTCGG 120
DB 261 GAGAGTTTCTTGTCTCTCTCCCTGCACACCCGCTGCGGAGCTGGGTCCAGCCCTCGG 320

QY 121 GCTGACATCGCGAGGCTGCAGTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGCGCA 180
DB 321 GCTGACATCGCGAGGCTGCAGTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGCGCA 380

QY 181 GCCCTCTGTGGAATCCCAACCCGAGCCCTGGCATCCGCGCTGTGGCGCACCCCTGCAAGTG 240
DB 381 GCCCTCTGTGGAATCCCAACCCGAGCCCTGGCATCCGCGCTGTGGCGCACCCCTGCAAGTG 440

QY 241 GGCTGGA 247
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Db 441 GGCTGGA 447

|||||||

RESULT 9

US-09-945-015-49

; Sequence 49, Application US/09945015

; Patent No. US20020132768A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerlitsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tamas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/945,015

; CURRENT FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: 09/866,028

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/067,411

; PRIOR FILING DATE: December 3, 1997

; PRIOR APPLICATION NUMBER: 60/069,334

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,335

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,278

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,425

; PRIOR FILING DATE: December 12, 1997

; PRIOR APPLICATION NUMBER: 60/069,696

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,694

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,702

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,870

; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/069,873

; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/068,017

; PRIOR FILING DATE: December 18, 1997

; PRIOR APPLICATION NUMBER: 60/070,440

; PRIOR FILING DATE: January 5, 1998

; PRIOR APPLICATION NUMBER: 60/074,086

; PRIOR FILING DATE: February 9, 1998

; PRIOR APPLICATION NUMBER: 60/074,092

; PRIOR FILING DATE: February 9, 1998

; PRIOR APPLICATION NUMBER: 60/075,945

; PRIOR FILING DATE: February 25, 1998

; PRIOR APPLICATION NUMBER: 60/112,850

; PRIOR FILING DATE: December 16, 1998

; PRIOR APPLICATION NUMBER: 60/113,296

; PRIOR FILING DATE: December 22, 1998

; PRIOR APPLICATION NUMBER: 60/146,222

; PRIOR FILING DATE: July 28, 1999

; PRIOR APPLICATION NUMBER: PCT/US98/19330

; PRIOR FILING DATE: September 16, 1998

; PRIOR APPLICATION NUMBER: PCT/US98/25108

; PRIOR FILING DATE: December 1, 1998

; PRIOR APPLICATION NUMBER: 09/216,021


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; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-945-015-49

Query Match          100.0%; Score 247; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 1.2e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGTGTGCGCCACCCAGCTGCGAGGACGCTCCGATGCGCGAGCCCTGAACGGAAG 60
    |||||
Db 201 GAGGTGTGCGCCACCCAGCTGCGAGGACGCTCCGATGCGCGAGCCCTGAACGGAAG 260
    |||||

QY 61 GAGAGTTTCTTGCTCTCTCCCTGCGACAAACCGCTGCGCGAGCTGGGTCCAGCCCTCGG 120
    |||||
Db 261 GAGAGTTTCTTGCTCTCTCCCTGCGACAAACCGCTGCGCGAGCTGGGTCCAGCCCTCGG 320
    |||||

QY 121 GCTGACATCGGAGGCTGGAGTGGAGTGCAGAGCTGCGCCCACTGGCTCAAGCCAGGCA 180
    |||||
Db 321 GCTGACATCGGAGGCTGGAGTGGAGTGCAGAGCTGCGCCCACTGGCTCAAGCCAGGCA 380
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QY 181 GGCCTCTGTGGAATCCCAACCCGAGCGCTGGCATCGCGGCTGTGGCGACCCCTCAAGTG 240
    |||||
Db 381 GGCCTCTGTGGAATCCCAACCCGAGCGCTGGCATCGCGGCTGTGGCGACCCCTCAAGTG 440
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QY 241 GCGTGA 247
Db 441 GCGTGA 447

RESULT 10
US-09-944-396-49
; Sequence 49, Application US/09944396
; Patent No. US20020132981A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
```

```
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PIC1
; CURRENT APPLICATION NUMBER: US/09/944,396
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
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; PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-396-49

Query Match          100.0%; Score 247; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 1.2e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGTGTGGCCACCCAGCTGCAGGAGCAGCTCCGATGGCCGGAGCCCTGAACAGGAAG 60
    |||||||
Db 201 GAGGTGTGGCCACCCAGCTGCAGGAGCAGCTCCGATGGCCGGAGCCCTGAACAGGAAG 260

QY 61 GAGAGTTTCTTGCTCTCCCTGCACAAACCGCTGCGAGCTGGGTCCAGCCCTCGG 120
    |||||||
Db 261 GAGAGTTTCTTGCTCTCCCTGCACAAACCGCTGCGAGCTGGGTCCAGCCCTCGG 320

QY 121 GCTGACATGCGGGAGGCTGGACTGAGTGACAGCTGGCCCACTGGCTCAAGCCAGGGCA 180
    |||||||
Db 321 GCTGACATGCGGGAGGCTGGACTGAGTGACAGCTGGCCCACTGGCTCAAGCCAGGGCA 380

QY 181 GCCTCTGTGGTAATCCCAACCCGAGCTGCGATCCGCGCTGTGGCGCACCTGCAAGTG 240
    |||||||
Db 381 GCCTCTGTGGTAATCCCAACCCGAGCTGCGATCCGCGCTGTGGCGCACCTGCAAGTG 440

QY 241 GGCTGGA 247
    |||||||
Db 441 GGCTGGA 447

RESULT 11
US-09-944-097-49
; Sequence 49, Application US/09944097
; Patent No. US20020133675A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
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; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,097
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
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; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020133675A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020133675A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
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; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-097-49

Query Match      100.0%; Score 247; DB 10; Length 1876;
Best local similarity 100.0%; Pred. No. 1.2e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGCCCGGAGCCCTGAACAGGAAG 60
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Db      201  GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGCCCGGAGCCCTGAACAGGAAG 260

QY      61  GAGAGTTTCTTGCTCTCTCTCCCTGCACAAACCGCTCGGAGCTGGTTCAGACCCCTCGG 120
        |||
Db      261  GAGAGTTTCTTGCTCTCTCTCCCTGCACAAACCGCTCGGAGCTGGTTCAGACCCCTCGG 320

QY      121  GCTGACATCGGAGGCTGACACTGGATGACAGCCTGGCCCAACTGCTCAAGCCAGGGCA 180
        |||
Db      321  GCTGACATCGGAGGCTGACACTGGATGACAGCCTGGCCCAACTGCTCAAGCCAGGGCA 380

QY      181  GCCTCTGTGGAATCCCAACCCCGAGCCCTGGCATCCGCTGTGGCGCACCCCTGCAAGTG 240
        |||
Db      381  GCCTCTGTGGAATCCCAACCCCGAGCCCTGGCATCCGCTGTGGCGCACCCCTGCAAGTG 440

QY      241  GGCTGGA 247
        |||
Db      441  GGCTGGA 447

RESULT 12
US-09-944-432-49
; Sequence 49, Application US/09944432
; Patent No. US20020142419A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fellvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Nepier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/09/944,432
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997

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US-09-944-432-49

Query Match 100.0%; Score 247; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 1.2e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGTGTGGCCACCCAGCTGCAGGAGCAGCTCCGATGGCCGGAGCCCTGAACAGGAAG 60
|||||
DB 201 GAGGTGTGGCCACCCAGCTGCAGGAGCAGCTCCGATGGCCGGAGCCCTGAACAGGAAG 260
|||||

QY 61 GAGAGTTTCTTGCTCTCTCCCTGCACAAACCCGCTGGCAGCTGGGTCCAGCCCTGGG 120
|||||
DB 261 GAGAGTTTCTTGCTCTCTCCCTGCACAAACCCGCTGGCAGCTGGGTCCAGCCCTGGG 320
|||||

QY 121 GCTGACATGGCGGAGCTGGAGTGGAGTGACAGCCTGGGCCCACTGGCTCAAGCCAGGCA 180
|||||
DB 321 GCTGACATGGCGGAGCTGGAGTGGAGTGACAGCCTGGGCCCACTGGCTCAAGCCAGGCA 380
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QY 181 GCCTCTGTGAATCCCAACCCGAGCCTGGCATCCGGCTGTGGCGCACCCCTGCAAGTG 240
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DB 381 GCCTCTGTGAATCCCAACCCGAGCCTGGCATCCGGCTGTGGCGCACCCCTGCAAGTG 440
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QY 241 GGCTGGA 247
DB 441 GGCTGGA 447

RESULT 13

US-09-943-762-49

Sequence 49, Application US/09943762
Patent No. US20020142958A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerriksen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

TITLE REFERENCE: P2548P1C1

CURRENT APPLICATION NUMBER: US/09/943,762

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 09/866,028

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/067,411

PRIOR FILING DATE: December 3, 1997

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,335

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,425

PRIOR FILING DATE: December 12, 1997

PRIOR APPLICATION NUMBER: 60/069,696

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,694

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,702

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,870

PRIOR FILING DATE: December 17, 1997

PRIOR APPLICATION NUMBER: 60/069,873

PRIOR FILING DATE: December 17, 1997

PRIOR APPLICATION NUMBER: 60/068,017

PRIOR FILING DATE: December 18, 1997

PRIOR APPLICATION NUMBER: 60/070,440

PRIOR FILING DATE: January 5, 1998

PRIOR APPLICATION NUMBER: 60/074,086

PRIOR FILING DATE: February 9, 1998

PRIOR APPLICATION NUMBER: 60/074,092

PRIOR FILING DATE: February 9, 1998

PRIOR APPLICATION NUMBER: 60/075,945

PRIOR FILING DATE: February 25, 1998

PRIOR APPLICATION NUMBER: 60/112,850

PRIOR FILING DATE: December 16, 1998

PRIOR APPLICATION NUMBER: 60/113,296

PRIOR FILING DATE: December 22, 1998

PRIOR APPLICATION NUMBER: 60/146,222

PRIOR FILING DATE: July 28, 1999

PRIOR APPLICATION NUMBER: PCT/US98/19330

PRIOR FILING DATE: September 16, 1998

PRIOR APPLICATION NUMBER: PCT/US98/25108

PRIOR FILING DATE: December 1, 1998

PRIOR APPLICATION NUMBER: 09/216,021

PRIOR FILING DATE: December 16, 1998

PRIOR APPLICATION NUMBER: 09/218,517

PRIOR FILING DATE: December 22, 1998

PRIOR APPLICATION NUMBER: 09/254,311

PRIOR FILING DATE: March 3, 1999

PRIOR APPLICATION NUMBER: PCT/US99/12252

PRIOR FILING DATE: June 22, 1999

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: September 15, 1999

PRIOR APPLICATION NUMBER: PCT/US99/28409

PRIOR FILING DATE: No. US20020142958A1ember 30, 1999

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: No. US20020142958A1ember 30, 1999

PRIOR APPLICATION NUMBER: PCT/US99/28301

PRIOR FILING DATE: December 1, 1999

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: December 16, 1999

PRIOR APPLICATION NUMBER: PCT/US00/03565

PRIOR FILING DATE: February 11, 2000

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: February 22, 2000

PRIOR APPLICATION NUMBER: PCT/US00/05841

PRIOR FILING DATE: March 2, 2000

PRIOR APPLICATION NUMBER: PCT/US00/08439

PRIOR FILING DATE: March 30, 2000

PRIOR APPLICATION NUMBER: PCT/US00/14042

PRIOR FILING DATE: May 22, 2000

PRIOR APPLICATION NUMBER: PCT/US00/20710

PRIOR FILING DATE: July 28, 2000

PRIOR APPLICATION NUMBER: PCT/US00/32678

PRIOR FILING DATE: December 1, 2000

PRIOR APPLICATION NUMBER: PCT/US01/06520

PRIOR FILING DATE: February 28, 2001

NUMBER OF SEQ ID NOS: 120

SEQ ID NO 49

LENGTH: 1876

TYPE: DNA

ORGANISM: Homo Sapien

US-09-943-762-49

Query Match 100.0%; Score 247; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 1.2e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGTGTGGCCACCCAGCTGCAGGAGCAGCTCCGATGGCCGGAGCCCTGAACAGGAAG 60
|||||
DB 201 GAGGTGTGGCCACCCAGCTGCAGGAGCAGCTCCGATGGCCGGAGCCCTGAACAGGAAG 260
|||||

QY 61 GAGAGTTTCTTGCTCTCTCCCTGCACAAACCCGCTGGCAGCTGGGTCCAGCCCTGGG 120
|||||

Db 261 GAGAGTTTCTGCTCTCCCTGACAAACCGCTGGCAGCTGGTCCAGCCCTCGG 320
QY 121 GCTGACATCGGAGGTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGCA 180
Db 321 GCTGACATCGGAGGTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGCA 380
QY 181 GCCTCTGTGGAATCCCAACCCGAGGCTGGCATCCGCGCTGTGGCGCACCTGCAAGTG 240
Db 381 GCCTCTGTGGAATCCCAACCCGAGGCTGGCATCCGCGCTGTGGCGCACCTGCAAGTG 440
QY 241 GGCTGGA 247
Db 441 GGCTGGA 447
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US-09-944-654-49
; Sequence 49, Application US/09944654
; Patent No. US20020142959A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,654
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998

; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/114,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020142959A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020142959A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-654-49

Query Match 100.0%; Score 247; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 1.2e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGTGTGGCCACCCAGCTGCGAGGAGGCTCGGATGGCGGAGCCCTGAACAGGAAG 60
Db 201 GAGGTGTGGCCACCCAGCTGCGAGGAGGCTCGGATGGCGGAGCCCTGAACAGGAAG 260
QY 61 GAGAGTTTCTGCTCTCCCTGACAAACCGCTGGCAGCTGGTCCAGCCCTCGG 120
Db 261 GAGAGTTTCTGCTCTCCCTGACAAACCGCTGGCAGCTGGTCCAGCCCTCGG 320
QY 121 GCTGACATCGGAGGCTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGCA 180
Db 321 GCTGACATCGGAGGCTGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGCA 380
QY 181 GCCTCTGTGGAATCCCAACCCGAGGCTGGCATCCGCGCTGTGGCGCACCTGCAAGTG 240
Db 381 GCCTCTGTGGAATCCCAACCCGAGGCTGGCATCCGCGCTGTGGCGCACCTGCAAGTG 440
QY 241 GGCTGGA 247
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Db 441 GGCTGGA 447

RESULT 15

US-09-943-851A-49

Sequence 49, Application US/09943851A

Patent No. US20020150976A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Botstein, David

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleone

APPLICANT: Flivaro, Ellen

APPLICANT: Geriitsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher

APPLICANT: Gurney, Austin

APPLICANT: Hillan, Kenneth

APPLICANT: Kijavin, Ivar

APPLICANT: Napier, Mary

APPLICANT: Roy, Margaret

APPLICANT: Tumas, Daniel

APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P2548P1C1

CURRENT APPLICATION NUMBER: US/09/943,851A

CURRENT FILING DATE: 2001-08-30

PRIOR APPLICATION NUMBER: US/09/866,028

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/067,411

PRIOR FILING DATE: December 3, 1997

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,335

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,425

PRIOR FILING DATE: December 12, 1997

PRIOR APPLICATION NUMBER: 60/069,696

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,694

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,702

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,870

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PRIOR APPLICATION NUMBER: 60/069,873

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PRIOR APPLICATION NUMBER: 60/068,017

PRIOR FILING DATE: December 18, 1997

PRIOR APPLICATION NUMBER: 60/070,440

PRIOR FILING DATE: January 5, 1998

PRIOR APPLICATION NUMBER: 60/074,086

PRIOR FILING DATE: February 9, 1998

PRIOR APPLICATION NUMBER: 60/074,092

PRIOR FILING DATE: February 9, 1998

PRIOR APPLICATION NUMBER: 60/075,945

PRIOR FILING DATE: February 25, 1998

PRIOR APPLICATION NUMBER: 60/112,850

PRIOR FILING DATE: December 16, 1998

PRIOR APPLICATION NUMBER: 60/113,296

PRIOR FILING DATE: December 22, 1998

PRIOR APPLICATION NUMBER: 60/146,222

PRIOR FILING DATE: July 28, 1999

PRIOR APPLICATION NUMBER: PCT/US98/19330

PRIOR FILING DATE: September 16, 1998

PRIOR APPLICATION NUMBER: PCT/US98/25108

PRIOR FILING DATE: December 1, 1998

PRIOR APPLICATION NUMBER: 09/216,021

PRIOR FILING DATE: December 16, 1998

PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020150976A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020150976A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 49
LENGTH: 1876
TYPE: DNA
ORGANISM: Homo Sapien
US-09-943-851A-49

Query Match 100.0%; Score 247; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 1.2e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCGGAGCCCTGAACAGGAAG 60
Db 201 GAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCGGAGCCCTGAACAGGAAG 260
QY 61 GAGAGTTTCTTGTCTCTCCCTGCACAAACCCCTGCAGCTGGTCCAGCCCTCGCG 120
Db 261 GAGAGTTTCTTGTCTCTCCCTGCACAAACCCCTGCAGCTGGTCCAGCCCTCGCG 320
QY 121 GCTGACATGCGGAGGCTGGACTGGAGTGACAGCCCTGGCCCAACTGGCTCAAGCCAGGCA 180
Db 321 GCTGACATGCGGAGGCTGGACTGGAGTGACAGCCCTGGCCCAACTGGCTCAAGCCAGGCA 380
QY 181 GCCTCTGTGGAATCCCAACCCCGAGCTGGCATCCGGCTGTGGCGGACCCCTGCAAGTG 240
Db 381 GCCTCTGTGGAATCCCAACCCCGAGCTGGCATCCGGCTGTGGCGGACCCCTGCAAGTG 440
QY 241 GGCTGGA 247
Db 441 GGCTGGA 447

Search completed: December 28, 2002, 23:04:35
Job time : 21.1055 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 20:45:48 ; Search time 376 Seconds
(without alignments)
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Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1876	100.0	1876	20	AA880053
3	1876	100.0	1876	21	AAA46918
4	1876	100.0	1876	21	AAA49561
5	1029	54.9	1775	22	AAZ12570
6	1029	54.9	1856	20	AAZ23299
7	1029	54.9	1856	24	AAZ35331
8	1029	54.9	1923	22	AAF24152
9	1008	53.7	1338	20	AAZ23300

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10.0	1519	23	AAS76344	DNA encoding novel
95.9	690	21	AAA70010	Human ovarian carc
95.9	690	24	ABN72904	Ovarian carcinoma
94.9	855	21	AAZ50926	Human Protease and
91.2	602	23	AAS81209	DNA encoding novel
90.7	1934	23	AAS91790	DNA encoding novel
88.6	906	23	AAS76343	DNA encoding novel
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80.7	512	22	AAK91830	Human cDNA 5'-end
80.7	512	22	AAK93233	Human cDNA clone r
6.5	1482	23	AAS81210	DNA encoding novel
5.3	3660	23	AAS88505	DNA encoding novel
5.3	3660	23	AAS89242	DNA encoding novel
5.2	480	23	AAS81207	DNA encoding novel
5.0	168	23	AAS91789	DNA encoding novel
5.0	1239	23	AAS73137	DNA encoding novel
4.6	792	23	AAS76345	DNA encoding novel
4.2	3660	23	AAS88505	DNA encoding novel
4.2	3660	23	AAS89242	DNA encoding novel
3.8	915	23	AAS81206	DNA encoding novel
2.4	45	20	AAH80091	Human PRO347 probe
2.4	45	21	AAA46921	Probe used to scre
2.4	45	21	AAA49497	Probe for cDNA enc
1.6	30	24	AAD33532	PCR primer #1 used
1.4	27	20	AAH87290	PRO347 probe 44176
1.4	27	21	AAA46958	PCR primer used to
1.4	27	21	AAA49533	Probe for analysin
1.3	24	20	AAH80090	Human PRO347 PCR p
1.3	24	20	AAH80089	Human PRO347 PCR p
1.3	24	21	AAA46919	PCR primer used to
1.3	24	21	AAA46920	PCR primer used to
1.3	24	21	AAA49495	primer for isolati
1.3	24	21	AAA49496	primer for isolati
1.1	7216	17	AAT12249	Cytochrome p450 is
1.1	8778	24	ABK84266	Human cDNA differe
1.1	2780	24	ABK12674	Selectin L Lymphoc
1.1	138169	21	AAF34791	Human adenosine re
1.1	141589	21	AAF20913	Human ELAM-1 polyn
1.1	141589	21	AAF21127	Human low adenosin
1.1	141589	21	AAF21152	Human low adenosin
1.1	141589	21	AAF35005	Human adenosine re
1.1	141589	21	AAF35030	Human adenosine re
1.1	146981	21	AAF21442	Human ELAM-1 polyn
1.1	209273	21	AAF21437	Human factor-relat
1.1	20	24	AAD33533	PCR primer #2 used
1.1	20	24	AAD33535	PCR primer #2 used
1.1	404	22	AAI85499	Human polynucleoti
1.1	619	22	AAK61749	Human immune/haema
1.1	669	22	AAF92355	Bovine mammary tis
1.1	737	15	AAQ44862	SPAI gene. Sus sc
1.1	2798	23	ABL28360	Drosophila melanog
1.1	8448	22	AAI06080	DNA encoding human
1.1	8448	22	AAI06568	Human reproductive
1.1	9566	22	AAI060682	DNA encoding human
1.1	9566	22	AAI06570	Human reproductive
1.1	14221	22	AAI060681	DNA encoding human
1.1	14221	22	AAI06569	Human reproductive
1.1	24740	21	AAC87743	Human Lmp-1 (HLMp-
1.0	19	20	AAH87291	PRO347 reverse PCR
1.0	19	21	AAA46959	Probe used to isol
1.0	19	21	AAA49534	Primer for analysi
1.0	171	23	ABV19710	Human prostate exp
1.0	219	22	AAF44532	Mouse dextran sodi
1.0	291	23	ABV49477	Human prostate exp
1.0	401	22	ABAI2083	Human nervous syst
1.0	500	24	ABQ63265	Genomic amplicon o
1.0	538	23	ABV48174	Human prostate exp
1.0	647	22	AAS41083	CDNA encoding nove
1.0	647	22	AAS26892	Human cDNA encodin
1.0	993	21	AAA30765	Human G protein-co
1.0	993	21	AAA30778	DNA encoding human
1.0	1002	21	AAC99844	Human secreted pro

Human full-length
DNA encoding novel
Human ovarian carc
Ovarian carcinoma
Human Protease and
DNA encoding novel
DNA encoding novel
DNA encoding novel
Human EST-derived
Human cDNA 5'-end
Human cDNA clone r
DNA encoding novel
DNA encoding novel
DNA encoding novel
DNA encoding novel
DNA encoding novel
DNA encoding novel
DNA encoding novel
Human PRO347 probe
Probe used to score
PCR primer #1 used
PRO347 probe 44176
PCR primer used to
Probe for analysis
Human PRO347 PCR p
Human PRO347 PCR p
PCR primer used to
PCR primer used to
Primer for isolati
Cytochrome P450 is
Human cDNA differe
Selectin L Lymphoc
Human adenosine re
Human ELAM-1 polyn
Human low adenosin
Human low adenosin
Human adenosine re
Human adenosine re
Human ELAM-1 polyn
Human factor-relat
PCR primer #2 used
PCR primer #2 used
Human polynucleoti
Human immune/haema
Bovine mammary tis
SPAI gene. Sus sc
Drosophila melanog
DNA encoding human
Human reproductive
DNA encoding human
Human reproductive
DNA encoding human
Human LMP-1 (HLMF-
PRO347 reverse PCR
Probe used to isol
Primer for analysi
Human prostate exp
Mouse dextran sodi
Human prostate exp
Human nervous syst
Genomic amplicon o
Human prostate exp
cDNA encoding nove
Human cDNA encodin
Human G protein-co
DNA encoding human
Human secreted pro

83	19	1.0	1021	21	AZ46516	Murine TREX2m poly	156	18	1.0	494	22	AAF92072	Human PRO831 cDNA.
84	19	1.0	1051	22	ABA16863	Human nervous syst	157	18	1.0	494	22	AAF54216	DNA encoding prote
85	19	1.0	1051	22	AAK72782	Human immune/haema	c 158	18	1.0	517	22	AAK61862	Human immune/haema
86	19	1.0	1060	21	AAC77732	Human cancer assoc	c 159	18	1.0	540	22	ABA63776	Human foetal liver
87	19	1.0	1129	22	AA521354	Human cDNA sequenc	c 160	18	1.0	540	22	ABA30968	Probe #9434 for ge
88	19	1.0	1329	22	AAV34300	Human secreted pro	c 161	18	1.0	540	22	AAK12291	Human brain expres
89	19	1.0	1616	20	AAK33961	Human GCR9 coding se	c 162	18	1.0	540	22	AAK38012	Human bone marrow
90	19	1.0	1619	20	AAZ20647	CBMACD04 coding se	c 163	18	1.0	540	22	AAI18782	Probe #8715 for ge
91	19	1.0	1667	22	AA514091	Human FCTR5a DNA s	c 164	18	1.0	540	22	AAI43895	Probe #12581 used
92	19	1.0	1691	22	AA514092	Human FCTR5b DNA s	c 165	18	1.0	540	22	ABS12015	Human genome-deriv
93	19	1.0	1725	24	ABK83879	Human cDNA differe	c 166	18	1.0	547	20	AAV86937	EST clone BK41. H
94	19	1.0	1835	21	AAFI8013	Lung cancer associ	167	18	1.0	555	22	ABA07617	Human ovarian and
95	19	1.0	2260	19	AAV41995	Human HTAD50 (G-p	168	18	1.0	555	22	AAAL02245	Human reproductive
96	19	1.0	2424	23	AA577710	DNA encoding novel	c 169	18	1.0	559	22	ABA31338	Probe #9804 for ge
97	19	1.0	2486	22	AA579944	Nucleotide sequenc	c 170	18	1.0	559	22	AAK38383	Human bone marrow
98	19	1.0	2924	23	ABV22970	Human prostate exp	171	18	1.0	562	16	AAQ97689	Human A10-4 thymok
99	19	1.0	2924	23	ABV25468	Human prostate exp	172	18	1.0	593	22	AA527157	CDNA encoding nove
100	19	1.0	2924	23	ABV28804	Human prostate exp	173	18	1.0	593	23	ABK43978	DNA encoding novel
101	19	1.0	3094	21	AAA93124	Human secreted pro	174	18	1.0	629	19	AAV59567	Human secreted pro
102	19	1.0	3230	22	AA530094	Human lung antigen	175	18	1.0	640	23	ABK43702	DNA encoding novel
103	19	1.0	3475	13	AAQ21453	Sequence encoding	176	18	1.0	641	22	AA583624	B. melitensis viru
104	19	1.0	4169	22	AAH77992	Nucleotide sequenc	177	18	1.0	654	19	AAV69616	Human secreted pro
105	19	1.0	7185	22	AAH21860	Mouse N-calcium ch	c 178	18	1.0	669	21	AAZ80258	Human colon cancer
106	19	1.0	21989	22	ABA15942	Human nervous syst	c 179	18	1.0	681	21	AAZ86699	C. pneumoniae CPN1
107	19	1.0	35100	20	AAV73804	KSHV LUR DNA (nucl	c 180	18	1.0	718	15	AAQ57027	Synthetic F. solan
108	19	1.0	137507	19	AAV19941	KSHV long unique c	c 181	18	1.0	718	15	AAQ68583	Synthetic gene enc
109	19	1.0	155074	24	ABN85735	Human genomic regi	c 182	18	1.0	718	15	AAQ68591	Synthetic gene enc
110	19	1.0	155074	24	ABN85735	Human genomic regi	c 183	18	1.0	730	24	AAI37809	Corc KCP-like prot
111	18	1.0	18	20	AA87289	PRO347 forward PCR	c 184	18	1.0	739	22	AAH05420	Human cDNA clone (
112	18	1.0	18	21	AA46957	PCR primer used to	c 185	18	1.0	745	22	AAI96827	Human neuroblastom
113	18	1.0	18	21	AA49532	Primer for analysi	c 186	18	1.0	752	22	AAH05752	Human cDNA clone (
114	18	1.0	25	21	AA95939	HLA HLA-B gene PCR	c 187	18	1.0	759	22	AAH0561	Receptor #49 parti
115	18	1.0	25	21	AA95939	HLA HLA-B gene PCR	c 187	18	1.0	759	22	AAH0561	T cell mixed lymph
116	18	1.0	229	22	AA966672	HLA HLA-A gene PCR	c 188	18	1.0	768	19	AAV37734	Human gene express
117	18	1.0	229	22	AB476048	Human foetal liver	c 189	18	1.0	785	20	AA216222	Human secreted pro
118	18	1.0	229	22	AB476048	Human foetal liver	c 190	18	1.0	785	24	AAI33237	Human secreted pro
119	18	1.0	229	22	AB476048	Human foetal liver	c 191	18	1.0	792	22	AAK31954	Human cDNA 5'-end
120	18	1.0	229	22	AAK50724	Human brain expres	c 192	18	1.0	792	22	AAK31954	Human cDNA 5'-end
121	18	1.0	229	22	AAK50963	Human bone marrow	c 193	18	1.0	804	22	AAI96176	Human neuroblastom
122	18	1.0	229	22	AAI27738	Human bone marrow	c 194	18	1.0	804	22	AAI96176	Human neuroblastom
123	18	1.0	229	22	AAI27738	Human bone marrow	c 195	18	1.0	850	21	AAZ28698	C. pneumoniae CPN1
124	18	1.0	229	22	AAI56705	Probe #17671 for g	c 196	18	1.0	936	21	AAZ77689	Human cancer assoc
125	18	1.0	229	24	AB524196	Human genome-deriv	c 197	18	1.0	963	21	AAZ65111	Membrane-bound pro
126	18	1.0	234	24	ABL68642	Kidney cancer rela	c 198	18	1.0	963	21	AAZ21504	Human cDNA sequenc
127	18	1.0	235	15	AAQ76534	Human genome fragm	c 199	18	1.0	963	22	AAZ44257	Human PRO1384 (UNQ
128	18	1.0	242	21	AA706620	Single nucleotide	c 200	18	1.0	979	20	AAZ79052	Human secreted pro
129	18	1.0	242	21	AA706620	Single nucleotide	c 201	18	1.0	1001	21	AAH51416	Human UGT1A7 relat
130	18	1.0	261	21	AA006652	SPAN-X gene relate	c 202	18	1.0	1001	21	AAH51417	Human UGT1A7 relat
131	18	1.0	261	21	AA006652	SPAN-X gene relate	c 203	18	1.0	1027	22	AAH51417	CDNA encoding nove
132	18	1.0	275	15	AAQ57026	PUR7209, cassette	c 204	18	1.0	1030	22	AAZ26560	Human cDNA encodin
133	18	1.0	280	15	AAQ68582	Cassette 3 of synt	c 205	18	1.0	1040	22	AAZ26560	Human cDNA encodin
134	18	1.0	280	15	AAQ68590	Cassette 3 of synt	c 206	18	1.0	1062	23	AAZ59697	Propionibacterium
135	18	1.0	290	24	ABN87658	Human prostate spe	c 207	18	1.0	1106	21	AAZ34556	Human secreted pro
136	18	1.0	345	22	AAI98677	Human excretory re	c 208	18	1.0	1125	24	ABL90022	Human polynucleoti
137	18	1.0	345	22	AAI63073	Human kidney relat	c 209	18	1.0	1182	22	AAZ63810	Human secreted pro
138	18	1.0	372	21	AA669542	Pinus radiata myrc	c 210	18	1.0	1200	22	AAK66438	Human immune/haema
139	18	1.0	391	21	AA798556	Human secreted pro	c 211	18	1.0	1200	22	AAK66439	Human immune/haema
140	18	1.0	400	22	AAI92400	Human polynucleoti	c 212	18	1.0	1210	21	AAZ37485	Arabidopsis thalia
141	18	1.0	408	22	AA511158	DNA encoding cance	c 213	18	1.0	1221	12	AAQ12560	Substance P recept
142	18	1.0	431	22	AB45521	Human breast cell	c 214	18	1.0	1224	23	ABI98002	Non-endogenous hum
143	18	1.0	431	22	AB56017	Human foetal liver	c 215	18	1.0	1224	24	ABK12170	Human cDNA for the
144	18	1.0	431	22	AB56017	Probe #4145 for ge	c 216	18	1.0	1230	13	AAQ29179	Human recombinant
145	18	1.0	431	22	AAK04222	Human brain expres	c 217	18	1.0	1230	13	AAZ21027	Human low adenosin
146	18	1.0	431	22	AAK29709	Human bone marrow	c 218	18	1.0	1230	21	AAA34905	Human adenosine re
147	18	1.0	431	22	AAI35667	Probe #4223 for ge	c 219	18	1.0	1230	24	ABK63836	CDNA encoding neur
148	18	1.0	431	22	AAI04125	Probe #4116 used t	c 220	18	1.0	1244	21	AAZ35944	Arabidopsis thalia
149	18	1.0	431	24	AB504264	Human genome-deriv	c 221	18	1.0	1251	20	AAZ86148	CDNA clone HFKBC47
150	18	1.0	441	24	ABK53613	Human eosinophil-m	c 222	18	1.0	1261	22	AAI10138	Mouse alpha-1 coll
151	18	1.0	456	23	ABV45778	Human prostate exp	c 223	18	1.0	1261	22	ABL35074	Murine cDNA isolat
152	18	1.0	460	20	AAV87027	EST clone BG160.	c 224	18	1.0	1332	21	AAZ65049	Membrane-bound pro
153	18	1.0	472	21	AA566631	Eucalyptus grandis	c 225	18	1.0	1332	22	AAZ21465	Human cDNA sequenc
154	18	1.0	474	24	ABL86924	Human ovarian cnc	c 226	18	1.0	1332	22	AAZ44195	Human PRO1184 (UNQ
155	18	1.0	493	21	AAZ37028	Human PRO831 (UNQ4	c 227	18	1.0	1332	24	ABL86147	Human angliogenesis
							c 228	18	1.0	1332	24	ABL86147	Human PRO1184 CDNA

229	1.0	1333	21	AAC58386	Human PRO1184 nucl	302	18	1.0	2502	22	AA161014	Human polynucleoti
230	1.0	1333	21	AAF58607	Human PRO1184 prot	303	18	1.0	2517	21	AAC90463	DNA encoding uncoupling p
231	1.0	1400	22	AAF28258	Murine TANGO 300 D	304	18	1.0	2541	20	AA51704	DNA encoding a hum
232	1.0	1488	21	AA26420	Human secreted pro	305	18	1.0	2568	18	AA788419	Human glial cell l
233	1.0	1538	20	AA35555	Secreted protein c	306	18	1.0	2568	20	AA799310	Glial cell-line de
234	1.0	1534	20	AA41342	Human normal uteru	307	18	1.0	2569	22	AAF27789	Murine TANGO 272 c
235	1.0	1553	20	AA26851	Consensus sequence	308	18	1.0	2620	24	ABA92669	Human NOV8c encodi
236	1.0	1554	22	AA158910	Human polynucleoti	309	18	1.0	2632	24	ABK55561	Human cDNA encodin
237	1.0	1558	23	ABV23229	Human prostate exp	310	18	1.0	2632	24	ABK55561	Human cDNA encodin
238	1.0	1558	23	ABV29072	Human prostate exp	311	18	1.0	2694	22	AAF94452	Human hydrophobic
239	1.0	1588	20	AA40810	Secreted protein E	312	18	1.0	2722	21	AA59922	Human secreted pro
240	1.0	1588	21	AA400016	Human secreted pro	313	18	1.0	2732	22	AA508630	Human cDNA (DNA148
241	1.0	1588	21	AA422255	Human human homolo	314	18	1.0	2732	22	AA508630	Human cDNA (DNA148
242	1.0	1588	20	AA511752	DNA encoding a hum	315	18	1.0	2732	24	ABK47278	CDNA encoding huma
243	1.0	1613	24	AA145968	Human retinoic aci	316	18	1.0	2732	24	ABK33575	CDNA encoding huma
244	1.0	1626	23	AB123609	Drosophila melanog	317	18	1.0	2777	22	AA508632	Human cDNA (DNA148
245	1.0	1674	21	AA211065	Human low adenosin	318	18	1.0	2777	24	ABK47280	cDNA encoding huma
246	1.0	1674	21	AA34943	Human adenosine re	319	18	1.0	2876	21	AA590467	Human uncoupling p
247	1.0	1678	22	AAH23086	Osteoarthritis tis	320	18	1.0	2930	22	AAF2750	Human prostate can
248	1.0	1682	19	AAV00247	Human Ret ligand r	321	18	1.0	3021	21	AAC80579	Human secreted pro
249	1.0	1709	22	AAK60647	Human immune/haema	322	18	1.0	3021	20	AA599312	Glial cell-line de
250	1.0	1724	22	AAH64906	Human secreted pro	323	18	1.0	3037	22	AA159428	Human polynucleoti
251	1.0	1727	21	AA23451	CDNA encoding huma	324	18	1.0	3037	21	AA581710	Human secreted pro
252	1.0	1766	14	AAQ37210	Substance P recept	325	18	1.0	3033	21	AA65058	Membrane-bound pro
253	1.0	1766	21	AA211066	Human low adenosin	326	18	1.0	3033	21	AA65058	Membrane-bound pro
254	1.0	1766	21	AA34944	Human adenosine re	327	18	1.0	3034	22	AA592086	Human PRO1106 cDNA
255	1.0	1793	22	AA158855	Human polynucleoti	328	18	1.0	3034	22	AA592086	Human PRO1106 cDNA
256	1.0	1797	24	ABD31756	Rice HMG-CoA lyase	329	18	1.0	3037	21	AA56886	Human MAGI polyep
257	1.0	1811	24	AB054401	Human ovarian anti	330	18	1.0	3037	22	AA590324	Human NOGO-A cDNA
258	1.0	1815	24	AAH77240	DNA of haloperoxid	331	18	1.0	3611	22	AAQ94326	Human full-length
259	1.0	1815	24	ABA03638	Drosophila hartleb	332	18	1.0	3775	23	AA581656	Human protein tyro
260	1.0	1826	22	AAH16610	Human cDNA sequenc	333	18	1.0	3786	21	AAZ46153	DNA encoding novel
261	1.0	1838	22	AA32649	Human cDNA encodin	334	18	1.0	3786	20	AAZ40483	CDNA sequence enco
262	1.0	1844	20	AA224588	Human lung tumor a	335	18	1.0	3815	22	AAZ40483	Human ZC1 DNA. Ho
263	1.0	1844	21	AA65827	Human lung cancer-	336	18	1.0	3837	23	ABL22528	Human immune/haema
264	1.0	1844	24	AB149046	Human lung tumour	337	18	1.0	3842	23	ABL22528	Drosophila melanog
265	1.0	1859	22	AA526561	Human cDNA encodin	338	18	1.0	3864	23	AA581657	DNA encoding novel
266	1.0	1879	22	AA505386	Rat caspase recrui	339	18	1.0	3925	22	AA581657	Human kinase (PKIN
267	1.0	1893	21	AA596353	CDNA encoding a no	340	18	1.0	3929	21	AA581657	Human low adenosin
268	1.0	1893	22	AA521288	Human cDNA sequenc	341	18	1.0	3929	21	AA581657	Human adenosine re
269	1.0	1911	22	AA521288	Human PRO5990 cDNA	342	18	1.0	3929	23	AA559617	Proionibacterium
270	1.0	1911	22	AA160641	Human polynucleoti	343	18	1.0	3953	22	AA559617	Human secreted pro
271	1.0	1927	20	AA599315	GDNFR-alpha cDNA c	344	18	1.0	3953	22	AA559617	Human secreted pro
272	1.0	1927	20	AA599315	GDNFR-alpha cDNA c	345	18	1.0	4053	22	AA59453	Human cDNA encodin
273	1.0	1947	22	ABA45817	Human breast cell	346	18	1.0	4093	21	AA523454	CDNA encoding huma
274	1.0	1947	22	ABA56332	Human foetal liver	347	18	1.0	4093	21	AA523454	Human lung cancer
275	1.0	1947	22	ABA25973	Probe #4439 for ge	348	18	1.0	4166	24	ABK09737	Human ovarian tumo
276	1.0	1947	22	AAK04511	Human brain expres	349	18	1.0	4182	21	AAF21030	Human low adenosin
277	1.0	1947	22	AAK30013	Human bone marrow	350	18	1.0	4182	21	AA581655	Human adenosine re
278	1.0	1947	22	AA114603	Probe #4536 for ge	351	18	1.0	4266	23	AA581655	DNA encoding novel
279	1.0	1947	22	AA135975	Probe #4661 used t	352	18	1.0	4266	24	ABK11027	DNA encoding huma
280	1.0	1947	22	AA104418	Probe #4409 used t	353	18	1.0	4740	22	AA57867	Human polynucleoti
281	1.0	1947	22	AB504584	Human genome-deriv	354	18	1.0	4859	21	AA593109	Human secreted pro
282	1.0	1962	24	ABA92863	Human NOV8a encodi	355	18	1.0	4885	24	ABN59757	Novel human coding
283	1.0	1967	22	AAK94647	Human full-length	356	18	1.0	4969	23	AA581653	DNA encoding novel
284	1.0	1985	22	AAZ32066	Human METH2 relate	357	18	1.0	5143	22	AAF32793	Human secreted pro
285	1.0	1985	22	AAZ32066	U31814 cDNA clone.	358	18	1.0	7332	23	ABL07409	Drosophila melanog
286	1.0	1985	22	AAZ32066	Human histone deac	359	18	1.0	7752	22	AA541793	Genomic sequence #
287	1.0	1985	22	AAZ32066	Human cDNA encodin	360	18	1.0	7752	22	AA541793	Genomic sequence #
288	1.0	2001	22	ABK87716	Human hydrophobic	361	18	1.0	7752	22	AA541888	Genomic sequence #
289	1.0	2012	24	ABA92866	Human NOV8b encodi	362	18	1.0	7752	22	AA541888	Human reproductive
290	1.0	2013	14	AA590380	Rat interleukin-1-	363	18	1.0	7752	22	AA541888	Human immune/haema
291	1.0	2014	14	AAQ49457	Rat IL-1alpha. Ra	364	18	1.0	7752	22	AA541888	Human immune/haema
292	1.0	2028	22	AAH14186	Human breast and o	365	18	1.0	7752	22	AA541888	Human immune/haema
293	1.0	2028	22	AAH14186	Human cDNA sequenc	366	18	1.0	7752	22	AA541888	Human immune/haema
294	1.0	2295	22	AAH14186	Human secreted pro	367	18	1.0	8646	24	AA43177	Arbidopsis thalia
295	1.0	2345	19	AAH15842	Human cDNA sequenc	368	18	1.0	9159	22	AAK83488	Nucleotide sequenc
296	1.0	2386	19	AAV30920	Human secreted pro	369	18	1.0	10079	16	AAQ88057	Human immune/haema
297	1.0	2386	22	AAH15842	Human cDNA clone B	370	18	1.0	10079	18	AAQ88057	Human EC-SOD gene.
298	1.0	2386	22	AAH15842	Human cDNA clone B	371	18	1.0	10079	18	AAQ88057	Human EC-SOD gene.
299	1.0	2397	20	AA522270	Protein PRO268 cDN	372	18	1.0	10079	21	AA522270	Human superoxide d
300	1.0	2397	22	AA545939	Human DNA encoding	373	18	1.0	12447	21	AA522270	Human low adenosin
301	1.0	2397	22	AA545939	Human PRO268 cDNA	374	18	1.0	12447	21	AA545939	Human adenosine re
		2467	23	ABL29342	Drosophila melanog				14346	22	AA532551	Human genomic DNA

c 375	18	1.0	16173	22	AAL07101	Human reproductive	448	17	0.9	339	23	ABV00329	Human prostate exp
c 376	18	1.0	17070	22	AAK80632	Human immune/haema	c 449	17	0.9	343	21	ABV056137	Eucalyptus grandis
c 377	18	1.0	17156	23	ABL07408	Drosophila melanog	450	17	0.9	344	20	AAV87204	EST clone BN48. H
c 378	18	1.0	17341	21	AAAL4872	Genomic DNA sequen	c 451	17	0.9	347	24	AAK93866	Gene #364 used to
c 379	18	1.0	17341	21	AAAL43176	Arabidopsis thalia	452	17	0.9	356	22	AAJ183287	Human polynucleoti
c 380	18	1.0	20377	22	ABA07231	Human pancreatic c	453	17	0.9	366	22	ABNL8614	Human ORFX polynuc
c 381	18	1.0	20377	22	AAK89872	Human digestive sy	454	17	0.9	379	22	AAH83634	Human polynucleoti
c 382	18	1.0	23587	22	AAL07100	Human reproductive	455	17	0.9	380	24	AAK62272	Rat sequence diffe
c 383	18	1.0	52616	22	AAK70459	Human immune/haema	456	17	0.9	380	24	ABL63351	Breast cancer rela
c 384	18	1.0	52616	22	AAK78930	Human immune/haema	457	17	0.9	380	24	ABL69719	Prostate cancer re
c 385	18	1.0	84495	24	AAK20588	Human methionine a	458	17	0.9	384	22	AAK59178	Human cancer relat
c 386	18	1.0	97835	24	ABK84796	Human cDNA differe	c 459	17	0.9	387	22	AAK68035	Corynebacterium gl
c 387	18	1.0	98690	24	ABK12169	Human DNA differe	460	17	0.9	387	24	ABL91351	Chlamydia pneumoni
c 388	18	1.0	99014	24	ABN96931	Human DNA represen	461	17	0.9	389	23	AAK30674	Human prostate exp
c 389	18	1.0	100848	22	AAF28552	Genomic fragment #	c 462	17	0.9	391	23	ABV13606	Human prostate exp
c 390	18	1.0	110096	24	ABN95044	Gene #1542 used to	c 463	17	0.9	397	22	AAF66281	Novel human polynu
c 391	18	1.0	147419	24	ABK83574	Human cDNA differe	464	17	0.9	402	22	AAH83007	Human polynucleoti
c 392	18	1.0	147419	24	ABK83574	Human cDNA differe	465	17	0.9	403	21	AAAD00654	SPAN-x gene relate
c 393	18	1.0	148834	24	ABK83570	Human cDNA differe	c 466	17	0.9	404	22	AAK96670	Human neurogulin g
c 394	18	1.0	236303	22	AAAL11614	Human genomic DNA	c 467	17	0.9	404	22	AAK98163	Human neurogulin g
c 395	17	0.9	17	23	ABK01170	Human NIGO Inozyme	c 468	17	0.9	411	24	ABK64778	Human benign prost
c 396	17	0.9	17	23	ABK011940	Human NIGO Zinzyne	c 469	17	0.9	411	24	ABL69259	Prostate cancer re
c 397	17	0.9	17	23	AAK33534	PCR primer #1 used	c 470	17	0.9	413	20	AAK30334	DNA encoding a hum
c 398	17	0.9	21	16	AAQ75754	Reverse transcript	c 471	17	0.9	421	14	AAK060935	Human brain Expres
c 399	17	0.9	25	21	AAK96222	16s rRNA gene PCR	c 472	17	0.9	424	22	AAK85826	Human immune/haema
c 400	17	0.9	25	21	AAK96230	16s rRNA gene PCR	c 473	17	0.9	424	23	ABV34720	Human prostate exp
c 401	17	0.9	29	21	AAK79653	Oligonucleotide us	c 474	17	0.9	424	23	ABV43575	Human prostate exp
c 402	17	0.9	42	13	AAK26693	PDGF-B primer 6	475	17	0.9	435	23	ABV38994	Human prostate exp
c 403	17	0.9	42	14	AAQ49384	Mature human PDGF-	476	17	0.9	435	23	ABV44781	Human prostate exp
c 404	17	0.9	65	24	ABN53279	Mouse spliced tran	477	17	0.9	450	23	AAH88187	CNS disorder-relat
c 405	17	0.9	74	22	AAF98688	Human ovarian canc	478	17	0.9	451	24	ABN73614	Bovine embryonic g
c 406	17	0.9	131	24	ABL85723	Human ovarian canc	479	17	0.9	456	22	AAAL03288	Human reproductive
c 407	17	0.9	152	23	ABV05739	Human prostate exp	480	17	0.9	456	22	AAAL03289	Human reproductive
c 408	17	0.9	152	23	ABV14908	Human prostate exp	481	17	0.9	457	17	AAK13979	Human reproductive
c 409	17	0.9	160	24	ABL83305	Human prostate exp	482	17	0.9	457	19	AAV09080	Human reproductive
c 410	17	0.9	162	24	ABL83306	Human ovarian canc	483	17	0.9	457	20	AAK03742	Mouse fat-specific
c 411	17	0.9	169	22	AAI85207	Human ovarian canc	484	17	0.9	457	21	AAK03742	Mouse body weight-
c 412	17	0.9	173	16	AAQ97266	Human polynucleoti	485	17	0.9	457	21	AAK52252	Mouse fat-specific
c 413	17	0.9	181	22	ABA73523	TFE3-like cDNA clo	486	17	0.9	470	20	AAK27436	Human secreted pro
c 414	17	0.9	181	22	ABA38804	Human foetal liver	487	17	0.9	471	24	ABN65311	Human cancer relat
c 415	17	0.9	181	22	AAK21969	Probe #17270 for g	c 488	17	0.9	473	22	ABN57686	Human foetal liver
c 416	17	0.9	181	22	AAK48132	Human brain expres	c 488	17	0.9	473	22	AAK05744	Human brain expres
c 417	17	0.9	181	22	AAI26132	Human bone marrow	c 489	17	0.9	473	22	AAK05744	Human brain expres
c 418	17	0.9	181	22	AAI53962	Probe #16065 for g	c 490	17	0.9	473	22	AAK31367	Human bone marrow
c 419	17	0.9	181	22	AAI53962	Probe #22648 used	c 491	17	0.9	473	22	AAI37260	Probe #5946 used t
c 420	17	0.9	181	24	ABS22038	Human genome-deriv	c 492	17	0.9	473	22	AAK06119	Human genome-deriv
c 421	17	0.9	192	21	AAK97711	Human genome-deriv	c 493	17	0.9	478	22	ABA52304	Human foetal liver
c 422	17	0.9	195	24	ABL88404	Bridge-1 related p	494	17	0.9	478	22	ABA22102	Human foetal liver
c 423	17	0.9	198	18	AAI50922	Pain regulated cDN	495	17	0.9	478	22	AAK00578	Probe #568 for gen
c 424	17	0.9	203	23	ABV47873	Rat brain rgss-7 g	496	17	0.9	478	22	AAK26028	Human brain expres
c 425	17	0.9	206	23	ABV57830	Human prostate exp	497	17	0.9	478	22	AAI10657	Human bone marrow
c 426	17	0.9	210	24	ABL86092	Human prostate exp	498	17	0.9	478	22	AAI131910	Probe #596 used to
c 427	17	0.9	222	24	ABN78687	Human ovarian canc	499	17	0.9	478	22	AAI00587	Probe #578 used to
c 428	17	0.9	257	24	ABN94467	Human ORF3634 cDNA	500	17	0.9	478	24	ABS00609	Human genome-deriv
c 429	17	0.9	257	24	ABL67007	Gene #965 used to	501	17	0.9	483	23	ABV56848	Human prostate exp
c 430	17	0.9	257	24	ABL67414	Thyroid cancer rel	502	17	0.9	494	24	ABL63405	Breast cancer rela
c 431	17	0.9	257	24	ABL67886	Thyroid cancer rel	503	17	0.9	495	21	AAK95482	Human secreted pro
c 432	17	0.9	265	22	AAK29043	Ovary cancer relat	504	17	0.9	515	22	AAK34270	Human cDNA encodin
c 433	17	0.9	283	23	ABV49472	cDNA encoding for	c 505	17	0.9	516	24	ABN93616	Gene #114 used to
c 434	17	0.9	287	24	AAK35795	Human prostate exp	c 506	17	0.9	516	24	ABL63363	Breast cancer rela
c 435	17	0.9	288	24	ABN24438	BS203 cDNA clone,	c 507	17	0.9	516	24	ABL63772	Breast cancer rela
c 436	17	0.9	288	20	AAK98389	Human ORFX polynuc	c 508	17	0.9	516	24	ABL64470	Stomach cancer rel
c 437	17	0.9	288	24	AAI69041	Human cancer cell	c 509	17	0.9	516	24	ABL65524	Lung cancer relate
c 438	17	0.9	296	24	ABN27082	Activated T-cell d	c 510	17	0.9	516	24	ABL65949	Lung cancer relate
c 439	17	0.9	298	23	ABV09498	Human prostate exp	c 511	17	0.9	517	24	AAAL45836	Human secreted pro
c 440	17	0.9	300	20	AAZ12854	Human prostate exp	c 512	17	0.9	532	22	AAAL45836	Human secreted pro
c 441	17	0.9	300	20	AAK98454	Human gene expres	513	17	0.9	540	23	AAK74005	DNA encoding novel
c 442	17	0.9	300	21	AAK24171	Human cancer cell	c 514	17	0.9	540	23	AAK91199	DNA encoding novel
c 443	17	0.9	302	23	ABV19705	Human secreted pro	c 515	17	0.9	545	24	ABK71601	Human dithp polynu
c 444	17	0.9	309	21	AAK18368	Human prostate exp	516	17	0.9	550	21	AAZ48826	Human delta1 codin
c 445	17	0.9	318	23	AAK90099	Lung cancer associ	517	17	0.9	561	24	AAK36939	Human phospholipas
c 446	17	0.9	330	24	ABK62764	DNA encoding novel	518	17	0.9	565	22	AAK62009	Human immune/haema
c 447	17	0.9	332	20	AAV90094	Rat sequence diffe	c 519	17	0.9	568	22	AAH04370	Human cDNA clone (
c 448	17	0.9	338	22	AAL10319	EST clone CY3. Ho	520	17	0.9	569	22	AAH187726	Human polynucleoti
c 449	17	0.9	338	22	AAL10319	Human breast cancer	521	17	0.9	569	22	AAH187726	Human polynucleoti

c 521	17	0.9	578	21	AAC97734	Bridge-1 related p	594	17	0.9	966	24	ABT04196	Human G-protein co
c 522	17	0.9	582	22	AAK64467	Human immune/haema	595	17	0.9	972	22	AAH31705	Human olfactory re
c 523	17	0.9	582	22	AAK63875	Human tankyrasyl r	596	17	0.9	975	23	AAS67820	DNA encoding novel
c 524	17	0.9	583	22	ABA61009	Human foetal liver	597	17	0.9	978	22	AAS42325	Human CDNA encoding
c 525	17	0.9	583	22	ABA28937	Probe #7403 for ge	598	17	0.9	978	24	ABK68498	Human DNA for olfa
c 526	17	0.9	583	22	AAK09302	Human brain expres	599	17	0.9	978	24	ABK37611	DNA encoding G-cou
c 527	17	0.9	583	22	AAK35191	Human bone marrow	600	17	0.9	982	24	ABN74298	Bovine embryonic g
c 528	17	0.9	583	22	AAI16941	Probe #6874 for ge	601	17	0.9	982	24	ABN74299	Bovine embryonic g
c 529	17	0.9	583	22	AAI40907	Probe #9593 used t	602	17	0.9	990	21	AAZ97102	Human secreted pro
c 530	17	0.9	583	22	ABS09623	Human genome-deriv	603	17	0.9	1002	22	AAF97887	Human secreted pro
c 531	17	0.9	584	22	AAK87649	Human immune/haema	604	17	0.9	1017	18	AAF89198	Human complement c
c 532	17	0.9	584	22	ABQ57972	Human colon cancer	605	17	0.9	1017	18	AAF68956	Blackcurrant PRIB6
c 533	17	0.9	598	22	ABA62677	Human foetal liver	606	17	0.9	1021	22	AAF91908	Human secreted pro
c 534	17	0.9	598	22	AAK11055	Human brain expres	607	17	0.9	1048	24	ABL51015	Human EDAL-II exon
c 535	17	0.9	600	22	AAK87646	Human immune/haema	608	17	0.9	1050	22	AAF97919	Human secreted pro
c 536	17	0.9	600	22	AAK87647	Human immune/haema	609	17	0.9	1052	21	AAZ93148	Human secreted pro
c 537	17	0.9	600	22	AAK87648	Human immune/haema	610	17	0.9	1056	18	AAI79681	Sequence encoding
c 538	17	0.9	601	22	AAH99617	Human prostate exp	611	17	0.9	1071	22	AAF97918	BRCA2 cancer suscep
c 539	17	0.9	613	22	AAH99617	Human prostate exp	612	17	0.9	1086	22	AAF97921	Human secreted pro
c 540	17	0.9	613	22	AAH99617	Human prostate exp	613	17	0.9	1086	22	AAF97921	Human secreted pro
c 541	17	0.9	614	23	ABV39658	Human breast cance	614	17	0.9	1090	22	AAH33778	Human secreted pro
c 542	17	0.9	614	23	ABV39658	Human breast cance	615	17	0.9	1097	21	AAZ76652	Human colon cancer
c 543	17	0.9	618	13	AAO22004	Human prostate exp	616	17	0.9	1121	11	AAO5859	Human ORFX ORF2207
c 544	17	0.9	623	9	AAH81233	Sequence encoding	617	17	0.9	1121	11	AAO5859	Cutinase gene of F
c 545	17	0.9	623	9	AAH81233	Sequence encoding	618	17	0.9	1138	22	AAF97917	Human secreted pro
c 546	17	0.9	642	23	AAH81233	Human breast cance	619	17	0.9	1138	22	AAF97917	Human secreted pro
c 547	17	0.9	643	20	AAK20436	DNA encoding novel	620	17	0.9	1149	22	AAF97920	Human secreted pro
c 548	17	0.9	645	24	ABQ66005	Human secreted pro	621	17	0.9	1153	19	AAV59541	Human secreted pro
c 549	17	0.9	650	22	AAK87646	Human secreted pro	622	17	0.9	1153	24	ABL89521	Human polynucleoti
c 550	17	0.9	657	23	ABV00345	Human secreted pro	623	17	0.9	1189	24	ABN98281	Human polynucleoti
c 551	17	0.9	666	21	AAFI4360	Human prostate exp	624	17	0.9	1193	24	ABL01575	Arabidopsis thalia
c 552	17	0.9	678	22	AAK92219	Human prostate exp	625	17	0.9	1200	23	AAZ92828	Human secreted pro
c 553	17	0.9	682	22	AAK93481	Human CDNA 5'-end	626	17	0.9	1217	21	AAZ60146	DNA encoding novel
c 554	17	0.9	683	22	AAK81509	Human immune/haema	627	17	0.9	1217	22	AAZ60146	Capsicum annuum (r
c 555	17	0.9	686	23	AAK81509	Human immune/haema	628	17	0.9	1225	20	AAZ59565	Incompatible peppe
c 556	17	0.9	697	22	AAK67224	DNA encoding novel	629	17	0.9	1225	20	AAZ59565	Nucleotide sequenc
c 557	17	0.9	708	22	AAK92283	Bovine HB-Egf codi	630	17	0.9	1242	20	AAZ59547	Nucleotide sequenc
c 558	17	0.9	713	23	AAK66834	Human CDNA 5'-end	631	17	0.9	1255	23	AAZ59547	Nucleotide sequenc
c 559	17	0.9	722	22	AAK84951	Human CDNA clone r	632	17	0.9	1262	21	AAZ26404	DNA encoding novel
c 560	17	0.9	724	23	AAZ91434	DNA encoding novel	633	17	0.9	1264	20	AAZ20927	Human secreted pro
c 561	17	0.9	730	23	ABV30690	Human immune/haema	634	17	0.9	1279	21	AAZ59018	Nucleotide sequenc
c 562	17	0.9	733	22	AAK84461	Human prostate exp	635	17	0.9	1281	21	AAZ59018	Human secreted pro
c 563	17	0.9	733	22	AAK84462	Human prostate exp	636	17	0.9	1297	24	ABN98249	Arabidopsis thalia
c 564	17	0.9	745	22	AAK63234	Human immune/haema	637	17	0.9	1322	20	AAZ20165	Arabidopsis thalia
c 565	17	0.9	747	20	ABN71146	Human immune/haema	638	17	0.9	1323	16	AAO87844	Arabidopsis thalia
c 566	17	0.9	759	24	ABN66883	DNA encoding a hum	639	17	0.9	1326	24	AAZ35796	Bovine pregnancy a
c 567	17	0.9	764	20	AAZ15568	Streptococcus poly	640	17	0.9	1335	21	AAZ98086	Cladosporium herba
c 568	17	0.9	772	22	AAI22379	Streptococcus poly	641	17	0.9	1335	22	AAZ98086	BS203 consensus CD
c 569	17	0.9	772	22	AAI22379	Human gene express	642	17	0.9	1335	21	AAZ98086	Human secreted pro
c 570	17	0.9	772	22	AAI22379	Human breast cance	643	17	0.9	1346	22	ABK69795	Human secreted pro
c 571	17	0.9	795	21	AAZ39171	Human neuroblastom	644	17	0.9	1350	20	AAZ00716	Human secreted pro
c 572	17	0.9	798	17	AAI14025	Human neuroblastom	645	17	0.9	1351	20	AAZ00716	Human secreted pro
c 573	17	0.9	799	23	ABV09514	Zea mays DNA fragm	646	17	0.9	1352	21	AAZ00716	Human secreted pro
c 574	17	0.9	825	23	ABV20242	Drosophila dCREB1	647	17	0.9	1352	21	AAZ00716	Human secreted pro
c 575	17	0.9	825	23	ABV20248	Human prostate exp	648	17	0.9	1353	20	AAZ90669	M. persicae ecodys
c 576	17	0.9	825	23	ABV26072	Human prostate exp	649	17	0.9	1393	21	AAZ76386	Human ORFX ORF1941
c 577	17	0.9	825	23	ABV26079	Human prostate exp	650	17	0.9	1399	22	AAH47052	Human ORFX ORF1941
c 578	17	0.9	826	22	AAI59195	Human prostate exp	651	17	0.9	1405	23	AAZ83864	Murine maspin CDNA
c 579	17	0.9	833	22	AAH34261	Human polynucleoti	652	17	0.9	1416	20	AAZ84498	DNA encoding novel
c 580	17	0.9	836	24	ABO88913	Human colon cancer	653	17	0.9	1416	20	AAZ84498	Human secreted pro
c 581	17	0.9	849	24	ABZ94453	Human neuroblastom	654	17	0.9	1431	22	AAZ59568	Human secreted pro
c 582	17	0.9	861	22	AAI59365	Human prostate exp	655	17	0.9	1431	22	AAZ59568	Mutant pitx3 gene
c 583	17	0.9	897	23	AAZ70691	Human manganese su	656	17	0.9	1434	18	AAZ90172	Human CDNA encodin
c 584	17	0.9	900	22	AAI00303	DNA encoding novel	657	17	0.9	1452	22	AAZ90172	Oil seed rape cyst
c 585	17	0.9	903	24	ABK77440	Human reproductive	658	17	0.9	1459	21	AAZ90172	Corynebacterium gl
c 586	17	0.9	918	21	AAZ51472	Bacillus clausii g	659	17	0.9	1465	22	AAZ90172	DNA encoding a hum
c 587	17	0.9	927	22	AAH31701	Human insulin-like	660	17	0.9	1465	22	AAZ90172	Human foetal liver
c 588	17	0.9	929	22	AAZ50840	Human olfactory re	661	17	0.9	1465	22	AAI11766	Human bone marrow
c 589	17	0.9	934	22	AAI97760	Human cDNA clone H	662	17	0.9	1465	22	AAI133076	Probe #1699 for ge
c 590	17	0.9	945	22	AAZ77969	Human neuroblastom	663	17	0.9	1465	22	AAI133076	Probe #1682 used t
c 591	17	0.9	948	21	AAZ61703	Corynebacterium gl	664	17	0.9	1465	24	ABS01730	Human genome-deriv
c 592	17	0.9	948	21	AAZ61703	Corynebacterium gl	665	17	0.9	1501	21	AAZ61703	Lung cancer associ
c 593	17	0.9	964	23	AAZ70645	DNA encoding novel	666	17	0.9	1512	18	AAZ72172	Alzheimer's diseas
c 594	17	0.9	964	23	AAZ70645	DNA encoding novel	667	17	0.9	1521	22	ABA66047	Human foetal liver

667	17	0.9	1521	22	AAK40210	Human bone marrow	740	17	0.9	2181	24	ABK11714	DNA encoding novel
668	17	0.9	1521	22	AAI20978	Probe #10911 for g	741	17	0.9	2193	24	ABK34911	Human cDNA encoding
669	17	0.9	1521	22	AAI46225	Probe #14911 used t	742	17	0.9	2280	21	AAC59224	Human secreted pro
670	17	0.9	1521	22	AAI06691	Probe #6682 used t	743	17	0.9	2280	22	AAI98091	Human neuroblastom
671	17	0.9	1521	24	ABS14258	Human genome-deriv	744	17	0.9	2288	21	AAA91714	cDNA encoding huma
672	17	0.9	1527	22	AAK52530	Human polynucleoti	745	17	0.9	2296	22	AAI99514	Human polynucleoti
673	17	0.9	1587	23	AAK73550	DNA encoding novel	746	17	0.9	2302	22	AAD09948	Human drug metaboli
c 674	17	0.9	1600	21	AAK77190	Human OREF ORF2745	747	17	0.9	2332	22	AAS30684	DNA encoding novel
675	17	0.9	1642	21	AAZ36835	Partial nucleotide	748	17	0.9	2332	22	AAS28763	Genomic sequence #
676	17	0.9	1642	23	AAI67877	Human interleukin	749	17	0.9	2346	21	AAC98804	Human pancreatic c
677	17	0.9	1651	23	AAK86287	DNA encoding novel	750	17	0.9	2361	21	AAZ52201	Human transforming
c 678	17	0.9	1660	22	AAK27209	cDNA encoding novel	751	17	0.9	2362	24	ABK27553	DNA encoding Chlam
c 679	17	0.9	1660	23	ABK43910	DNA encoding novel	752	17	0.9	2370	21	AAA61509	A. vitis hypersens
680	17	0.9	1663	21	AAZ65293	Human secreted pro	753	17	0.9	2370	21	AAA61510	A. vitis hypersens
681	17	0.9	1680	24	AAQ54644	Human ovarian anti	754	17	0.9	2403	21	AAZ98123	Human signal pepti
c 682	17	0.9	1717	22	AAH13941	Human cDNA sequenc	755	17	0.9	2438	22	AAH14659	Human cDNA sequenc
c 683	17	0.9	1720	21	AAK39471	Human ADA2 DNA. H	756	17	0.9	2445	24	ABQ54621	Human ovarian anti
684	17	0.9	1737	21	AAK77792	Human cancer assoc	c 757	17	0.9	2502	18	AAT88991	Streptococcus pneu
685	17	0.9	1740	22	AAK89270	Human digestive sy	758	17	0.9	2514	22	AAT30308	Mouse Sox-9 cDNA.
686	17	0.9	1747	22	AAK51546	Human polynucleoti	759	17	0.9	2514	22	AAH16134	Human cDNA sequenc
687	17	0.9	1752	13	AAQ25808	Mouse thyrotropin-	760	17	0.9	2551	19	AAV29537	Homo sapiens PSPI-
c 688	17	0.9	1754	22	AAD08520	Human secreted pro	761	17	0.9	2566	20	AAZ27256	Human secreted pro
689	17	0.9	1756	19	AAV59667	Human secreted pro	762	17	0.9	2613	22	AAH15201	Human cDNA sequenc
c 690	17	0.9	1758	23	AAK53398	Haemophilus influe	763	17	0.9	2663	18	AAI70174	Human delta-1 prot
c 691	17	0.9	1785	22	AAH68408	C glutamicum codin	764	17	0.9	2663	20	AAI16817	Human delta-1 gene
692	17	0.9	1787	19	AAZ29522	Homo sapiens PSPI	765	17	0.9	2688	20	AAI19062	Human PPAP-gamma-1
693	17	0.9	1793	21	AAK77949	Human cancer assoc	766	17	0.9	2702	16	AAQ95323	GalNAC-alpha-2,6-s
c 694	17	0.9	1797	22	AAK32137	M persicae ecdyson	767	17	0.9	2728	22	AAQ95323	Eucalyptus grandis
c 695	17	0.9	1805	22	AAK42421	Human full-length	768	17	0.9	2832	22	AAQ95323	Human TANGO 243 CD
c 696	17	0.9	1808	21	AAK42421	Arabidopsis thalia	769	17	0.9	2832	22	AAI61894	Human adenocarcino
c 697	17	0.9	1814	22	AAK94853	Human full-length	770	17	0.9	2832	22	AAI61894	Human GTP-binding
c 698	17	0.9	1821	22	AAK30446	Wheat apoptosis in	771	17	0.9	2834	23	ABL26522	Drosophila melanog
c 699	17	0.9	1829	22	AAH17638	Human cDNA sequenc	772	17	0.9	2888	21	AAA11239	C. reinhardtii chl
c 700	17	0.9	1831	21	AAK61882	cDNA encoding a hu	c 773	17	0.9	2921	21	AAC69547	Human secreted pro
c 701	17	0.9	1832	22	AAK94520	Human full-length	774	17	0.9	2921	21	AAK54105	Human secreted pro
c 702	17	0.9	1835	21	AAK98821	Human proliferatio	775	17	0.9	2933	21	AAK54105	PRO172 cDNA. Homo
c 703	17	0.9	1835	21	AAK98102	Human proliferatio	776	17	0.9	2933	21	AAK54105	PRO172 cDNA. Homo
c 704	17	0.9	1835	24	AAD29932	Human pharmaceutical	777	17	0.9	2933	21	AAK54105	Human PRO172 prote
705	17	0.9	1846	21	AAK26992	Maize PCNA p120 ge	778	17	0.9	2933	21	AAK54105	Human PRO172 prote
706	17	0.9	1854	21	AAK59664	Human secreted pro	779	17	0.9	2933	22	AAK54105	PRO172 DNA5916-11
707	17	0.9	1860	22	AAH81748	Human differential	780	17	0.9	2933	22	AAK54105	Human cDNA sequenc
708	17	0.9	1860	22	AAH02889	Human shear stress	781	17	0.9	2935	22	AAK54105	Human angio genesis
709	17	0.9	1860	24	ABN95120	Gene #1618 used to	782	17	0.9	3010	21	AAZ65071	cDNA encoding nove
c 710	17	0.9	1865	22	AAD08498	Human secreted pro	783	17	0.9	3010	22	AAZ65071	Membrane-bound pro
711	17	0.9	1866	19	AAV62478	Human MAP kinase,	784	17	0.9	3012	21	AAC58609	Human PRO1346 nucl
712	17	0.9	1866	24	ABK84604	Human cDNA differe	785	17	0.9	3026	22	AAI60845	Human polynucleoti
713	17	0.9	1870	22	AAH98408	Human EST-derived	786	17	0.9	3036	24	ABQ90503	M. capsulatus gene
714	17	0.9	1884	24	ABK83500	Human cDNA differe	787	17	0.9	3059	21	AAK60191	Hydrophobic domain
715	17	0.9	1885	21	AAK77018	Human OREF ORF2573	c 788	17	0.9	3099	22	AAK60191	Human cDNA encoding
716	17	0.9	1904	24	ABA02343	Human pax protein	c 789	17	0.9	3111	19	AAV54586	Human secretory pr
717	17	0.9	1921	20	AAI19487	Human secreted pro	790	17	0.9	3111	20	AAZ25606	Human secreted pro
c 718	17	0.9	1951	21	AAK72422	Human nucleic acid	791	17	0.9	3147	24	ABK48437	DNA encoding human
719	17	0.9	1956	21	AAK46328	Arabidopsis thalia	792	17	0.9	3162	21	AAZ98679	Human delta protei
720	17	0.9	1978	22	AAK40969	cDNA encoding nove	793	17	0.9	3218	23	ABV25411	Human prostate exp
721	17	0.9	1980	18	AAI59454	H-Delta-1 contig c	794	17	0.9	3218	23	ABV25411	Nucleotide sequenc
722	17	0.9	1989	24	ABL58249	Human transferase	795	17	0.9	3300	22	AAH42258	Drosophila melanog
723	17	0.9	2004	24	AAK99456	Human 32144 cDNA s	796	17	0.9	3340	23	ABL19058	Drosophila melanog
724	17	0.9	2011	22	AAK24683	Nucleotide sequenc	c 797	17	0.9	3421	23	ABL26860	DNA encoding novel
725	17	0.9	2011	22	AAK24705	Nucleotide sequenc	798	17	0.9	3421	23	AAI71804	Bovine butyrophilli
726	17	0.9	2038	22	AAI59495	Human polynucleoti	799	17	0.9	3452	19	AAV57908	Human cDNA differe
727	17	0.9	2046	20	AAV83110	Chicken 17.5.3 pro	800	17	0.9	3452	24	ABK64749	Human benign prost
728	17	0.9	2114	22	AAI59059	Human polynucleoti	c 801	17	0.9	3505	22	AAK22758	Human cDNA encoding
729	17	0.9	2138	22	AAD21395	R. sanguineus glut	802	17	0.9	3542	22	AAD08295	Human secreted pro
730	17	0.9	2163	21	AAK50081	Arabidopsis herbic	c 803	17	0.9	3551	22	AAD22522	Human cDNA encoding
731	17	0.9	2168	24	AAD23973	Human neurotransmi	804	17	0.9	3770	24	AAD31617	Rat wild-type IRP-
732	17	0.9	2172	24	ABL58248	Human transferase	805	17	0.9	3803	22	AAH14485	Human polynucleoti
c 733	17	0.9	2181	20	AAZ33935	Nucleotide sequenc	806	17	0.9	3803	22	AAH14485	Human cDNA sequenc
c 734	17	0.9	2181	20	AAK81769	DNA40628 encoding	807	17	0.9	3923	24	ABN97440	Gene #3938 used to
c 735	17	0.9	2181	20	AAK81771	Human PRO362 encod	808	17	0.9	3923	24	ABL68030	Ovary cancer relat
c 736	17	0.9	2181	21	AAK78472	Human PRO362 nucle	809	17	0.9	3934	17	AAT30309	Human SOX-9 cDNA.
c 737	17	0.9	2181	21	AAK58231	Human PRO362 nucle	810	17	0.9	4305	23	ABV22380	Human prostate exp
c 738	17	0.9	2181	21	AAK58594	Human PRO362 prote	811	17	0.9	4305	23	ABV22380	Human prostate exp
c 739	17	0.9	2181	21	AAA49725	Human PRO362 cDNA	812	17	0.9	4324	23	ABL16366	Drosophila melanog

813	17	0.9	4361	23	ABL05620	Drosophila melanog	c 886	17	0.9	11523	22	AAS45467	Chemically pretrea
814	17	0.9	4446	23	ABL02990	Drosophila melanog	c 887	17	0.9	11523	22	AAS46641	Tumour suppressor
815	17	0.9	4619	23	AAH29917	C albicans apoptos	c 888	17	0.9	11523	24	ABL34001	Human DNA for stag
816	17	0.9	4629	16	AAO76016	B-domain deleted F	c 889	17	0.9	11523	24	ABL33922	Human immune syst
817	17	0.9	4629	20	AAO76016	Human Factor VIII	c 890	17	0.9	11523	24	ABL33922	DNA transcription
818	17	0.9	4629	24	AAO76016	Human Factor VIII	c 891	17	0.9	11523	24	ABL33922	Human immune/haema
819	17	0.9	4670	24	ABN84384	Human B domain-del	c 892	17	0.9	11617	22	AAK75374	Human immune/haema
820	17	0.9	4670	19	AAV23339	Human Factor VIII	c 893	17	0.9	11617	22	AAI62937	Human genomic DNA
821	17	0.9	4832	19	AAV15581	Human Factor VIII	c 894	17	0.9	11632	22	AAK80647	Human immune/haema
822	17	0.9	4832	19	AAV15338	Human Factor VIII	c 895	17	0.9	11639	22	ABAO7806	Human ovarian and
823	17	0.9	4839	22	AAK90965	Human digestive sy	c 896	17	0.9	11639	22	AAO36005	Human reproductive
824	17	0.9	4839	22	AAK90965	Human liver associ	c 897	17	0.9	11655	22	AAK71335	Human immune/haema
825	17	0.9	4839	24	ABN90355	Human liver antige	c 898	17	0.9	11770	19	AAV52305	Streptococcus pneu
826	17	0.9	5077	21	AAO50096	Arabidopsis herbic	c 899	17	0.9	11846	20	AAK82261	Factor VIII protei
827	17	0.9	5086	15	AAO54631	Human oncogene bcl	c 900	17	0.9	12022	20	AAK82260	Factor VIII protei
828	17	0.9	5086	16	AAO86661	Human bcl-2 gene.	c 901	17	0.9	12022	20	AAK82260	Human immune/haema
829	17	0.9	5086	19	AAO75766	Human bcl2 proto-o	c 902	17	0.9	12212	24	ABK12920	Human SLC26A2 (sol
830	17	0.9	5086	24	ABL54166	DNA sequence. Hom	c 903	17	0.9	12212	24	ABK12920	Human SLC26A2 (sol
831	17	0.9	5087	22	AAH15284	Human Bcl-2 protei	c 904	17	0.9	12445	21	AAK49232	Vector HSRNeo fo
832	17	0.9	5105	9	AAH15292	Sequence of bcl-2	c 905	17	0.9	12902	23	ABL07916	Drosophila melanog
833	17	0.9	5259	21	AAA64328	cDNA sequence enco	c 906	17	0.9	12961	22	ABA20012	Human nervous syst
834	17	0.9	5322	22	ABA19018	Human nervous syst	c 907	17	0.9	14044	22	AAF54793	Nucleotide sequenc
835	17	0.9	5322	22	AAO5921	Human reproductive	c 908	17	0.9	15580	22	ABA15958	Human nervous syst
836	17	0.9	5322	23	ABU98485	Human testicular a	c 909	17	0.9	15651	22	AAK81510	Human immune/haema
837	17	0.9	5433	23	ABU09704	Drosophila melanog	c 910	17	0.9	16106	22	AAK83468	Human immune/haema
838	17	0.9	5640	22	AAK53426	Human polynucleoti	c 911	17	0.9	16161	22	AAK83469	Human immune/haema
839	17	0.9	6032	22	AAK84600	Human BCL-2 protei	c 912	17	0.9	17764	20	AAK13238	Enterococcus faeca
840	17	0.9	6096	24	ABK92513	Human prostate spe	c 913	17	0.9	22319	23	ABL26686	Drosophila melanog
841	17	0.9	6120	23	AAK566225	DNA encoding novel	c 914	17	0.9	22735	23	AAF87198	Human ion3 coding
842	17	0.9	6398	23	ABU12502	Drosophila melanog	c 915	17	0.9	23024	22	AAF25499	Nucleotide sequenc
843	17	0.9	6865	22	AAK52011	Human polynucleoti	c 916	17	0.9	24268	22	AAK67462	Human immune/haema
844	17	0.9	6867	22	AAK52995	Human polynucleoti	c 917	17	0.9	29521	22	AAK32517	Human genomic DNA
845	17	0.9	6867	22	AAK52996	Human polynucleoti	c 918	17	0.9	29543	22	AAK32516	Human genomic DNA
846	17	0.9	7059	9	AAH81543	Human Factor VIII	c 919	17	0.9	30032	22	ABA17086	Human nervous syst
847	17	0.9	7093	22	AAK52012	Human polynucleoti	c 920	17	0.9	30826	22	AAO7345	Human pancreatic c
848	17	0.9	7285	23	ABL16216	Drosophila melanog	c 921	17	0.9	30826	22	AAK32772	Human genomic DNA
849	17	0.9	7405	22	AAK83850	Human immune/haema	c 922	17	0.9	32132	22	AAK35943	Human musculoskele
850	17	0.9	7620	23	ABL03159	Drosophila melanog	c 923	17	0.9	32132	22	AAO7060	Human reproductive
851	17	0.9	7881	19	AAV27865	Human telomerase R	c 924	17	0.9	37322	23	ABL06898	Drosophila melanog
852	17	0.9	8144	22	AAK46634	Tumour suppressor	c 925	17	0.9	39287	24	ABN05533	Human P450(cytochr
853	17	0.9	8241	9	AAH81439	Factor VIII cDNA 1	c 926	17	0.9	40023	24	ABL51954	Human solute carri
854	17	0.9	8241	9	AAH81096	cDNA sequence enco	c 927	17	0.9	41648	23	AAK59551	Propionibacterium
855	17	0.9	8396	21	AAZ59353	Human STP2 (phenol	c 928	17	0.9	45845	24	ABK12809	Human tumour suppr
856	17	0.9	8839	19	AAV25989	Human telomerase e	c 929	17	0.9	49999	24	ABO90984	M. capsulatus gene
857	17	0.9	8967	17	AAK31031	Factor-VIII full-l	c 930	17	0.9	74962	22	AAK15256	Human phosphatase
858	17	0.9	8967	22	AAK87526	Human factor VIII	c 931	17	0.9	105325	24	ABK94407	DNA encoding endot
859	17	0.9	8975	6	AAH50054	Human factor VIII	c 932	17	0.9	144460	21	AAZ93815	Olfactory receptor
860	17	0.9	8975	21	AAK38604	Human full-length	c 933	17	0.9	178896	24	ABO98816	Human osteoblast d
861	17	0.9	9009	14	AAO50185	Human Factor VIII	c 934	17	0.9	215980	24	AAK38337	Complementary stra
862	17	0.9	9009	18	AAK61548	Factor VIII:C (Arg	c 935	17	0.9	349980	22	AAH68526	C glutamicum codin
863	17	0.9	9009	19	AAV18884	Homo sapiens facto	c 936	17	0.9	349980	22	AAH68527	C glutamicum codin
864	17	0.9	9009	19	AAV25810	Human factor VIII	c 937	17	0.9	349980	22	AAH68533	C glutamicum codin
865	17	0.9	9009	19	AAV12112	Homo sapiens facto	c 938	17	0.9	465237	24	ABO87681	Human oestrogen re
866	17	0.9	9009	20	AAK91162	Human factor VIII	c 939	17	0.9	465237	24	ABA90193	Human oestrogen re
867	17	0.9	9009	22	AAK18637	Human factor VIII	c 940	17	0.9	1230025	20	AAK91990	Nucleotide sequenc
868	17	0.9	9009	22	AAK90508	Human factor VIII	c 941	17	0.9	1503900	22	AAK95240	Human neuregulin-1
869	17	0.9	9009	24	ABK49525	Human factor VIII	c 942	17	0.9	1503900	22	AAK96733	Human neuregulin-1
870	17	0.9	9029	22	AAK60309	cDNA encoding huma	c 943	17	0.9	4403765	22	AAI99683	Mycobacterium tube
871	17	0.9	9068	19	AAV15359	Human factor VIII	c 944	17	0.9	4403765	22	AAI99683	Human NOGO Inozyme
872	17	0.9	9080	19	AAV15359	Human factor VIII	c 945	17	0.9	4403765	22	AAI99683	Reverse transcript
873	17	0.9	9164	20	AAH82259	Beta-domain delete	c 946	17	0.9	4403765	22	AAI99683	Reverse transcript
874	17	0.9	9354	18	AAK73164	cDNA encoding huma	c 947	17	0.9	4403765	22	AAI99683	Reverse transcript
875	17	0.9	9358	24	ABK84319	Human cDNA differe	c 948	17	0.9	4403765	22	AAI99683	Primer for amplify
876	17	0.9	9358	24	ABK84319	Colon adenocarcino	c 949	17	0.9	4403765	22	AAI99683	Sequencing primer
877	17	0.9	9695	23	ABL03140	Drosophila melanog	c 950	17	0.9	4403765	22	AAI99683	HLA DPB1 gene PCR
878	17	0.9	9820	23	ABL03140	Drosophila melanog	c 951	17	0.9	4403765	22	AAI99683	HLA DPB1 gene PCR
879	17	0.9	10221	22	AAK58417	Human oligonucleot	c 952	17	0.9	4403765	22	AAI99683	HLA DQA1 gene PCR
880	17	0.9	10837	22	ABAL7063	Human nervous syst	c 953	17	0.9	4403765	22	AAI99683	HLA DQA1 gene PCR
881	17	0.9	10927	22	AAK3763	Human immune/haema	c 954	17	0.9	4403765	22	AAI99683	HLA DQB1 gene PCR
882	17	0.9	10927	22	AAK3763	Human immune/haema	c 955	17	0.9	4403765	22	AAI99683	HLA DQB1 gene PCR
883	17	0.9	11096	24	ABK81962	cDNA encoding mous	c 956	17	0.9	4403765	22	AAI99683	HLA HLA-A gene PCR
884	17	0.9	11216	22	AAK39593	Genomic sequence #	c 957	17	0.9	4403765	22	AAI99683	HLA HLA-B gene PCR
885	17	0.9	11216	22	AAK88992	Human digestive sy	c 958	17	0.9	4403765	22	AAI99683	16s rRNA gene PCR

c 959 16 0.9 25 21 AAC96201
 c 960 16 0.9 25 21 AAC96263
 c 961 16 0.9 25 21 AAC96284
 c 962 16 0.9 25 21 AAC96392
 c 963 16 0.9 25 21 AAC96404
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 c 965 16 0.9 25 21 AAC96616
 c 966 16 0.9 25 21 AAC96624
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 c 968 16 0.9 25 21 AAC96783
 c 969 16 0.9 25 21 AAC96876
 c 970 16 0.9 25 21 AAA75773
 c 971 16 0.9 29 21 AAA71173
 c 972 16 0.9 29 21 AAA71190
 c 973 16 0.9 30 18 AAT69677
 c 974 16 0.9 30 21 AAA94323
 c 975 16 0.9 30 21 AAA63198
 c 976 16 0.9 31 19 AAV48095
 c 977 16 0.9 33 21 AAA94322
 c 978 16 0.9 34 19 AAV48094
 c 979 16 0.9 36 21 AAA94321
 c 980 16 0.9 37 16 AAO85920
 c 981 16 0.9 37 16 AAO75035
 c 982 16 0.9 37 19 AAV48093
 c 983 16 0.9 39 21 AAA94320
 c 984 16 0.9 40 13 AAQ25023
 c 985 16 0.9 40 19 AAV48092
 c 986 16 0.9 40 22 AAH20358
 c 987 16 0.9 42 21 AAA94319
 c 988 16 0.9 43 19 AAV48091
 c 989 16 0.9 44 21 AAA59200
 c 990 16 0.9 44 21 AAA59202
 c 991 16 0.9 45 22 AAL32265
 c 992 16 0.9 50 22 AAL29684
 c 993 16 0.9 50 22 AAI77401
 c 994 16 0.9 51 22 AAL30293
 c 995 16 0.9 51 22 AAI74150
 c 996 16 0.9 51 22 AAI74151
 c 997 16 0.9 51 23 ABI00401
 c 998 16 0.9 59 21 AAC14025
 c 999 16 0.9 60 24 ABN37626
 c1000 16 0.9 60 24 ABN46425

ALIGNMENTS

RESULT 1
 AAX87260
 ID AAX87260 standard; cDNA; 1876 BP.

AC AAX87260;

DT 27-SEP-1999 (first entry)

XX cDNA clone encoding human PRO347, amplified in tumour cells.

XX PRO347; UNQ306; cancer; tumour; diagnosis; therapy; human; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 123..1490

FT sig_peptide /*tag= a

FT mat_peptide /*tag= b

FT /*tag= c

XX WO9935170-A2.

XX 15-JUL-1999.

XX

16s rRNA gene PCR
 HLA DPB1 gene PCR
 HLA DPB1 gene PCR
 HLA DPB1 gene PCR
 HLA DQA1 gene PCR
 HLA DQA1 gene PCR
 HLA DRB345 gene PCR
 HLA DRB345 gene PCR
 HLA HLA-A gene PCR
 HLA HLA-A gene PCR
 HLA HLA-A gene PCR
 HLA HLA-C gene PCR
 PCR primer for a h
 Molecular interact
 Molecular interact
 Downstream primer
 RNA-protein fusion
 Cassava S-hydroxyn
 Oligonucleotide 31
 RNA-protein fusion
 Oligonucleotide 34
 RNA-protein fusion
 Hepatitis C virus
 PCR primer for the
 Oligonucleotide 37
 RNA-protein fusion
 Anti-sense oligonu
 Oligonucleotide 40
 HHV6 virus p41 gen
 RNA-protein fusion
 Oligonucleotide 43
 3' PCR primer used
 Human SNP oligonuc
 Human silent SNP c
 Human SNP oligonuc
 Human silent SNP c
 Human silent SNP c
 Human secreted pro
 Human spliced tran
 Human spliced tran

PF 05-JAN-1999; 99WO-US00106.
 XX 20-NOV-1998; 98US-0109304.
 PR 05-JAN-1998; 98US-0070440.
 PR 29-APR-1998; 98US-0083500.
 PR 22-MAY-1998; 98US-0086414.
 PR 10-JUN-1998; 98US-0088742.
 PR 10-NOV-1998; 98US-0107783.
 XX (GETH) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
 PI Roy MA, Wood WI;
 DR WPI; 1999-430385/36.
 DR P-PSDB; AAY06483.

XX Antibody against proteins expressed in neoplastic cells, useful for
 tumor diagnosis and treatment

PS Example 1; Fig 13; 162pp; English.

XX This is the nucleotide sequence of cDNA clone DNA44176 (ATCC 209532)
 CC coding for human PRO347 (UNQ306) (see AAY06482). The clone was
 CC isolated from a foetal kidney library. Amplification of DNA44176
 CC occurs in various tumours, suggesting an association with tumour
 CC formation or growth. Antagonists (e.g. antibodies) directed against
 CC PRO347 may have use in cancer therapy. The invention identifies 14
 CC genes (see AAX87254-67) that are amplified in the genome of tumour
 CC cells. Such amplification is expected to be associated with
 CC overexpression of the gene product and to contribute to
 CC tumorigenesis. The encoded proteins (see AAY06477-90) may be useful
 CC targets for the diagnosis and/or treatment (including prevention)
 CC of certain cancers, and may act as predictors of the prognosis of
 CC tumour treatment.

XX SQ Sequence 1876 BP; 387 A; 568 C; 574 G; 347 T; 0 other;

Query Match 100.0%; Score 1876; DB 20; Length 1876;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTTTTCCACAGCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTG 60
 DB 1 CTCCTTTTCCACAGCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTG 60
 QY 61 AGAAACAAGCCGGTGGCTGAGCGAGCTGTGCACGAGCACCTGACGGGCCCCAACAGAC 120
 DB 61 AGAAACAAGCCGGTGGCTGAGCGAGCTGTGCACGAGCACCTGACGGGCCCCAACAGAC 120
 QY 121 CCATGCTGCATCCAGAGAGCTCCCTTGGCGGGGGGATCTCTCTGGTGTGTCTCTGGGCC 180
 DB 121 CCATGCTGCATCCAGAGAGCTCCCTTGGCGGGGGGATCTCTCTGGTGTGTCTCTGGGCC 180
 QY 181 TCCTTGGCACCACCTGGGCAGAGGTGGCCACCCAGCTGCGAGGACAGGCTCCGATGG 240
 DB 181 TCCTTGGCACCACCTGGGCAGAGGTGGCCACCCAGCTGCGAGGACAGGCTCCGATGG 240
 QY 241 CCGGAGCCCTGAACAGGAGAGAGTTCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
 DB 241 CCGGAGCCCTGAACAGGAGAGAGTTCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
 QY 301 GCTGGTCCAGCCCTTGGCTGACATGCGGAGGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 360
 DB 301 GCTGGTCCAGCCCTTGGCTGACATGCGGAGGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 360
 QY 361 AACTGGCTTAAGCCAGGCGAGCCCTCTGTGGAATCCAAACCCAGGCTGGCATCCGGCC 420
 DB 361 AACTGGCTTAAGCCAGGCGAGCCCTCTGTGGAATCCAAACCCAGGCTGGCATCCGGCC 420
 QY 421 TGTGGCGCACCTGCAAGTGGGTGGAACATGCAGTGTGCGCGCGCGGTGGCGTCT 480
 DB 421 TGTGGCGCACCTGCAAGTGGGTGGAACATGCAGTGTGCGCGCGCGGTGGCGTCT 480

QY 481 TTGTTGAAGTGGTCAGGCTATGTTTSCAGAGGGGACAGCGGTACAGCCACCGCGCAGGAG 540
Db 481 TTGTTGAAGTGGTCAGGCTATGTTTSCAGAGGGGACAGCGGTACAGCCACCGCGCAGGAG 540
QY 541 AGTGTGCTCGCAACGCCACCTGCACCCACTACAGCGAGCTCGTGTGGCCACCTCAAGCC 600
Db 541 AGTGTGCTCGCAACGCCACCTGCACCCACTACAGCGAGCTCGTGTGGCCACCTCAAGCC 600
QY 601 AGCTGGGCTGTGGCGGACCTGTGCTCTGCAGGCCACAGACGATAGAAAGCTTTGTCT 660
Db 601 AGCTGGGCTGTGGCGGACCTGTGCTCTGCAGGCCACAGACGATAGAAAGCTTTGTCT 660
QY 661 GTCCCTACTCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAAATCATCCCTTATAAGA 720
Db 661 GTCCCTACTCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAAATCATCCCTTATAAGA 720
QY 721 AGGGTGCCTGGTGTGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACC 780
Db 721 AGGGTGCCTGGTGTGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACC 780
QY 781 ATCAGGGGGGCTCTGTGAGTGTCCCAAGGAATCCTTCTCGCATGAGCTGCCAGAACCATG 840
Db 781 ATCAGGGGGGCTCTGTGAGTGTCCCAAGGAATCCTTCTCGCATGAGCTGCCAGAACCATG 840
QY 841 GACGTCTCAACATCAGCACTGCCACTGCCACTGTCCCTCTGCTACACGGGCGAGATACT 900
Db 841 GACGTCTCAACATCAGCACTGCCACTGCCACTGTCCCTCTGCTACACGGGCGAGATACT 900
QY 901 GCCAAGTGAAGTGCAGGCTCAGTGTGTGCAAGGCCGGTTCGGGGAGGAGAGTGTCTCGT 960
Db 901 GCCAAGTGAAGTGCAGGCTCAGTGTGTGCAAGGCCGGTTCGGGGAGGAGAGTGTCTCGT 960
QY 961 GCCTGTGTGACATCGGCTACGGGGAGCCAGTGTGCAAGGCCGGTTCGGGGAGGAGAGTGTCT 1020
Db 961 GCCTGTGTGACATCGGCTACGGGGAGCCAGTGTGCAAGGCCGGTTCGGGGAGGAGAGTGTCT 1020
QY 1021 ACACCTGTGACCTGAGGATCGAGGAGTGTCTCATGTTCTTCAGAGGCGAGACACT 1080
Db 1021 ACACCTGTGACCTGAGGATCGAGGAGTGTCTCATGTTCTTCAGAGGCGAGACACT 1080
QY 1081 ATTACAGAGCCAGGATGAATGTTCAGAGGAAAGCGGGGTGCTGGCCAGATCAAGAGCC 1140
Db 1081 ATTACAGAGCCAGGATGAATGTTCAGAGGAAAGCGGGGTGCTGGCCAGATCAAGAGCC 1140
QY 1141 AGAAGTGAAGGACATCTCGCTCTTCTATCTGGGCCGCTTGGAGACCAACAGAGTGA 1200
Db 1141 AGAAGTGAAGGACATCTCGCTCTTCTATCTGGGCCGCTTGGAGACCAACAGAGTGA 1200
QY 1201 CTGACAGTGAATTCAGACAGGAACTTCTGATCGGGCTCACCTACAAGACCGCCCAAGG 1260
Db 1201 CTGACAGTGAATTCAGACAGGAACTTCTGATCGGGCTCACCTACAAGACCGCCCAAGG 1260
QY 1261 ACTCCTTCGCTGGGCGACAGGGAGCACAGGCTTTCACAGTTTTCGCTTGGGCGAGC 1320
Db 1261 ACTCCTTCGCTGGGCGACAGGGAGCACAGGCTTTCACAGTTTTCGCTTGGGCGAGC 1320
QY 1321 CTGACAAACACAGGCTGTGCTGAGTGTGCTGCTGATGGGGTTCGCAACTTCGCTGGAGC 1380
Db 1321 CTGACAAACACAGGCTGTGCTGAGTGTGCTGCTGATGGGGTTCGCAACTTCGCTGGAGC 1380
QY 1381 TGCAGGCTTCAGCTGCTTCACTTGAACGACGAGCTGCAAAACCCGAAACCGTTACA 1440
Db 1381 TGCAGGCTTCAGCTGCTTCACTTGAACGACGAGCTGCAAAACCCGAAACCGTTACA 1440
QY 1441 TCTGCCAGTTTGGCCAGGAGCACATCTCCGGTGGGGCCAGGCTCTCTGAGGCGCTGACCA 1500
Db 1441 TCTGCCAGTTTGGCCAGGAGCACATCTCCGGTGGGGCCAGGCTCTCTGAGGCGCTGACCA 1500
QY 1501 CATGGCTCCCTCGGCTGGGAGCACGGCTCTGCTTACCTGCTCTGCCACCTGTCT 1560
Db 1501 CATGGCTCCCTCGGCTGGGAGCACGGCTCTGCTTACCTGCTCTGCCACCTGTCT 1560

QY 1561 GGAACAAGGGCCAGGTTAAGACACACATGCTCATGTCCAAGAGGTCTCAGACCTTGCAC 1620
Db 1561 GGAACAAGGGCCAGGTTAAGACACACATGCTCATGTCCAAGAGGTCTCAGACCTTGCAC 1620
QY 1621 AATGCCAGAGTGGGCAG 1680
Db 1621 AATGCCAGAGTGGGCAG 1680
QY 1681 AGAAGAAGCTGGGGCCCTTCGCTGCTTTTGTATTGGGAAGATGGGCTTCAATTAGATGGC 1740
Db 1681 AGAAGAAGCTGGGGCCCTTCGCTGCTTTTGTATTGGGAAGATGGGCTTCAATTAGATGGC 1740
QY 1741 GAAG 1800
Db 1741 GAAG 1800
QY 1801 TGTGGGGCAGCGAGCTTCCCTGTGCGATGACGACCCACGCGGGTATTAAATATGAATCAG 1860
Db 1801 TGTGGGGCAGCGAGCTTCCCTGTGCGATGACGACCCACGCGGGTATTAAATATGAATCAG 1860
QY 1861 CTGAAAAAATAAAAAA 1876
Db 1861 CTGAAAAAATAAAAAA 1876
RESULT 2
AAAX80053
ID AAAX80053 standard; cDNA; 1876 BP.
XX
AC AAAX80053;
XX
DT 12-AUG-1999 (first entry)
XX
DE Human PRO347 nucleotide sequence.
XX
KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
secreted protein; transmembrane protein; inflammation disorder; ss.
XX
OS Homo sapiens.
XX
FN WO9928462-A2.
XX
PD 10-JUN-1999.
XX
PF 01-DEC-1998; 98WO-US25108.
XX
PR 25-FEB-1998; 98US-0075945.
PR 03-DEC-1997; 97US-0067411.
PR 11-DEC-1997; 97US-0069278.
PR 11-DEC-1997; 97US-0069334.
PR 11-DEC-1997; 97US-0069335.
PR 12-DEC-1997; 97US-0069425.
PR 16-DEC-1997; 97US-0069694.
PR 16-DEC-1997; 97US-0069702.
PR 17-DEC-1997; 97US-0069870.
PR 17-DEC-1997; 97US-0069873.
PR 18-DEC-1997; 97US-0068017.
PR 05-JAN-1998; 98US-0070440.
PR 09-FEB-1998; 98US-0074086.
PR 09-FEB-1998; 98US-0074092.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;
PI Yuan J;
XX
XX WPI; 1999-371118/31.
DR P-PSDB; AAY17828.
XX
PT Nucleic acids encoding PRO secreted and transmembrane proteins
XX
PS Claim 2; Fig 22; 123pp; English.

XX The present invention describes nucleic acids encoding PRO secreted and
CC transmembrane proteins used therapeutically. The PRO proteins have
CC cytotatic, anti-inflammatory, anti-proliferative and immunosuppressive
CC activity. The proteins and polynucleotides can be used in therapy,
CC identification of homologues, raising antibodies and design of probes
CC and primers. They can be used in a range of diseases related to proteins
CC that they have homology with, e.g. a PRO protein having homology to
CC complement proteins may be used in inflammatory responses.

XX
SQ Sequence 1876 BP; 387 A; 568 C; 574 G; 347 T; 0 other;

Query Match 100.0%; Score 1876; DB 20; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCTTTGTCACACAGCCAGCCCTGACTCCTCGGAGATTGTGAATAGCTCCATCCAGCCTG 60
DB 1 CTCTTTGTCACACAGCCAGCCCTGACTCCTCGGAGATTGTGAATAGCTCCATCCAGCCTG 60
QY 61 AGAAACAAGCCGGGTGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGAC 120
DB 61 AGAAACAAGCCGGGTGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGAC 120
QY 121 CCATGCTGCATCCAGAGACCTCCCTGGCCGGGGGCACTCTCTGGCTGTGCTCTGGGCC 180
DB 121 CCATGCTGCATCCAGAGACCTCCCTGGCCGGGGGCACTCTCTGGCTGTGCTCTGGGCC 180
QY 181 TCCTTGGCACCACTGGGCGAGAGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGG 240
DB 181 TCCTTGGCACCACTGGGCGAGAGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGG 240
QY 241 CCGAGGCCCTGAACAGGAAGAGAGTTTCTTGCTCTCTCCCTGCACAAACCCCTCGCGCA 300
DB 241 CCGAGGCCCTGAACAGGAAGAGAGTTTCTTGCTCTCTCCCTGCACAAACCCCTCGCGCA 300
QY 301 GCTGGGTCCAGCCCTCGCGCTGACATGCGGAGGCTGAGTGAAGTGAACGCTGGGCC 360
DB 301 GCTGGGTCCAGCCCTCGCGCTGACATGCGGAGGCTGAGTGAAGTGAACGCTGGGCC 360
QY 361 AACTGGCTCAAGCCAGGCGAGCCCTCTGTGAATCCCAACCCAGCCTGGCATCGGCC 420
DB 361 AACTGGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCAGCCTGGCATCGGCC 420
QY 421 TGTGGCGCACCCCTGCAAGTGGGCTGGAACATGCAGTCTGCTCCCGCGGCTTGGCGTCT 480
DB 421 TGTGGCGCACCCCTGCAAGTGGGCTGGAACATGCAGTCTGCTCCCGCGGCTTGGCGTCT 480
QY 481 TTGTTGAAGTGGTCAGCCTATGTTTGCAGAGGGCAGCGGTACAGCCACGCGGAGAG 540
DB 481 TTGTTGAAGTGGTCAGCCTATGTTTGCAGAGGGCAGCGGTACAGCCACGCGGAGAG 540
QY 541 AGTGTGCTCGCAACGCCACCTGCACCCACTACACGCACTCGTGTGGGCCACTCAAGCC 600
DB 541 AGTGTGCTCGCAACGCCACCTGCACCCACTACACGCACTCGTGTGGGCCACTCAAGCC 600
QY 601 AGCTGGGCTGTGGCGGCACCTGTGCTCTGCAGGCCAGACGCGATAGAAGCCTTGTCT 660
DB 601 AGCTGGGCTGTGGCGGCACCTGTGCTCTGCAGGCCAGACGCGATAGAAGCCTTGTCT 660
QY 661 GTGCCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGA 720
DB 661 GTGCCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGA 720
QY 721 AGGGTGCCTGTGCTCTGCACAGCCAGTGTCTCAGGCTGTCAAGGCTGGGACC 780
DB 721 AGGGTGCCTGTGCTCTGCACAGCCAGTGTCTCAGGCTGTCAAGGCTGGGACC 780
QY 781 ATGACGGGGGCTCTGTGAGGTCCCCAGGAATCTTGTGCGATGAGTCCCAAGACCATG 840
DB 781 ATGACGGGGGCTCTGTGAGGTCCCCAGGAATCTTGTGCGATGAGTCCCAAGACCATG 840
QY 841 GACGTCTCAACATCAGCACCTGCCACTGTCCCTGTCCCTGTACAGGGCAGATACT 900

DB 841 GACGTCTCAACATCAGCACCTGCCACTGTCCCTGTCCCTGTACACGGCAGATACT 900
QY 901 GCCAAGTGAAGTGCAGCCTGCACTGTGTGCACGGCGGTTCCGGAGGAGTGTCTCGT 960
DB 901 GCCAAGTGAAGTGCAGCCTGCACTGTGTGCACGGCGGTTCCGGAGGAGTGTCTCGT 960
QY 961 GCGTCTGTGACATCGGCTACGGGGAGCCAGTGTGCCCAAGGTCAATTTCCCTTCC 1020
DB 961 GCGTCTGTGACATCGGCTACGGGGAGCCAGTGTGCCCAAGGTCAATTTCCCTTCC 1020
QY 1021 ACACCTGTGACCTGAGGATCGAGAGACTGTCTATGTGTCTTACAGAGCAGACACT 1080
DB 1021 ACACCTGTGACCTGAGGATCGAGAGACTGTCTATGTGTCTTACAGAGCAGACACT 1080
QY 1081 ATTACAGAGCCAGGATGAATCTCAGAGAAAGCGGGTGTGGCCCAAGATCAAGAGCC 1140
DB 1081 ATTACAGAGCCAGGATGAATCTCAGAGAAAGCGGGTGTGGCCCAAGATCAAGAGCC 1140
QY 1141 AGAAGTGCAGGACATCCTCGCCTTCTATCTGGCGCCCTGGAGACCACCAACGAGTGA 1200
DB 1141 AGAAGTGCAGGACATCCTCGCCTTCTATCTGGCGCCCTGGAGACCACCAACGAGTGA 1200
QY 1201 CTGACAGTGACTTCAGAGCAGGAACTTCTGATCGGGCTCAGCTACAGACCCTCAAG 1260
DB 1201 CTGACAGTGACTTCAGAGCAGGAACTTCTGATCGGGCTCAGCTACAGACCCTCAAG 1260
QY 1261 ACTCCTTCCGCTGGGCCACAGGGGAGCACAGGCCCTTACACAGTTTGGCTTTGGGCGAG 1320
DB 1261 ACTCCTTCCGCTGGGCCACAGGGGAGCACAGGCCCTTACACAGTTTGGCTTTGGGCGAG 1320
QY 1321 CTGACAACACAGGGCTGTGTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1380
DB 1321 CTGACAACACAGGGCTGTGTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1380
QY 1381 TGCAGGCTTCAAGTGCCTTCAACTGGAACGACAGCGCTGCAAAACCCGAAACCGTTACA 1440
DB 1381 TGCAGGCTTCAAGTGCCTTCAACTGGAACGACAGCGCTGCAAAACCCGAAACCGTTACA 1440
QY 1441 TCTGCCAGTTTCCAGGAGCACATCTCCGCTGGGGCCAGGGTCTCTGAGGCTGACCA 1500
DB 1441 TCTGCCAGTTTCCAGGAGCACATCTCCGCTGGGGCCAGGGTCTCTGAGGCTGACCA 1500
QY 1501 CATGGCTCCCTCGCCTGGGAGCACCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1560
DB 1501 CATGGCTCCCTCGCCTGGGAGCACCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1560
QY 1561 GGAACAGGGCCAGGTTAAGACCATGCTCATGTCCAAAGAGGTCTCAGACCTTGCAC 1620
DB 1561 GGAACAGGGCCAGGTTAAGACCATGCTCATGTCCAAAGAGGTCTCAGACCTTGCAC 1620
QY 1621 AATGCCAGAAGTTGGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
DB 1621 AATGCCAGAAGTTGGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
QY 1681 AGAAGAAGCTGGGGCCCTTCGCTTGTGATTTGGAAGAGAGGAGGAGGAGGAGGAGGAGGAG 1740
DB 1681 AGAAGAAGCTGGGGCCCTTCGCTTGTGATTTGGAAGAGATGGGCTTCAATTAGATGGC 1740
QY 1741 GAAGGAGGAGACCGCCAGTGGTCCAAAGAGGCTCTCTTCCACCTGGCCCGAGACCC 1800
DB 1741 GAAGGAGGAGACCGCCAGTGGTCCAAAGAGGCTCTCTTCCACCTGGCCCGAGACCC 1800
QY 1801 TGTGGGGCAGGAGCTTCCCTGTGCTGATGAACCCAGCGGTATTAATATTAATATTAATAT 1860
DB 1801 TGTGGGGCAGGAGCTTCCCTGTGCTGATGAACCCAGCGGTATTAATATTAATATTAATAT 1860
QY 1861 CTGAAAAAATAAAAA 1876
DB 1861 CTGAAAAAATAAAAA 1876

RESULT 3

Db 1201 CTGACAGTCTCGAGACAGAACTCTGGATCGGGCTCACCTACAGACCGCAAGG 1260
Qy 1261 ACTCTCTTCGGCTGGGCGACAGGGAGCACCAGGCTTTCACCAAGTTTTCCTTTGGGCGAC 1320
Db 1261 ACTCTCTTCGGCTGGGCGACAGGGAGCACCAGGCTTTCACCAAGTTTTCCTTTGGGCGAC 1320
Qy 1321 CTGACAAACACCGGCTGGTGGCTGAGTGTGCTGCCATGGGCTTTGGCAACTGCGTGGAGC 1380
Db 1321 CTGACAAACACCGGCTGGTGGCTGAGTGTGCTGCCATGGGCTTTGGCAACTGCGTGGAGC 1380
Qy 1381 TGCAGCTTCAGTCTGCTTCAACTGGACGACGCTGCAAAACCCGAACCGTTTACA 1440
Db 1381 TGCAGCTTCAGTCTGCTTCAACTGGACGACGCTGCAAAACCCGAACCGTTTACA 1440
Qy 1441 TCTGCCAGTTTGGCCAGGACATCTCCCGGTGGGCGCCAGGCTCCCTGAGGCCCTGACCA 1500
Db 1441 TCTGCCAGTTTGGCCAGGACATCTCCCGGTGGGCGCCAGGCTCCCTGAGGCCCTGACCA 1500
Qy 1501 CATGGCTCCCTCGCCCTGGGAGCACCAGGCTCTGCTTACCTGTCTGCTGCCACCTGTCT 1560
Db 1501 CATGGCTCCCTCGCCCTGGGAGCACCAGGCTCTGCTTACCTGTCTGCTGCCACCTGTCT 1560
Qy 1561 GGNACAAAGGCCAGTTAAGACACATCTCTCATCTGTCCTCAAGAGGCTCTCAGACCTTGCAC 1620
Db 1561 GGAACAAGGCCAGTTAAGACACATCTCTCATCTGTCCTCAAGAGGCTCTCAGACCTTGCAC 1620
Qy 1621 AATGCCAGAAAGTTGGGCGAGAGAGGAGGAGCCAGTGTAGGGGCGAGGAGTGTGT 1680
Db 1621 AATGCCAGAAAGTTGGGCGAGAGAGGAGGAGCCAGTGTAGGGGCGAGGAGTGTGT 1680
Qy 1681 AGAAGAGCTGGGGCCCTTCGCTGCTTTTGAATGGGAAGATGGGCTTCAATTAGATGCG 1740
Db 1681 AGAAGAGCTGGGGCCCTTCGCTGCTTTTGAATGGGAAGATGGGCTTCAATTAGATGCG 1740
Qy 1741 GRAGGAGGACACCGCAGTGTCTCAAAAGGCTGCTCTTCCACCTGGCCGACGCC 1800
Db 1741 GRAGGAGGACACCGCAGTGTCTCAAAAGGCTGCTCTTCCACCTGGCCGACGCC 1800
Qy 1801 TGTGGGCGACGGAGCTTCCCTGTGGCATGAACCCCGGGGTATTAAATATGAATCAG 1860
Db 1801 TGTGGGCGACGGAGCTTCCCTGTGGCATGAACCCCGGGGTATTAAATATGAATCAG 1860
Qy 1861 CTGAAAAAANAANA 1876
Db 1861 CTGAAAAAANAANA 1876

RESULT 4

AAA49561
ID AAA49561 standard; cDNA; 1876 BP.
XX AC AAA49561;
XX AC AAA49561;
DT 25-SEP-2000 (first entry)
XX Human PRO347 cDNA.
XX PRO; membrane bound protein; secreted protein; PRO327;
KW PRO243; PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347;
KW PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;
KW antibody; screening; detection; inhibition; probe; primer; human;
ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 123..1490
FT /*tag= a
FT /product= PRO347 polypeptide
XX
XX PN WO200032776-A2.
XX

PD 08-JUN-2000.
XX
PF 01-DEC-1999; 99WO-US28301.
XX
PR 01-DEC-1998; 98WO-US25108.
PR 16-DEC-1998; 98US-0112850.
PR 22-DEC-1998; 98US-0113296.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E,
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Woney WI;
XX
DR WPI; 2000-412324/35.
XX P-PSDB; AAB01319.
XX
PT New human nucleic acids encoding secreted and transmembrane
PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
PT and diagnostic agents
XX
PS Claim 2; Fig 19; 187pp; English.
XX
CC New human nucleic acids encoding secreted and transmembrane
CC polypeptides which are designated as PRO polypeptides are described
CC The membrane-bound proteins have various industrial applications,
CC including as pharmaceutical and diagnostic agents. The membrane-bound
CC proteins can also be employed for screening of potential peptide or
CC small molecule inhibitors of the relevant receptor/ligand interaction.
CC Anti-PRO antibodies are useful for the affinity purification of PRO
CC from recombinant cell culture or natural sources.
XX
SQ Sequence 1876 BP; 387 A; 568 C; 574 G; 347 T; 0 other;

Query Match 100.0%; Score 1876; DB 21; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTTTTGTCCACAGCCAGCCTGACTGAGATTGTGATAGCTCCATCAGCCTG 60
Db 1 CTCCTTTTGTCCACAGCCAGCCTGACTGAGATTGTGATAGCTCCATCAGCCTG 60
Qy 61 AGAACAAGCCGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGAGGGCCCAACAGAC 120
Db 61 AGAACAAGCCGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGAGGGCCCAACAGAC 120
Qy 121 CCATGCTGCATCCAGAGACCTCCCTGGCCGGGGGATCTCTCTGCTGTCTCTGCCCC 180
Db 121 CCATGCTGCATCCAGAGACCTCCCTGGCCGGGGGATCTCTCTGCTGTCTCTGCCCC 180
Qy 181 TCCTTGGCACCCCTGGGCGAGAGGTGTGGCCACCCAGCTGCGAGGAGCGCTCCGATGG 240
Db 181 TCCTTGGCACCCCTGGGCGAGAGGTGTGGCCACCCAGCTGCGAGGAGCGCTCCGATGG 240
Qy 241 CCGGAGCCCTGAACAGGAAGAGAGTTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
Db 241 CCGGAGCCCTGAACAGGAAGAGAGTTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
Qy 301 GCTGGGTCCAGCCCTCGCGCTGACATCGCGAGGCTGGACTGGAGTGACAGCTGGCCCC 360
Db 301 GCTGGGTCCAGCCCTCGCGCTGACATCGCGAGGCTGGACTGGAGTGACAGCTGGCCCC 360
Qy 361 AACTTGGCTCAAGCCAGGCGAGCCCTCTGTGTGAATCCCAACCCCGAGCCTGGCATCCG 420
Db 361 AACTTGGCTCAAGCCAGGCGAGCCCTCTGTGTGAATCCCAACCCCGAGCCTGGCATCCG 420
Qy 421 TGTGGCGCACCTCGAAGTGGGCTGGAACATGCAGCTGTGCCCCGGGGCTTGGCGTCTCT 480
Db 421 TGTGGCGCACCTCGAAGTGGGCTGGAACATGCAGCTGTGCCCCGGGGCTTGGCGTCTCT 480
Qy 481 TTGTTGAAGTGGTCAAGCTATGTTTGCAGAGGGCGAGCGGTACACCCAGCGCAGAG 540
Db 481 TTGTTGAAGTGGTCAAGCTATGTTTGCAGAGGGCGAGCGGTACACCCAGCGCAGAG 540

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QY 541 AGTGTGCTCGCAAGCCACCTGCACCCACTACACACAGAGCTCGTGTGGGCCACCTCAAGCC 600
Db 541 AGTGTGCTCGCAAGCCACCTGCACCCACTACACACAGAGCTCGTGTGGGCCACCTCAAGCC 600
QY 601 AGCTGGGCTGTGGGGGACCTGTGCTCTGAGGCGCAGACAGCATAGAGCGTTTGTCT 660
Db 601 AGCTGGGCTGTGGGGGACCTGTGCTCTGAGGCGCAGACAGCATAGAGCGTTTGTCT 660
QY 661 GTGCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCATTAAGA 720
Db 661 GTGCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCATTAAGA 720
QY 721 AGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 780
Db 721 AGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 780
QY 781 ATGAGGGGGCTGTGTAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 840
Db 781 ATGAGGGGGCTGTGTAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 840
QY 841 GAGTCTCAACATCAGCACCTGCCACTGCCACTGCCACTGCCACTGCCACTGCCACTGCCACT 900
Db 841 GAGTCTCAACATCAGCACCTGCCACTGCCACTGCCACTGCCACTGCCACTGCCACTGCCACT 900
QY 901 GCCAAGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGT 960
Db 901 GCCAAGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGT 960
QY 961 GCCTGTGTGATCGGTACGGGTACGGGTACGGGTACGGGTACGGGTACGGGTACGGGTACGGT 1020
Db 961 GCCTGTGTGATCGGTACGGGTACGGGTACGGGTACGGGTACGGGTACGGGTACGGGTACGGT 1020
QY 1021 ACACCTGTGACCTGAGTATCAGGAGACTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1021 ACACCTGTGACCTGAGTATCAGGAGACTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 ATTACAGAGCCAGGATGAATGTGAGAGGAAGGCGGGTGTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1081 ATTACAGAGCCAGGATGAATGTGAGAGGAAGGCGGGTGTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 1141 AGAAGTGCAGGACATCTCGCTCTCTATCTGCGCGCGCTGAGAGCACCAACAGAGGTGA 1200
Db 1141 AGAAGTGCAGGACATCTCGCTCTCTATCTGCGCGCGCTGAGAGCACCAACAGAGGTGA 1200
QY 1201 CTGACACTGACTTCGAGACAGGACTTCTGATGGGCTCACCTACAGACCGCCAAAG 1260
Db 1201 CTGACACTGACTTCGAGACAGGACTTCTGATGGGCTCACCTACAGACCGCCAAAG 1260
QY 1261 ACTCTTCCGCTGGGCGCACAGGGAGCACAGGCGCTTACACAGTTTGTGCTTTGGGCAGC 1320
Db 1261 ACTCTTCCGCTGGGCGCACAGGGAGCACAGGCGCTTACACAGTTTGTGCTTTGGGCAGC 1320
QY 1321 CTGACAAACAGGCGTGGTGTGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
Db 1321 CTGACAAACAGGCGTGGTGTGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
QY 1381 TGCAGGCTTCAGCTGCTTCACTTGAACGACGACGCGCTGCAAAACCCGAAACCGTTACA 1440
Db 1381 TGCAGGCTTCAGCTGCTTCACTTGAACGACGACGCGCTGCAAAACCCGAAACCGTTACA 1440
QY 1441 TCTGCCAGTTTGGCCAGGAGCACATCTCCCGGTGGGGCCAGGGTCTGTGAGGCGCTGACCA 1500
Db 1441 TCTGCCAGTTTGGCCAGGAGCACATCTCCCGGTGGGGCCAGGGTCTGTGAGGCGCTGACCA 1500
QY 1501 CATGGCTCCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
Db 1501 CATGGCTCCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1561 GGAACAGGGCCAGGTTAAGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
Db 1561 GGAACAGGGCCAGGTTAAGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
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QY 1621 AATGCCAGAAGTTGGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1680
Db 1621 AATGCCAGAAGTTGGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1680
QY 1681 AGAAGAAGCTGGGCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCC 1740
Db 1681 AGAAGAAGCTGGGCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCC 1740
QY 1741 GAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
Db 1741 GAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
QY 1801 TGTGGGCGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
Db 1801 TGTGGGCGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
QY 1861 CTGAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1876
Db 1861 CTGAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1876

RESULT 5
AADI2570
ID AADI2570 standard; cDNA; 1775 BP.
XX
AC AADI2570;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human protein having hydrophobic domain encoding cDNA clone HP10760.
XX
KW Human; hydrophobic domain; gene therapy; nutritional supplement;
KW cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
KW haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
KW contraceptive; antiinfertility; antiinflammatory; ss.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
CDS 62..1402
FT /*tag= a
FT /product= "Human protein having hydrophobic domain"
FT /note= "CDS is specifically is claimed in claim 3"
FT sig_peptide 62..142
FT FT
FT mat_peptide 143..1399
FT FT
FT /*tag= c
FT /product= "Mature human protein with hydrophobic domain"
XX
WO200149728-A2.
PN
XX
PD 12-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-JP09359.
XX
PR 06-JAN-2000; 2000JP-0000585.
PR 06-JAN-2000; 2000JP-0000588.
PR 11-JAN-2000; 2000JP-0002299.
PR 03-FEB-2000; 2000JP-0026862.
PR 03-MAR-2000; 2000JP-0058367.
XX
PA (PROT-) PROTEGENE INC.
PA (SAGA ) SAGAMI CHEM RES CENT.
XX
PI Kato S, Kimura T;
XX
WPI; 2001-418355/44.
DR P-PSDB; AAE06575.
XX
PT Human proteins with hydrophobic domains and the nucleic acids encoding
```

PT them, useful for preventing diagnosing and treating e.g. cancer,
PT Alzheimer's and inflammation -
XX
PS
PS
XX Claim 4; Page 271-275; 563pp; English.
XX
CC The present sequence is human protein with hydrophobic domain encoding
CC cDNA clone HP10760. The polynucleotide and polypeptide of the invention
CC may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The polynucleotides
CC may be used to produce the polypeptide, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the protein. The
CC polynucleotides and its complementary sequences may also be used as DNA
CC probes in diagnostic assays and also used in gene therapy. The
CC polypeptides may also be used as antigens in the production of antibodies
CC and in assays to identify modulators of polypeptide expression and
CC activity. The polypeptides and nucleic acids may be used as nutritional
CC supplements, to modulate cytokine and cell proliferation activity, to
CC modulate immune stimulation or suppression (e.g. for the treatment of
CC microbial infections and autoimmune disorders such as multiple sclerosis,
CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
CC haematopoiesis, to modulate tissue growth activity (e.g. for the
CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
CC disease), to modulate activin and inhibin activity (e.g. for controlling
CC fertility), to modulate chemotactic and chemokinetic activity, to
CC modulate haemostatic and thrombolytic activity, to modulate receptor
CC ligand activity, to modulate inflammation and to inhibit tumour growth.
XX
SQ Sequence 1775 BP; 360 A; 541 C; 549 G; 325 T; 0 other;

Query Match 54.9%; Score 1029; DB 22; Length 1775;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 102 CTGTGAGGGGCCCCAACAGACCCATCTGTCATCCAGAGACTCCCTCCGCGGGGGCATCTC 161
DB 41 CTGTGAGGGGCCCCAACAGACCCATCTGTCATCCAGAGACTCCCTCCGCGGGGGCATCTC 100
QY 162 CTGGCTGTGTCTCTGGCCCTCTTGGACACCACTTGGGAGAGAGTGTGGCCACCCAGCTG 221
DB 101 CTGGCTGTGTCTCTGGCCCTCTTGGACACCACTTGGGAGAGAGTGTGGCCACCCAGCTG 160
QY 222 CAGGACAGGCTCGATGGCGGAGCCCTGAACAGGAGAGAGTTCCTGTCTCTCTCC 281
DB 161 CAGGACAGGCTCGATGGCGGAGCCCTGAACAGGAGAGTTCCTGTCTCTCTCC 220
QY 282 CTGCACAAACCGCTGCGAGCTGGGTTCAGCCCTGCGGTGACATCGGAGGCTGGAC 341
DB 221 CTGCACAAACCGCTGCGAGCTGGGTTCAGCCCTGCGGTGACATCGGAGGCTGGAC 280
QY 342 TGGAGTGACAGCTGGCCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACC 401
DB 281 TGGAGTGACAGCTGGCCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACC 340
QY 402 CCGAGCTGTCATCCGCGCTGTGGCGACACCTGCAAGTGGGCTGGAACATGACGTGCTG 461
DB 341 CCGAGCTGTCATCCGCGCTGTGGCGACACCTGCAAGTGGGCTGGAACATGACGTGCTG 400
QY 462 CCGCGGGCTGTGGCTGCTTGTGTAAGTGGTACGCTATGTTTGCAGAGGGGCGAGCGG 521
DB 401 CCGCGGGCTGTGGCTGCTTGTGTAAGTGGTACGCTATGTTTGCAGAGGGGCGAGCGG 460
QY 522 TACAGCCACCGCGCAGAGAGTGTGCTCGCAACCCACCTGCACCCACTACACGAGCTC 581
DB 461 TACAGCCACCGCGCAGAGAGTGTGCTCGCAACCCACCTGCACCCACTACACGAGCTC 520
QY 582 GTGTGGGCGACCTCAAGCCAGCTGGGCTGTGGGCGGCGACCTGTGCTGTGAGGCCAGACA 641
DB 521 GTGTGGGCGACCTCAAGCCAGCTGGGCTGTGGGCGGCGACCTGTGCTGTGAGGCCAGACA 580
QY 642 GCGATAGAGCCCTTGTCTGTCTACTTCCGCCGAGGCAACTGGGAGGTCAACGGGAAG 701
DB 581 GCGATAGAGCCCTTGTCTGTCTACTTCCGCCGAGGCAACTGGGAGGTCAACGGGAAG 640

QY 702 ACAATCATCCCTATAGAAGGGTGCCTGGTGTCTGCTGTGCACAGCCAGTGTCTCAGGC 761
DB 641 ACAATCATCCCTATAGAAGGGTGCCTGGTGTCTGCTGTGCACAGCCAGTGTCTCAGGC 700
QY 762 TGCCTTCAAGGCTTGGGACCATCCAGGGGGCTCTGTGAGTCCCAAGGAATCTTGTCTGC 821
DB 701 TGCCTTCAAGGCTTGGGACCATCCAGGGGGCTCTGTGAGTCCCAAGGAATCTTGTCTGC 760
QY 822 ATGAGCTGCCAGAACCATGAGCTCTCAACATCAGCACCTGCCACTGCCACTGTCCCT 881
DB 761 ATGAGCTGCCAGAACCATGAGCTCTCAACATCAGCACCTGCCACTGCCACTGTCCCT 820
QY 882 GGCTACAGGGGAGACTACTGCCAAGTGAAGTGCAGCTGCAGTGTGTGCAGCGCGGTTC 941
DB 821 GGCTACAGGGGAGACTACTGCCAAGTGAAGTGCAGCTGCAGTGTGTGCAGCGCGGTTC 880
QY 942 CCGGAGGAGGAGTGTCTGTGCTGTGTGACATCGGCTACGGGGGAGCCCAAGTGTGCCACC 1001
DB 881 CCGGAGGAGGAGTGTCTGTGCTGTGTGACATCGGCTACGGGGGAGCCCAAGTGTGCCACC 940
QY 1002 AAGGTGCAATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGAGACTGCTTTCATGGTG 1061
DB 941 AAGGTGCAATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGAGACTGCTTTCATGGTG 1000
QY 1062 TCTTTCAGAGGAGACACCTATTACAGAGCCAGGATGAAATGTTCAGAGGAAAGCGGGTG 1121
DB 1001 TCTTTCAGAGGAGACACCTATTACAGAGCCAGGATGAAATGTTCAGAGGAAAGCGGGTG 1060
QY 1122 CTGCCCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCTTCTATCTGGGCGGCTG 1181
DB 1061 CTGCCCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCTTCTATCTGGGCGGCTG 1120
QY 1182 GAGACCAACCAAGGAGTGTGACAGTGTTCGAGACCAAGGAATCTTCTGATCGGCTC 1241
DB 1121 GAGACCAACCAAGGAGTGTGACAGTGTTCGAGACCAAGGAATCTTCTGATCGGCTC 1180
QY 1242 ACCTACAAGACCGCCAAAGGACTCTTCCGCTGGGCCACAGGGGAGCACCAGGCTTCACC 1301
DB 1181 ACCTACAAGACCGCCAAAGGACTCTTCCGCTGGGCCACAGGGGAGCACCAGGCTTCACC 1240
QY 1302 AGTTTGGCTTTGGCAGCCTGTGACACACGCGG 1334
DB 1241 AGTTTGGCTTTGGCAGCCTGTGACACACGCGG 1273
RESULT 6
AAZ23299
ID AAZ23299 standard; cDNA; 1856 BP.
XX
AC AAZ23299;
XX
DT 31-JAN-2000 (first entry) *
XX
DE Human T139 protein encoding cDNA.
XX
KW Human; T139 polypeptide; immune system disorder; spermatogenesis; ss;
KW sperm-egg fusion; testicular disorder; testicular cancer; gene mapping.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 95..1435
FT /*tag= a
FT /product= "T139 protein"
XX
PN WO954343-A2.
XX
PD 28-OCT-1999.
XX
PF 23-APR-1999; 99WO-US08896.
XX
PR 23-APR-1998; 98US-0065661.
XX

(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

Holzman D;

WPI: 1999-633969/54.

P-P5DB: AAY41266.

Human T139 nucleic acids and polypeptides, useful for treating
proliferative disorders associated with aberrant T139 expression or
activity -

Claim 2; Fig 1; 115pp; English.

This cDNA encodes a human T139 polypeptide. The T139 polypeptide can be expressed by standard recombinant methodology. The T139 cDNA insert is deposited with ATCC under accession number 98694. The T139 polypeptides and polynucleotides can be administered therapeutically or prophylactically to treat/prevent disorders associated with aberrant T139 expression or activity, especially proliferative or differentiative disorders, e.g. of the immune system. They can be used to modulate spermatogenesis, e.g. as a contraceptive to decrease spermatogenesis or to treat disorders related to defects in sperm-egg fusion. They may also be useful to treat testicular disorders e.g. testicular cancer. The polypeptides may be used to identify selectively binding compounds which may be useful for detecting the polypeptides in samples; and identifying compounds modulating polypeptide activity. The polynucleotides are useful for producing probes or primers that selectively hybridize to the polynucleotides which may be useful for detecting the polynucleotides in a sample, gene mapping; identifying cells or tissues expressing aberrant T139 levels; determining if a gene has been mutated or deleted to identify subjects at risk for or having a disorder associated with T139 expression or activity and to monitor therapeutic interventions; and for producing antisense sequences for therapeutic administration to modulate /prevent T139 expression.

Sequence 1856 BP; 402 A; 560 C; 564 G; 330 T; 0 other;

Query Match 54.9%; Score 1029; DB 20; Length 1856;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 102 CTTGAGGCGCCACAGACCCATGCTGCATCCAGAGACCTCCCTGCGGGGGGCATCTC 161

DB 74 CTTGAGGCGCCACAGACCCATGCTGCATCCAGAGACCTCCCTGCGGGGGGCATCTC 133

QY 162 CTGGCTGTGCTCTCTGCTCCCTCTTGGCACACCTGGGACAGGTGTGGCCACCCAGCTG 221

DB 134 CTGGCTGTGCTCTCTGCTCCCTCTTGGCACACCTGGGACAGGTGTGGCCACCCAGCTG 193

QY 222 CAGGACAGGCTCCGATGGCCGGAGCCCTGAACAGGAAGGAGAGTTTCTTCTCTCTCC 281

DB 194 CAGGACAGGCTCCGATGGCCGGAGCCCTGAACAGGAAGGAGAGTTTCTTCTCTCTCC 253

QY 282 CTGCACAACGGCTGGCAGCTGGTGTCCAGCCCTGCGGCTGCATCGGAGGCTGGAC 341

DB 254 CTGCACAACGGCTGGCAGCTGGTGTCCAGCCCTGCGGCTGCATCGGAGGCTGGAC 313

QY 342 TGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGCGACCCCTCTCTGGAATCCCAACC 401

DB 314 TGGAGTGACAGCTGGCCCAACTGGCTCAAGCCAGGCGACCCCTCTCTGGAATCCCAACC 373

QY 402 CCGAGCTGGCATCGGCTGTGGCCACCCCTGCAAGTGGGCTGGAACATGCAGCTGCTG 461

DB 374 CCGAGCTGGCATCGGCTGTGGCCACCCCTGCAAGTGGGCTGGAACATGCAGCTGCTG 433

QY 462 CCGCGGGCTTGGCTGCTCTTGTGAAGTGGTGCAGCCATGTTGTTGAGAGGGGACGGG 521

DB 434 CCGCGGGCTTGGCTGCTCTTGTGAAGTGGTGCAGCCATGTTGTTGAGAGGGGACGGG 493

QY 522 TACAGCCAGCGGACGAGAGTGTGTCGAACGCCACCTGCACCCACTACACGAGCTC 581

DB 494 TACAGCCAGCGGACGAGAGTGTGTCGAACGCCACCTGCACCCACTACACGAGCTC 553

QY 582 GTGTGGGCGACCTCAAGCCAGCTGGGCTGTGGGCGGCACCTGTGCTCTGCAGGCCAGACA 641

DB 554 GTGTGGGCGACCTCAAGCCAGCTGGGCTGTGGGCGGCACCTGTGCTCTGCAGGCCAGACA 613

QY 642 GCGATAGAAGCCTTTGTGTGCTGCTACTCCCGGAGGCAACTGGGAGGTCAACGGGAAG 701

DB 614 GCGATAGAAGCCTTTGTGTGCTGCTACTCCCGGAGGCAACTGGGAGGTCAACGGGAAG 673

QY 702 ACAATCATCCCTATAAGAAGGCTGCTGTGCTCTGTCACACGCCAGTGTCTCAGGC 761

DB 674 ACAATCATCCCTATAAGAAGGCTGCTGTGCTCTGTCACACGCCAGTGTCTCAGGC 733

QY 762 TGTCTTAAAGCCTGGGACCATCGAGGGGGCTCTGTGAGGTGCCCCAGGAATCCTTGTGCG 821

DB 734 TGTCTTAAAGCCTGGGACCATCGAGGGGGCTCTGTGAGGTGCCCCAGGAATCCTTGTGCG 793

QY 822 ATGAGCTGCCAGAACCATGAGGCTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCT 881

DB 794 ATGAGCTGCCAGAACCATGAGGCTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCT 853

QY 882 GGCTACAGGGGAGATGCTGCCAAGTGAAGTGCAGCTGTGTCACGGCCGGGCTC 941

DB 854 GGCTACAGGGGAGATGCTGCCAAGTGAAGTGCAGCTGTGTCACGGCCGGGCTC 913

QY 942 CGGAGGAGGAGTGTGCTGCTGTGACATGCGGTACGGGGAGCCAGTGTGCGCAC 1001

DB 914 CGGAGGAGGAGTGTGCTGCTGTGACATGCGGTACGGGGAGCCAGTGTGCGCAC 973

QY 1002 AAGTGTGCTTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTCTTCATGGTG 1061

DB 974 AAGTGTGCTTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTCTTCATGGTG 1033

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DB 1034 TCTTCAGAGGCGACACACCTATTACAGAGCCAGGATGAAATGTTCAGAGGAAGCGGGGTG 1093

QY 1122 CTGCCCCAGATCAAGAGCCAGAAAGTGCAGGACATCTCGCCCTTCTATCTGGGCGCGCTG 1181

DB 1094 CTGCCCCAGATCAAGAGCCAGAAAGTGCAGGACATCTCGCCCTTCTATCTGGGCGCGCTG 1153

QY 1182 GAGACCCACCAAGGAGTGTGACAGTGTGACCTGAGGATCGACGGAGACTCTTCGATGGGCTC 1241

DB 1154 GAGACCCACCAAGGAGTGTGACAGTGTGACCTGAGGATCGACGGAGACTCTTCGATGGGCTC 1213

QY 1242 ACCTCAAGACCCGCAAGGACTCTTCCGCTGGGCGCACAGGGAGGACACAGGCTTCAC 1301

DB 1214 ACCTCAAGACCCGCAAGGACTCTTCCGCTGGGCGCACAGGGAGGACACAGGCTTCAC 1273

QY 1302 AGTTTGGCTTTGGGAGCCTTGACACACCGGG 1334

DB 1274 AGTTTGGCTTTGGGAGCCTTGACACACCGGG 1306

RESULT 7

AAD33531

ID AAD33531 standard; cDNA; 1856 BP.

XX AC AAD33531;

XX DT 01-JUL-2002 (first entry)

XX Human T139 (TANGO-139) cDNA.

DE Human; haematopoiesis; clotting; kidney failure; wound healing; cancer;

KW neoplasia; pancreatic disorder; pancreatitis; cerebrovascular disease;

KW heart disorder; ischaemic heart disease; neuroprotective; vulnary;

KW cardiovascular disorder; ischaemic heart disease; immunosuppressive;

KW glomerular disease; glomerulonephritis; uterine disorder; hyperplasia;

KW fetal spleen; prostate disorder; inflammatory disease; Crohn's disease;

KW proliferative disorder; gynaecological; haemostatic; antibacterial;

KW systemic lupus erythematosus; immunodeficiency disorder; antisthmatic;

KW cytostatic; nephrotropic; antidiabetic; cerebroprotective; tranquiliser;

KW hypotensive; tumour; injury; trauma; antiangiinal; vasotropic; antiulcer;

apoptotic disorder; rheumatoid arthritis; cardiant; renal disorder; hepatotropic; antipsoriatic; antiallergic; dermatological; virucide; T139; gene; ss.

Homo sapiens.

Key	Location/Qualifiers
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C  
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E
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/cag-
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specifically referred in claim

[illegible]

US2002028508-A1.

07-MAR-2003

07-MAR-2002.

21-FEB-2001: 2001US-0790264.

21 FEB 2001, 200103-0730Z04:

23-APR-1998; 98US-0065363.

23-APR-1998; 98US-0065661.

22-JUN-1998; 98US-0102705.

29-JUL-1998; 98US-0124538.

23-APR-1999; 99US-0298531.
22-JUN-1999; 99US-0337930

22-JUN-1999; 99US-0337930.
29-JUL-1999; 99US-0363630.

0-5066, 1, 666T, 500 67

(HOLT/) HOLTZMAN D A.

(GOOD//) GOODEARL A D J

(MCCA/) MCCARTHY S A.

Holtzman DA Gooden

Holtzman DA, Good

Novel TANGO polypeptides and nucleic acid molecules useful as modulating agents in regulating cellular processes and for diagnosing and treating heart, liver, lung, kidney, inflammatory and cellular proliferative disorders -

Claim 26; Fig 1; 138pp; English.

The invention relates to nucleic acids encoding a variety of proteins (human TANGO-139), T125 (TANGO-125), T110 (TANGO-110), murine T175 (TANGO-175), human T175 or murine WDNW-2), having diagnostic, preventive, therapeutic and other uses. Polypeptide of the invention has the ability to inhibit a proteinase activity, to modulate cell-cell interactions, haematopoiesis and the ability to modulate clotting. Polypeptide and polynucleotide of the invention are useful for diagnosing and treating disorders characterised by their aberrant expression or activity. The antibodies are useful as modulating agents in regulating a variety of cellular processes e.g. cell proliferation and/or cell differentiation. TANGO-139 is useful for treating kidney defects such as kidney failure. TANGO-125 is useful in wound healing and for treating cancer, TANGO-110 is useful for treating neoplasia, TANGO-177 or WDNW-2 is useful for treating cancer, are useful to treat pancreatic disorders, such as pancreatitis, cerebrovascular disease, and tumours, and injury or trauma to the brain. TANGO-125, 110, 175 molecules treat heart disorders, e.g., ischaemic heart disease, cardiovascular disorders, such as ischaemic heart disease. TANGO-139, 125, 110 and 175 molecules are useful to treat renal (kidney) disorders, such as glomerular disease (e.g., acute and chronic glomerulonephritis), TANGO-175 is useful to treat uric acid disorders, hyperplasia of the endometrium. TANGO-110 is useful to treat spleen, e.g., the fetal spleen, associated diseases and disorders. TANGO-125 treats prostate disorders, such as inflammatory diseases, Crohn's

Db 914 CGGAGGAGGAGTGCTGCTGCTGTGACATCGGCTACGGGGGAGCCAGTGTGCCACC 973
QY 1002 AAGGTGCAATTTCCCTCCACACCTGTGACCTGAGGATCGACGAGACTGTTTCATGGTG 1061
Db 974 AAGGTGCAATTTCCCTCCACACCTGTGACCTGAGGATCGACGAGACTGTTTCATGGTG 1033
QY 1062 TCTTCAGAGGAGACACCTATTATACAGAGCCAGGATGAAATGTCTAGAGGAAAGGGGGTG 1121
Db 1034 TCTTCAGAGGAGACACCTATTATACAGAGCCAGGATGAAATGTCTAGAGGAAAGGGGGTG 1093
QY 1122 CTGGCCAGATCAAGAGCCGAAAGTGCAGGACATCTCGCTTCTATCTGGCCGCGCTG 1181
Db 1094 CTGGCCAGATCAAGAGCCGAAAGTGCAGGACATCTCGCTTCTATCTGGCCGCGCTG 1153
QY 1182 GAGACACCAACAGAGTGACTGACAGTGACTTCGAGACCAAGGAATCTTGATCGGGCTC 1241
Db 1154 GAGACACCAACAGAGTGATGACAGTGACTTCGAGACCAAGGAATCTTGATCGGGCTC 1213
QY 1242 ACCTACAAGACCCCAAGGACTCTTCCGCTGGGCCACAGGGGAGCACAGGCCCTTCACC 1301
Db 1214 ACCTACAAGACCCCAAGGACTCTTCCGCTGGGCCACAGGGGAGCACAGGCCCTTCACC 1273
QY 1302 AGTTTTCCTTTGGGAGACCTGACACACCGGG 1334
Db 1274 AGTTTTCCTTTGGGAGACCTGACACACCGGG 1306

RESULT 8

AAF24152

ID AAF24152 standard; DNA; 1923 BP.

XX AC

AAF24152;

XX DT

23-MAR-2001 (first entry)

XX DE

Human secreted protein DNA #2.

XX KW

Secreted protein; gene therapy; vaccine; cancer; leukemia;

XX KW

autoimmune disease; allergy; inflammation; graft rejection;

XX KW

hyperproliferation; cardiovascular; infection; ds.

XX OS

Homo sapiens.

XX PN

W0200075375-A1.

XX PD

14-DEC-2000.

XX PF

02-JUN-2000; 2000WO-US15187.

XX PR

07-JUN-1999; 99US-0137725.

XX PR

(HUMA-) HUMAN GENOME SCI INC.

XX PA

Ruben SM, Birse CE, Duan RD, Soppet DR, Rosen CA, Shi Y;

XX PI

Lafleur DW, Olsen HS, Ebner R, Florence KA, Ni J, Young PE;

XX PI

WPI; 2001-061741/07.

XX DR

Nucleic acids encoding 26 human secreted polypeptides, useful e.g. for

XX PT

preventing, diagnosing and/or treating cancers and for promoting wound

XX PT

healing -

XX PS

Claim 1; Page 416-417; 530pp; English.

XX XX

The present invention relates to 26 secreted human proteins. The

XX CC

proteins may be used in the prevention, diagnosis and treatment of

XX CC

diseases associated with inappropriate polypeptide expression.

XX CC

For example, they may be used in gene therapy or in vaccines.

XX CC

Typical of diseases which are potentially treatable are cancers

XX CC

(including leukemia), autoimmune diseases, allergies, inflammation,

XX CC

graft rejection, hyperproliferation, cardiovascular diseases

XX CC

(particularly critical limb ischemia and coronary disease) and any

XX CC

involving abnormal angiogenesis, neurodegeneration and/or

CC infectious diseases.

XX XX

SQ Sequence 1923 BP; 444 A; 568 C; 569 G; 342 T; 0 other;

XX XX

Query Match 54.9%; Score 1029; DB 22; Length 1923;

XX XX

Best Local Similarity 99.7%; Pred. No. 0;

XX XX

Matches 1229; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 102 CCGAGCGGCCCAACAGACCATGCTGCCATCCAGAGACCTCCCTGCGCGGGGCATCTC 161
Db 119 CCGAGCGGCCCAACAGACCATGCTGCCATCCAGAGACCTCCCTGCGCGGGGCATCTC 178
QY 162 CTGGGTGTCTCTCTGCGCCCTCTTGGCACACACCTGGSCAGAGGTGTGCCACCCAGCTG 221
Db 179 CTGGGTGTCTCTCTGCGCCCTCTTGGCACACACCTGGSCAGAGGTGTGCCACCCAGCTG 238
QY 222 CAGGAGCAGGCTCCGATGGCCGAGCCCTGAACAGGAGAGAGTTTCTTGTCTCTCTCC 281
Db 239 CAGGAGCAGGCTCCGATGGCCGAGCCCTGAACAGGAGAGAGTTTCTTGTCTCTCTCC 298
QY 282 CTGCACAAACCGCTCGCGAGCTGGGTCCAGCCCTCGCGCTGACATGCGGAGGCTGGAC 341
Db 299 CTGCACAAACCGCTCGCGAGCTGGGTCCAGCCCTCGCGCTGACATGCGGAGGCTGGAC 358
QY 342 TGGAGTGCACAGCCTGGCCCAACTGGCTCAAGCCAGGSCAGCCCTCTCTGGAATCCCAACC 401
Db 359 TGGAGTGCACAGCCTGGCCCAACTGGCTCAAGCCAGGSCAGCCCTCTCTGGAATCCCAACC 418
QY 402 CCGAGCCTGGCATCCGGCTGTGGCGCACCCCTGCAAGTGGGCTGGGAACATGCAGCTGCTG 461
Db 419 CCGAGCCTGGCATCCGGCTGTGGCGCACCCCTGCAAGTGGGCTGGGAACATGCAGCTGCTG 478
QY 462 CCGCGGGCTTGGCGTCTTGTGAAGTGTGACGCTATGTTTGCAGAGGGCAGCGG 521
Db 479 CCGCGGGCTTGGCGTCTTGTGAAGTGTGACGCTATGTTTGCAGAGGGCAGCGG 538
QY 522 TACAGCCACCGCGCAGGAGAGTGTCTGCAACGCCACCTGCACCCACTACACAGCAGCTC 581
Db 539 TACAGCCACCGCGCAGGAGAGTGTCTGCAACGCCACCTGCACCCACTACACAGCAGCTC 598
QY 582 GTGTGGGCGCACCTCAAGCCAGCTGGGCTGTGGGGGCGCACCTGTCTCTGCAAGGCCAGACA 641
Db 599 GTGTGGGCGCACCTCAAGCCAGCTGGGCTGTGGGGGCGCACCTGTCTCTGCAAGGCCAGACA 658
QY 642 GCGATAGAAGCCTTGTCTGTGCTACTCCCGCGAGGCAACTGGGAGGTCAACGGGAAG 701
Db 659 GCGATAGAAGCCTTGTCTGTGCTACTCCCGCGAGGCAACTGGGAGGTCAACGGGAAG 718
QY 702 ACAATCATCCCTTATAAGAGGCTGCTGTGTTTCTGCTGCAACGCCAGCAGTGTCTCAGGC 761
Db 719 ACAATCATCCCTTATAAGAGGCTGCTGTGTTTCTGCTGCAACGCCAGCAGTGTCTCAGGC 778
QY 762 TGCTTCAAGCCTGGGACCATGAGGGGGCTCTGTGAGGTCCCGCAGGAATCCCTGTGCGC 821
Db 779 TGCTTCAAGCCTGGGACCATGAGGGGGCTCTGTGAGGTCCCGCAGGAATCCCTGTGCGC 838
QY 822 ATGAGCTGCGCAGAACCATGGACGCTCTCAACATCAGCAGCTGCCACTGTGCCCTTCCCT 881
Db 839 ATGAGCTGCGCAGAACCATGGACGCTCTCAACATCAGCAGCTGCCACTGTGCCCTTCCCT 898
QY 882 GGTACACGGGCGAGATCTACTGCCAAGTGAAGTGCAGCCTGCAAGTGTGTGACAGGGCGGTTTC 941
Db 899 GGTACACGGGCGAGATCTACTGCCAAGTGAAGTGCAGCCTGCAAGTGTGTGACAGGGCGGTTTC 958
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Db 959 CCGGAGGAGGAGTGTCTGCTGCTGTGACATCGGCTACGGGGGAGCCAGTGTGCCACC 1018
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QY 1062 TCTTACAGGSCAGACACCTATTACAGAGCCAGGATGAAATGTCAAGAGAAAGCGGGGTG 1121

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Db 1139 CTGGCCAGATCAAGAGCCAGAAAGTGAGGACATCTCGCTTCTTACTTGGCGCGCTG 1198
QY 1182 GAGACACCAACGAGGTGACTGACAGTGTGACAGTGTGAGACAGGAACTTCTGGATCGGGCTC 1241
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Db 1259 ACCTACAAGACCGCAGGACTCTTCGCTGGGCGCACAGGGAGACACAGGCGCTTCACC 1318
QY 1302 AGTTTTCCTTTGGGCGAGCTGACAAACACCGG 1334
Db 1319 AGTTTTCCTTTGGGCGAGCTGACAAACACCGG 1351
RESULT 9
AAZ23300
ID AAZ23300 standard; cDNA; 1338 BP.
XX
AC AAZ23300;
XX
DT 31-JAN-2000 (first entry)
XX
XX Human T139 protein coding sequence.
DE
XX
KW Human; T139 polypeptide; immune system disorder; spermatogenesis; ss;
KW sperm-egg fusion; testicular disorder; testicular cancer; gene mapping.
XX
OS Homo sapiens.
XX
PN WO954343-A2.
XX
PD 28-OCT-1999.
XX
PF 23-APR-1999; 99WO-US08896.
PR 23-APR-1998; 98US-0065661.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
XX Holtzman D;
XX
XX WPI; 1999-633969/54.
XX P-PSDB; AAY41266.
XX
PT Human T139 nucleic acids and polypeptides, useful for treating
PT proliferative disorders associated with aberrant T139 expression or
PT activity -
XX
PS Claim 2; Page 114; 115pp; English.
XX
CC This represents the coding sequence of the human T139 polypeptide. The
CC T139 polypeptide can be expressed by standard recombinant methodology.
CC The T139 cDNA insert is deposited with ATCC under accession number
CC 98694. The T139 polypeptides and polynucleotides can be administered
CC therapeutically or prophylactically to treat/prevent disorders associated
CC with aberrant T139 expression or activity, especially proliferative or
CC differentiative disorders, e.g. of the immune system. They can be used to
CC modulate spermatogenesis, e.g. as a contraceptive to decrease
CC spermatogenesis or to treat disorders related to defects in sperm-egg
CC fusion. They may also be useful to treat testicular disorders e.g.
CC testicular cancer. The polypeptides may be used to identify selectively
CC binding compounds which may be useful for detecting the polypeptides in
CC samples; and identifying compounds modulating polypeptide activity. The
CC polynucleotides are useful for producing probes or primers that
CC selectively hybridize to the polynucleotides which may be useful for
CC detecting the polynucleotides in a sample; gene mapping; identifying
CC cells or tissues expressing aberrant T139 levels; determining if a gene

CC has been mutated or deleted to identify subjects at risk for or having a
CC disorder associated with T139 expression or activity and to monitor
CC therapeutic interventions; and for producing antisense sequences for
CC therapeutic administration to modulate/prevent T139 expression.
XX
SQ Sequence 1338 BP; 259 A; 420 C; 413 G; 246 T; 0 other;
Query Match 53.7%; Score 1008; DB 20; Length 1338;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1208; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 123 ATGCTGATCCAGAGACCTCCCTGGCGGGGCGCATCTCTGTGCTGTGCTCTGGCCCTC 182
Db 1 ATGCTGATCCAGAGACCTCCCTGGCGGGGCGCATCTCTGTGCTGTGCTCTGGCCCTC 60
QY 183 CTGGCACCACCTGGGCGAGAGGTGTGGCCACCCAGCTGAGAGAGAGGTCCGATGGCC 242
Db 61 CTGGCACCACCTGGGCGAGAGGTGTGGCCACCCAGCTGAGAGAGAGGTCCGATGGCC 120
QY 243 GGAGCCCTGAACAGGAAGGAGAGTTTCTTGCTCTCTCCCTGCACACCCGCTGCGCAGC 302
Db 121 GGAGCCCTGAACAGGAAGGAGAGTTTCTTGCTCTCTCCCTGCACACCCGCTGCGCAGC 180
QY 303 TGGTCCAGCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCTGGCCCAA 362
Db 181 TGGTCCAGCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCTGGCCCAA 240
QY 363 CTGGCTCAAGCAGGCGAGCCCTCTGTGGAATCCNACCAGCTGGATCCGGGCTG 422
Db 241 CTGGCTCAAGCAGGCGAGCCCTCTGTGGAATCCNACCAGCTGGATCCGGGCTG 300
QY 423 TGGCCACCCCTGCAAGTGGGTGGAACATGACAGTGTCTCCCGGGCTTGGGCTCCTTT 482
Db 301 TGGCCACCCCTGCAAGTGGGTGGAACATGACAGTGTCTCCCGGGCTTGGGCTCCTTT 360
QY 483 GTTGAAGTGTGACCCCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACCGCGGAGAG 542
Db 361 GTTGAAGTGTGACCCCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACCGCGGAGAG 420
QY 543 TGTGCTCGACACGCGACCTGTCACCCACTACAGCGAGCTGTGTGGGCCACCTCAAGCAG 602
Db 421 TGTGCTCGACACGCGACCTGTCACCCACTACAGCGAGCTGTGTGGGCCACCTCAAGCAG 480
QY 603 CTGGGCTGTGGCGGCGACCTGTGCTCTGAGGCCAGACAGCGATAGAAGCTTTGTCTGT 662
Db 481 CTGGGCTGTGGCGGCGACCTGTGCTCTGAGGCCAGCGAGCGATAGAAGCTTTGTCTGT 540
QY 663 GCCTACTCCCGCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAG 722
Db 541 GCCTACTCCCGCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAG 600
QY 723 GGTGCTGTGTTGCTGCTGTGACAGCCAGTGTCTCAGGCTGTCTCAAGGCTGGGACCAT 782
Db 601 GGTGCTGTGTTGCTGCTGTGACAGCCAGTGTCTCAGGCTGTCTCAAGGCTGGGACCAT 660
QY 783 GCAGGGGGGCTCTGTGAGTCCCGAGGAATCTTGTGCGATGAGCTGCAGAACCATGGA 842
Db 661 GCAGGGGGGCTCTGTGAGTCCCGAGGAATCTTGTGCGATGAGCTGCAGAACCATGGA 720
QY 843 CGTCTCAACATFACAGACCTGCCACTGTCCCTGTGTACACGGGCGAGATACTGC 902
Db 721 CGTCTCAACATFACAGACCTGCCACTGTCCCTGTGTACACGGGCGAGATACTGC 780
QY 903 CAAGTAGGTGTGACGCTGTGACGCTGTGACGCGCGGTTCGCGAGGAGAGTCTGCTGC 962
Db 781 CAAGTAGGTGTGACGCTGTGACGCTGTGACGCGCGGTTCGCGAGGAGAGTCTGCTGC 840
QY 963 GTCTGTGACATCGGCTACGGGGGAGCCAGTGTGCGACCAAGGTGCATTTTCCCTTCCAC 1022
Db 841 GTCTGTGACATCGGCTACGGGGGAGCCAGTGTGCGACCAAGGTGCATTTTCCCTTCCAC 900
QY 1023 ACCTGTGACCTGAGGATCGACGGAGACTGTCTTCTGAGGTGTCTTACAGGCGACACCTAT 1082
|||||

Db 901 ACCTGTGACCTTGAGGATCGACGGAGACTGCTTCATGCTGTCTTCAGAGGCGACACACCTAT 960
QY 1083 TACAGAGCCAGGATGAATCTCAGAGAAAGGGGGTGTGGCCCGAGATCAAGAGCCAG 1142
Db 961 TACAGAGCCAGGATGAATCTCAGAGAAAGGGGGTGTGGCCCGAGATCAAGAGCCAG 1020
QY 1143 AAAGTCAGAGACATCTCGCCTTCTATCTGGGCGCCTGGAGAGCCACCAAGAGGTGACT 1202
Db 1021 AAAGTCAGAGACATCTCGCCTTCTATCTGGGCGCCTGGAGAGCCACCAAGAGGTGATT 1080
QY 1203 GACAGTGACTTCAGAGCAGGAATCTGTGATGGGCTACCTTACAGAGCCGCGCAAGGAC 1262
Db 1081 GACAGTGACTTCAGAGCAGGAATCTGTGATGGGCTACCTTACAGAGCCGCGCAAGGAC 1140
QY 1263 TCCTTCGGCTGGGCCACAGGGAGCACCAGGCTTACCAAGTTTGGCTTTGGGCGAGCT 1322
Db 1141 TCCTTCGGCTGGGCCACAGGGAGCACCAGGCTTACCAAGTTTGGCTTTGGGCGAGCT 1200
QY 1323 GACAACCCAGGG 1334
Db 1201 GACAACCCAGGG 1212

RESULT 10
AAK94246
ID AAK94246 standard; cDNA; 1786 BP.
XX
AC AAK94246;
XX
XX
DT 06-NOV-2001 (first entry)
XX
DE Human full-length cDNA, SEQ ID NO: 2850.
KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS Homo sapiens.
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-0114089.
XX
XX 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
XX
XX (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI: 2001-524255/58.
DR P-PSDB; AAM93326.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
XX Claim 8; SEQ ID NO 2850; 1380pp + sequence listing; English.
PS
CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesizing the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a full length
CC human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX

SQ Sequence 1786 BP; 361 A; 548 C; 553 G; 324 T; 0 other;
Query Match 41.3%; Score 774; DB 22; Length 1786;
Best Local Similarity 99.3%; Pred No. 0;
Matches 1224; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 102 CCTGACGGGCCCAACAGACCCTATGTCATCCAGAGACCTCCCTTGGCCGGGSCATCTC 161
Db 52 CTTGACGGGCCCAACAGACCCTATGTCATCCAGAGACCTCCCTTGGCCGGGSCATCTC 111
QY 162 CTGGCTGTGCTCTCTGGCCCTCTTGGCACCACCTGGCAGAGGTGTGGCCACCACCGACTG 221
Db 112 CTGGCTGTGCTCTCTGGCCCTCTTGGCACCACCTGGCAGAGGTGTGGCCACCACCGACTG 171
QY 222 CAGGAGCAGGCTCCGATGGCCGGAGCCCTGAACAGAGAGAGAGTTTCTTCTCTCTCC 281
Db 172 CAGGAGCAGGCTCCGATGGCCGGAGCCCTGAACAGAGAGAGAGTTTCTTCTCTCTCC 231
QY 282 CTGCACAACCGCTTCGCAGCTGGGTCCAGCCCCCTCGGCTGACATFGCGAGGCTGGAC 341
Db 232 CTGCACAACCGCTTCGCAGCTGGGTCCAGCCCCCTCGGCTGACATFGCGAGGCTGGAC 291
QY 342 TGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGCGACCCCTCTGTGGAATCCCAACC 401
Db 292 TGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGCGACCCCTCTGTGGAATCCCAACC 351
QY 402 CCGAGCTGGCATCCGGCCTGTGGCGCACCCCTCAAGTGGGCTGGAACATGCACTGCTG 461
Db 352 CCGAGCTGGCATCCGGCCTGTGGCGCACCCCTCAAGTGGGCTGGAACATGCACTGCTG 411
QY 462 CCCGGGGCTTGGCGCTCTTGTGAAGTGGTCAAGCCTATGTTTGCAGAGGGGACGCG 521
Db 412 CCCGGGGCTTGGCGCTCTTGTGAAGTGGTCAAGCCTATGTTTGCAGAGGGGACGCG 471
QY 522 TACAGCAGCGCGCAGGAGAGTGTCTGCAACGCCACCTGCAACCACTACAGCAGCTC 581
Db 472 TACAGCAGCGCGCAGGAGAGTGTCTGCAACGCCACCTGCAACCACTACAGCAGCTC 531
QY 582 GTGTGGGCGCACCTCAAGCCAGCTGGGCTGTGGCGGCGACCTGTCTCTGAGGCCAGCA 641
Db 532 GTGTGGGCGCACCTCAAGCCAGCTGGGCTGTGGCGGCGACCTGTCTCTGAGGCCAGCA 591
QY 642 GCGATAGAGCCCTTTCTCTGTGCTACTCCCGCGGAGGCAACTGGGAGGTCAACGGGAAG 701
Db 592 GCGATAGAGCCCTTTCTCTGTGCTACTCCCGCGGAGGCAACTGGGAGGTCAACGGGAAG 651
QY 702 ACAATCATCCCTATAAGAGGGTGTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 761
Db 652 ACAATCATCCCTATAAGAGGGTGTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 711
QY 762 TCGTTCAAAGCCTGGGAGCCATGAGGGGGCTCTGTGAGGTCCCGAGGAATCTTGTGCG 821
Db 712 TCGTTCAAAGCCTGGGAGCCATGAGGGGGCTCTGTGAGGTCCCGAGGAATCTTGTGCG 771
QY 822 ATGAGTGCAGAGCCATGAGCCCTCAACATCAGCAGCTGCGCCTGCGCCTGCGCCT 881
Db 772 ATGAGTGCAGAGCCATGAGCCCTCAACATCAGCAGCTGCGCCTGCGCCTGCGCCT 831
QY 882 GCGTACAGGGCAGATACCTGCGCAGTGTGAGGTGTGAGGTGTGAGGTGTGAGGTGTGAG 941
Db 832 GCGTACAGGGCAGATACCTGCGCAGTGTGAGGTGTGAGGTGTGAGGTGTGAGGTGTGAG 891
QY 942 CCGGAGGAGGAGTGTGCTGTGAGGTGTGAGGTGTGAGGTGTGAGGTGTGAGGTGTGAG 1001
Db 892 CCGGAGGAGGAGTGTGCTGTGAGGTGTGAGGTGTGAGGTGTGAGGTGTGAGGTGTGAG 951
QY 1002 AAGGTGCAATTTTCCCTTCCACACTGTGACCTGAGGATCGACGAGACTGCTTCAATG 1061
Db 952 AAGGTGCAATTTTCCCTTCCACACTGTGACCTGAGGATCGACGAGACTGCTTCAATG 1011
QY 1062 TCTTCAGAGCGCAGACACCTATTACAGAGCCAGGATGAATGTACAGAGAAAGCGGGGTG 1121
Db 1012 TCTTCAGAGCGCAGACACCTATTACAGAGCCAGGATGAATGTACAGAGAAAGCGGGGTG 1071

QY 1122 CTGGCCAGATCAAGCCAGAGAAAGTCCAGGACATCTCGCTTCTATCTATCTGGCGCCTG 1181
|||||
Db 1072 CTGGCCAGATCAAGCCAGAGAAAGTCCAGGACATCTCGCTTCTATCTATCTGGCGCCTG 1131
|||||
QY 1182 GAGACCACCAACGAGGTGACTGACAGTACTTCAGACAGGAACTTCTGGATCGGGCTC 1241
|||||
Db 1132 GAGACCACCAACGAGGTGATTGACAGTACTTCAGACAGGAACTTCTGGATCGGGCTC 1191
|||||
QY 1242 ACTCAAGACCCCAAGGACTCTTCCGCTGGGCCACAGGGAGCACCAGGCCCTTCACC 1301
|||||
Db 1192 ACTCAAGACCCCAAGGACTCTTCCGCTGGGCCACAGGGAGCACCAGGCCCTTCACC 1251
|||||
QY 1302 AGTTTTCCTTTGGGAGCCTGACAAACAGGG 1334
|||||
Db 1252 AGTTTTCCTTTGGGAGCCTGACAAACAGGG 1284
|||||

RESULT 11

AA576344
ID AAS76344 standard; cDNA; 1519 BP.

XX AAS76344;

XX 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #12148.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR P-PSDB; ABG12157.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 1; SEQ ID No 12148; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human

CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 1519 BP; 297 A; 462 C; 489 G; 271 T; 0 other;

Query Match 30.0%; Score 562; DB 23; Length 1519;

Best Local Similarity 99.6%; Pred No. 3 4e-236;

Matches 712; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 486 GAAGTGTGACCCATATGTTTTCAGAGGGGACGGGTACAGCCACGCGGAGAGAGTGT 545

Db 430 GAAGTGTGACCCATATGTTTTCAGAGGGGACGGGTACAGCCACGCGGAGAGAGTGT 489

QY 546 GCTCGCAACGCCACCTGCACCCACTACAGCAGCTCGTGTGGCCACCTCAAGCCAGCTG 605

Db 490 GCTCGCAACGCCACCTGCACCCACTACAGCAGCTCGTGTGGCCACCTCAAGCCAGCTG 549

QY 606 GGCTGTGGGGGCACCTGTGCTCTGCAGGCCAGACGCGATAGAAGCCTTTGTCTGTGCC 665

Db 550 GGCTGTGGGGGCACCTGTGCTCTGCAGGCCAGACGCGATAGAAGCCTTTGTCTGTGCC 609

QY 666 TACTTCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTTATAAGAGGGT 725

Db 610 TACTTCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTTATAAGAGGGT 669

QY 726 GCCTGGTGTGCTCTGCAGCCAGTCTCTCAGGCTGCTTCAAGCCCTGGGACCATGCA 785

Db 670 GCCTGGTGTGCTCTGCAGCCAGTCTCTCAGGCTGCTTCAAGCCCTGGGACCATGCA 729

QY 786 GGGGGGCTCTGTGAGTCCCGAGGAATCCTTGTGCGATGAGTGCAGAACCATGGACGT 845

Db 730 GGGGGGCTCTGTGAGTCCCGAGGAATCCTTGTGCGATGAGTGCAGAACCATGGACGT 789

QY 846 CTCAACATCAGCACTGCCACTGTCACCTGTCCTCCCTGCTACACGGGCGAGATACTGCCAA 905

Db 790 CTCAACATCAGCACTGCCACTGTCACCTGTCCTCCCTGCTACACGGGCGAGATACTGCCAA 849

QY 906 GTGAGGTGACGCCCTGCAGTGTGTCACGGCCGGTTCGGGGAGGAGAGTCTGTCGGTC 965

Db 850 GTGAGGTGACGCCCTGCAGTGTGTCACGGCCGGTTCGGGGAGGAGAGTCTGTCGGTC 909

QY 966 TGTGACATCGGCTACGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCACACC 1025

Db 910 TGTGACATCGGCTACGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCACACC 969

QY 1026 TGTGACCTGAGGATCGAGGAGACTGCTTCATGTTGTTCTTCAGAGGCGACACCTATTAC 1085

Db 970 TGTGACCTGAGGATCGAGGAGACTGCTTCATGTTGTTCTTCAGAGGCGACACCTATTAC 1029

QY 1086 AGAGCCAGGATGAATGTCAGAGGAAGCGGGGTGCTGGCCAGATCAGAGCCAGAAA 1145

Db 1030 AGAGCCAGGATGAATGTCAGAGGAAGCGGGGTGCTGGCCAGATCAGAGCCAGAAA 1089

QY 1146 GTGAGGACATCCTCGCCTTCTATCTGGCCCGCTTGGAGACCAACAGAGGTGA 1200

Db 1090 GTGAGGACATCCTCGCCTTCTATCTGGCCCGCTTGGAGACCAACAGAGGTGA 1144

RESULT 12

AAA70010

ID AAA70010 standard; cDNA; 690 BP.

XX AAA70010;

XX 07-NOV-2000 (first entry)

XX Human ovarian carcinoma antigen polynucleotide SEQ ID NO:321.

DE Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;

KW tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.

XX

OS Homo sapiens.
PN WO200036107-A2.
XX
XX 22-JUN-2000.
XX
XX 17-DEC-1999; 99WO-US30270.
XX
XX 17-DEC-1998; 98US-0215681.
XX 17-DEC-1998; 98US-0216003.
PR 23-JUN-1999; 99US-0338933.
PR 24-SEP-1999; 99US-0404879.
XX
XX (CORI-) CORIXA CORP.
XX
XX Mitcham JL, King GE, Algate PA, Frudakis TN;
PI WPI; 2000-431589/37.
XX
XX Immunogenic portion of an ovarian carcinoma protein and the nucleic
PT acid encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer -
XX
XX Claim 1; Page 177; 299pp; English.
XX
XX The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants).
CC ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytostatic activity and can be used in gene therapy and vaccines.
CC Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines
CC are useful for the prevention, diagnosis and treatment of cancer,
CC preferably ovarian cancer. AAG69691 to AAA70077 and AAB12552 to AAB12557
CC represent human ovarian carcinoma polynucleotides and proteins used in
CC the exemplification of the present invention.
XX
SQ Sequence 690 BP; 148 A; 197 C; 212 G; 131 T; 2 other;
Query Match 25.9%; Score 485; DB 21; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.9e-202;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 604 TGGGTGTGGGGGACCTGTGCTGTGAGGCGCAGACAGGATAGAGCCTTTGTCTGTG 663
DB 1 TGGGTGTGGGGGACCTGTGCTGTGAGGCGCAGACAGGATAGAGCCTTTGTCTGTG 60
QY 664 CCTACTCCCCGGAGCACTGGAGGTCAACGGGAGACAATCATCCCTATAAGAAGG 723
DB 61 CCTACTCCCCGGAGCACTGGAGGTCAACGGGAGACAATCATCCCTATAAGAAGG 120
QY 724 GTGCTGTGTGCTGTGCTGTGAGGCGCAGGCTCTCAAGCCTGGGACCATG 783
DB 121 GTGCTGTGTGCTGTGCTGTGAGGCGCAGGCTCTCAAGCCTGGGACCATG 180
QY 784 CAGGGGGGCTGTGAGGTCCTTGTCCAGGAATCCTTGTCCATGAGTGCACCAACCATGGAC 843
DB 181 CAGGGGGGCTGTGAGGTCCTTGTCCAGGAATCCTTGTCCATGAGTGCACCAACCATGGAC 240
QY 844 GTCTCAACATCAGCACTGCACTGCACTGCTCCCTGCTACACGGGAGATACCTGCC 903
DB 241 GTCTCAACATCAGCACTGCACTGCACTGCTCCCTGCTACACGGGAGATACCTGCC 300
QY 904 AAGTAGGTCGACCTGTGCTGTGACGCGCGGTTCCGGGAGGAGTGTCTCGTGGC 963
DB 301 AAGTAGGTCGACCTGTGCTGTGACGCGCGGTTCCGGGAGGAGTGTCTCGTGGC 360
QY 964 TCTGTGACATCGGCTACGGGGGAGCCAGTGTGTCACCAAGGTCATTTCCCTTCCACA 1023
DB 361 TCTGTGACATCGGCTACGGGGGAGCCAGTGTGTCACCAAGGTCATTTCCCTTCCACA 420
QY 1024 CTTGTGACCTGAGGATGCGAGGAGTGTCTTCAATGTTGCTTCAAGGAGCAGACACCTATT 1083
DB 421 CTTGTGACCTGAGGATGCGAGGAGTGTCTTCAATGTTGCTTCAAGGAGCAGACACCTATT 480

QY 1084 ACAGA 1088
DB 481 ACAGA 485
RESULT 13
ABN72904
ID ABN72904 standard; DNA; 690 BP.
XX
XX AC ABN72904;
XX
XX 02-JUL-2002 (first entry)
XX
XX Ovarian carcinoma antigen polynucleotide #9.
XX
XX Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; ds.
XX
XX Homo sapiens.
XX
XX WO200206317-A2.
XX
XX 24-JAN-2002.
XX
XX 17-JUL-2001; 2001WO-US22635.
XX
XX 17-JUL-2000; 2000US-0617747.
XX 10-AUG-2000; 2000US-0636801.
XX 20-SEP-2000; 2000US-0687857.
XX 04-APR-2001; 2001US-0827271.
XX 18-JUN-2001; 2001US-0884441.
XX
XX (CORI-) CORIXA CORP.
XX
XX Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX WPI; 2002-164781/21.
XX
XX Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer -
XX
XX Example 2; Page 296; 408pp; English.
XX
XX This invention relates to polypeptides comprising an immunogenic
CC portion of an ovarian carcinoma protein which acts as an
CC immunostimulant and is cytostatic. The polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells that express the polypeptides are useful for stimulating an
CC immune response in a patient and treating ovarian cancer. This
CC sequence represents DNA related to the invention.
XX
SQ Sequence 690 BP; 148 A; 197 C; 212 G; 131 T; 2 other;
Query Match 25.9%; Score 485; DB 24; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.9e-202;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 604 TGGGTGTGGGGGACCTGTGCTGTGAGGCGCAGACAGGATAGAGCCTTTGTCTGTG 663
DB 1 TGGGTGTGGGGGACCTGTGCTGTGAGGCGCAGACAGGATAGAGCCTTTGTCTGTG 60
QY 664 CCTACTCCCCGGAGCACTGGAGGTCAACGGGAGACAATCATCCCTATAAGAAGG 723
DB 61 CCTACTCCCCGGAGCACTGGAGGTCAACGGGAGACAATCATCCCTATAAGAAGG 120
QY 724 GTGCTGTGTGCTGTGCTGTGAGGCGCAGGCTCTCAAGCCTGGGACCATG 783
DB 121 GTGCTGTGTGCTGTGCTGTGAGGCGCAGGCTCTCAAGCCTGGGACCATG 180
QY 784 CAGGGGGGCTGTGAGGTCCTTGTCCAGGAATCCTTGTCCATGAGTGCACCAACCATGGAC 843
DB 181 CAGGGGGGCTGTGAGGTCCTTGTCCAGGAATCCTTGTCCATGAGTGCACCAACCATGGAC 240

QY 844 GTCTCAACATCAGACACCTGCCACTGCCACTGTCCCTGGCTACACGGCAGATAGTCC 903
Db 241 GTCTCAACATCAGACACCTGCCACTGCCACTGTCCCTGGCTACACGGCAGATAGTCC 300
QY 904 AAGTGAGTGCAGCTGCAGTGTGTGACAGCGCGGTTCGGGAGGAGAGTGTCTGTGCG 963
Db 301 AAGTGAGTGCAGCTGCAGTGTGTGACAGCGCGGTTCGGGAGGAGAGTGTCTGTGCG 360
QY 964 TCTGTGACATCGGTACGGGGAGCCAGTGTGCCACCAAGTGCATTTTCCCTTCCACA 1023
Db 361 TCTGTGACATCGGTACGGGGAGCCAGTGTGCCACCAAGTGCATTTTCCCTTCCACA 420
QY 1024 CCTGTGACCTGAGGATCGACGAGACTGCTTCATGCTGTCTTCAGAGGAGACACCTATT 1083
Db 421 CCTGTGACCTGAGGATCGACGAGACTGCTTCATGCTGTCTTCAGAGGAGACACCTATT 480
QY 1084 ACAGA 1088
Db 481 ACAGA 485

RESULT 14

AAZ50926

ID AAZ50926 standard; cDNA; 855 BP.

XX AAZ50926;

XX 05-JUN-2000 (first entry)

XX Human Protease and associated protein-9 (PPRG-9) encoding cDNA.

XX Protease and associated protein-9; PPRG-9; anti-PPRG antibody;

KW diagnosis; treatment; cell proliferative disorder; cancer; cirrhosis;
KW arteriosclerosis; atherosclerosis; bursitis; hepatitis; immune disorder;
KW AIDS; Addison's disease; adult respiratory distress syndrome; allergy;
KW ankylosing spondylitis; amyloidosis; cytostatic; antiarteriosclerotic;
KW hepatotrophic; antiinflammatory; virucide; antipsoriatic; anti-HIV;
KW antiallergic; immunosuppressive; antidiabetic; antianaemic;
KW neuroprotective; human; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FH CDS 233..733

FT /*tag= a

FT /product= "Human PPRG-9"

FT 233..310

FT /*tag= b

FT 311..730

FT /*tag= c

FT /product= "Mature PPRG-9"

FT 326..370

FT /*tag= d

FT /bound_moiety= "Probe or Primer"

XX WO200009709-A2.

XX 24-FEB-2000.

XX 06-AUG-1999; 99WO-US17818.

XX 10-AUG-1998; 98US-0096114.

XX 11-FEB-1999; 99US-0119768.

XX (INCY-) INCYTE PHARM INC.

XX Bandman O, Hillman JL, Baughn MR, Azimzai Y, Guegler KJ;

XX Corley NC, Yue H, Tang YT, Reddy R, Patterson C, Au-Young J;

XX Shih LL, Lu DAM;

XX WPI; 2000-224346/19.

XX P-PSDB; AAY70015.

XX DR

XX New human proteases, useful for diagnosis, treatment and prevention of
PT cell proliferative disorders such as atherosclerosis -
XX Claim 9; Page 105; 114pp; English.

XX The present sequence is a cDNA identified in Incyte clone 998626
CC derived from KIDNUT01 cDNA library. It encodes human protease and
CC associated protein-9 (PPRG-9), which is expressed in urologic
CC and musculoskeletal tissues. Anti-PPRG antibodies can be used
CC as therapeutic antagonists, reagents for diagnosis and monitoring
CC diseases and for isolating PPRG. PPRG nucleotide sequence can be used
CC as probe or primer for diagnosis and monitoring of PPRG-related
CC diseases and gene mapping. PPRG can be used in the treatment of cell
CC proliferative disorders like cancer, arteriosclerosis, atherosclerosis,
CC bursitis, cirrhosis and hepatitis, and immune disorders like AIDS,
CC Addison's disease, adult respiratory distress syndrome, allergies,
CC ankylosing spondylitis and amyloidosis.

XX Sequence 855 BP; 152 A; 283 C; 257 G; 162 T; 1 other;

Query Match 24.9%; Score 467; DB 21; Length 855;

Best Local Similarity 99.5%; Pred. No. 1.4e-194;

Matches 617; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTCTTTTGTCCACGAGCCAGCTGACTCTCTGGAGATTGTGAATAGCTCCATCCAGCCTG 60

Db 111 CTCTTTTGTCCACGAGCCAGCTGACTCTCTGGAGATTGTGAATAGCTCCATCCAGCCTG 170

QY 61 AGAACAAAGCCGGTGGCTGAGCCAGGCTGTGCACGAGCACCCTGACGGGCCCCAACAGAC 120

Db 171 AGAACAAAGCCGGTGGCTGAGCCAGGCTGTGCACGAGCACCCTGACGGGCCCCAACAGAC 230

QY 121 CCATGCTCATCCAGAGACCTCCCTGGCCGGGGGATCTCTCTGGCTGTCTCTGGGCC 180

Db 231 CCATGCTCATCCAGAGACCTCCCTGGCCGGGGGATCTCTCTGGCTGTCTCTGGGCC 290

QY 181 TCCTTGGCACCACCTGGCAGAGGTGTGCCACCCAGCTGACGAGCAGCTCCGATGG 240

Db 291 TCCTTGGCACCACCTGGCAGAGGTGTGCCACCCAGCTGACGAGCAGCTCCGATGG 350

QY 241 CCGAGCCCTGAACAGGAGAGAGTTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300

Db 351 CCGAGCCCTGAACAGGAGAGAGTTTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 410

QY 301 GCTGGTCCAGCCCTCGGCTGACATGCGGAGGCTGGAGTGGAGTGGAGTGGAGTGGAGT 360

Db 411 GCTGGTCCAGCCCTCGGCTGACATGCGGAGGCTGGAGTGGAGTGGAGTGGAGTGGAGT 470

QY 361 AACTGGCTCAAGCCAGGAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGCCC 420

Db 471 AACTGGCTCAAGCCAGGAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGCCC 530

QY 421 TGTGGCAGCCCTGCAAGTGGGCTGGAACATGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 480

Db 531 TGTGGCAGCCCTGCAAGTGGGCTGGAACATGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 590

QY 481 TTGTTGAAGTGGTCAAGTGGGCTGGAACATGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 540

Db 591 TTGTTGAAGTGGTCAAGTGGGCTGGAACATGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 650

QY 541 AGTGTGCTCGCAAGCCACCTGCACCCACTACACGAGCTCGTGTGGGCCACCTCAAGCC 600

Db 651 AGTGTGCTCGCAAGCCACCTGCACCCACTACACGAGCTCGTGTGGGCCACCTCAAGCC 710

QY 601 AGCTGGCTGTGGGGGAC 620

Db 711 AGCTGGCTGTGGGGGAC 730

RESULT 15

AAS81209/C

ID AAS81209 standard; cDNA; 602 BP.

CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1934 BP; 409 A; 577 C; 576 G; 372 T; 0 other;

Query Match 20.7%; Score 388; DB 23; Length 1934;
Best Local Similarity 98.8%; Pred. No. 5.5e-160;
Matches 1038; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 17 CCAGCTGACTCTGAGAGTGTGAATAGCTCATCCAGCTGAGAAACAGCCGGGTG 76
Db 75 CCAGCTGACTCTGAGAGTGTGAATAGCTCATCCAGCTGAGAAACAGCCGGGTG 134
QY 77 GCTGAGCAGGCTGTGACGAGGAGCAGCTGACGGGCCAACAGACCATGCTCATCCAGA 136
Db 135 GCTGAGCAGGCTGTGACGAGGAGCAGCTGACGGGCCAACAGACCATGCTCATCCAGA 194
QY 137 GACCTCCCTGGCGGGGGGATCTCTGGGTGTGCTCTGCGCCCTCTTGGCACCACCTG 196
Db 195 GACCTCCCTGGCGGGGGGATCTCTGGGTGTGCTCTGCGCCCTCTTGGCACCACCTG 254
QY 197 GGCAGAGGTGTGCGCCACCCAGCTGCGAGGAGCAGGCTCCGATGGCCGAGCCCTGAACAG 256
Db 255 GGCAGAGGTGTGCGCCACCCAGCTGCGAGGAGCAGGCTCCGATGGCCGAGCCCTGAACAG 314
QY 257 GAAGGAGGTTCTTGTCTCTCTCCCTGCACAAACCGCTGCGCAGCTGGTCCAGCCGCC 316
Db 315 GAAGGAGGTTCTTGTCTCTCTCCCTGCACAAACCGCTGCGCAGCTGGTCCAGCCGCC 374
QY 317 TCGGGCTGACATCGGAGGCTGAGCTGGAGTGACAGCTGCGCCCAACTGGCTCAAGCCAG 376
Db 375 TCGGGCTGACATCGGAGGCTGAGCTGGAGTGACAGCTGCGCCCAACTGGCTCAAGCCAG 434
QY 377 GGCAGCCCTCTGTGGAAATCCAAACCCGAGCTGCGATCCCGGCTTGGCTGAGTGGTCA 436
Db 435 GGCAGCCCTCTGTGGAAATCCAAACCCGAGCTGCGATCCCGGCTTGGCTGAGTGGTCA 494
QY 437 AGTGGCTGGAACATGAGCTGTGCTCCCGGGCTTGGCTGCTTGGTGAAGTGGTCA 496
Db 495 AGTGGCTGGAACATGAGCTGTGCTCCCGGGCTTGGCTGCTTGGTGAAGTGGTCA 554
QY 497 CCTATGTTGACAGGGGAGCGGTACAGCCAGCGGCTGCGGAGAGTGTCTCGCAAGCG 556
Db 555 CCTATGTTGACAGGGGAGCGGTACAGCCAGCGGCTGCGGAGAGTGTCTCGCAAGCG 614
QY 557 CACCTGCACCCACTACAGCAGCTGCTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGCG 616
Db 615 CACCTGCACCCACTACAGCAGCTGCTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGCG 674
QY 617 GCACCTGTGCTGTGAGGGCAGACAGGATAGAGCCTTTGTCTGTGCTACTCCCGCG 676
Db 675 GCACCTGTGCTGTGAGGGCAGACAGGATAGAGCCTTTGTCTGTGCTACTCCCGCG 734
QY 677 AGGCAACTGGAGGTCAAGGGGAGACAAATCATCCCTATAAGAGGCTGCTGGTGTTC 736
Db 735 AGGCAACTGGAGGTCAAGGGGAGACAAATCATCCCTATAAGAGGCTGCTGGTGTTC 794
QY 737 GCTCTGCACAGCAGTGTCTCAGGCTGCTTCAAGAGCTGGGACCATGACGGGGGCTGTG 796
Db 795 GCTCTGCACAGCAGTGTCTCAGGCTGCTTCAAGAGCTGGGACCATGACGGGGGCTGTG 854
QY 797 TGAGTCCCGAGGATCTTGTGCGATGAGTGCAGAACCATGGAGTCTCAACATCAG 856
Db 855 TGAGTCCCGAGGATCTTGTGCGATGAGTGCAGAACCATGGAGTCTCAACATCAG 914
QY 857 CACCTGCCACTGCCCTGCTCCCTGCTACAGGGCAGATAGTCCCAAGTGAAGTGCAG 916
Db 915 CACCTGCCACTGCCCTGCTCCCTGCTACAGGGCAGATAGTCCCAAGTGAAGTGCAG 974
QY 917 CCTGAGTGTGTGCAGCGCGGTTCGCGGAGGAGGAGTGTCTGCTGTGACATCGG 976

Db 975 CCTGCAGTGTGTGCACGCGCGGTTCGCGGAGGAGGAGTGTCTCGTGTGACATCGG 1034
QY 977 CTACGGGGAGCCCACTGTGCCACCAAGTGCAATTTTCCCTTCCACACCTGTGACCTGAG 1036
Db 1035 CTACGGGGAGCCCACTGTGCCACCAATGTGCAATTTTCCCTTCCACACCTGTGACCTGAG 1094
QY 1037 GATCAGCGAGAGTGTCTTCATGGTGTCTTCA 1067
Db 1095 GATCAGCGAGAGTGTCTTCATGGTGTCTTCA 1125

RESULT 17
AAS76343

ID AAS76343 standard; cDNA; 906 BP.

XX AAS76343;

XX 13-FEB-2002 (first entry)

DT DNA encoding novel human diagnostic protein #12147.

DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

PN 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

PR (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR P-PSDB; ABG12156.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

PS Claim 1; SEQ ID No 12147; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 906 BP; 175 A; 294 C; 286 G; 151 T; 0 other;

DR WPI: 2001-639362/73.
XX P-PSDB; ABG17023.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX
XX Claim 1; SEQ ID No 17014; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human
XX diagnostic coding sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 1482 BP; 395 A; 360 C; 431 G; 296 T; 0 other;
Query Match 6.5%; Score 122; DB 23; Length 1482;
Best Local Similarity 100.0%; Pred. No. 1.9e-43;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 677 AGGCACTGGGAGGTCAACGGGAAGACAATCATCCCTATAGAAGGTCCTGGTGTC 736
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 384 AGGCACTGGGAGGTCAACGGGAAGACAATCATCCCTATAGAAGGTCCTGGTGTC 443
QY 737 GCTCTGCACAGCAGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGCTCTG 796
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 444 GCTCTGCACAGCAGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGCTCTG 503
QY 797 TG 798
DB ||
DB 504 TG 505
RESULT 22
AAS88505
ID AAS88505 standard; cDNA; 3660 BP.
XX
XX AAS88505;
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #24309.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX P-PSDB; ABG24318.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 1; SEQ ID No 24309; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human
XX diagnostic coding sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 3660 BP; 901 A; 903 C; 1053 G; 803 T; 0 other;
Query Match 5.3%; Score 99; DB 23; Length 3660;
Best Local Similarity 100.0%; Pred. No. 2.1e-33;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1236 GGGCTACCTACAGACCGCCAGGACTCTTCGCTGGGCCACAGGGGACACAGGCC 1295
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 2935 GGGCTACCTACAGACCGCCAGGACTCTTCGCTGGGCCACAGGGGACACAGGCC 2994
QY 1296 TTCACCACTTTTGCCTTTGGGCAGCCTGACAACACCGG 1334
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 2995 TTCACCACTTTTGCCTTTGGGCAGCCTGACAACACCGG 3033
RESULT 23
AAS89242
ID AAS89242 standard; cDNA; 3660 BP.
XX
XX AAS89242;
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #25046.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
PI WPI; 2001-639362/73.
DR P-PSDB; ABG25055.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX Claim 1: SEQ ID No 25046; 103pp; English.
PS
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 3660 BP; 901 A; 903 C; 1053 G; 803 T; 0 other;
Query Match 5.3%; Score 99; DB 23; Length 3660;
Best Local Similarity 100.0%; Pred. No. 2.1e-33;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1236 GGGCTACCTACAGACCGCCAGGACTCCCTCCGCTGGCCACAGGGAGCACCAGGCC 1295
DB 2935 GGCTACCTACAGACCGCCAGGACTCCCTCCGCTGGCCACAGGGAGCACCAGGCC 2994
QY 1296 TTCACCAAGTTTGGCTTTGGCAGCCCTGACAAACACGGG 1334
DB 2995 TTCACCAAGTTTGGCTTTGGCAGCCCTGACAAACACGGG 3033
RESULT 24
AAS81207/c
ID AAS81207 standard; cDNA; 480 BP.
XX AAS81207;
XX
XX 13-FEB-2002 (first entry)
DT
XX DNA encoding novel human diagnostic protein #17011.
DE
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
OS
XX WO200175067-A2.
PN
PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.
PF
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
PI WPI; 2001-639362/73.
DR P-PSDB; ABG17020.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX Claim 1: SEQ ID No 17011; 103pp; English.
PS
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 480 BP; 110 A; 135 C; 105 G; 130 T; 0 other;
Query Match 5.2%; Score 97; DB 23; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.8e-32;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1104 CAGAGGAAGCGGGTGTCTGGCCAGATCAAGAGCCAGAAAGTCAGGACATCTCGCC 1163
DB 252 CAGAGGAAGCGGGTGTCTGGCCAGATCAAGAGCCAGAAAGTCAGGACATCTCGCC 193
QY 1164 TTCATCTCTGGCCGCTGGAGACCAACACGAGGTGA 1200
DB 192 TTCATCTCTGGCCGCTGGAGACCAACACGAGGTGA 156
RESULT 25
AAS91789
ID AAS91789 standard; cDNA; 168 BP.
XX AAS91789;
XX
XX 13-FEB-2002 (first entry)
DT
XX DNA encoding novel human diagnostic protein #27593.
DE
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
OS
XX WO200175067-A2.
PN

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XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Dmanac RT, Liu C, Tang YT;
XX DR WPI: 2001-639362/73.
XX DR P-PSDB; ABG27602.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 1; SEQ ID No 27593; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. AAS64197-AAS94564 represent novel human
XX CC diagnostic coding sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 168 BP; 41 A; 45 C; 56 G; 26 T; 0 other;

Query Match 5.0%; Score 94; DB 23; Length 168;
Best Local Similarity 100.0%; Pred. No. 3.9e-31;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1107 AGGAAGGCGGGTGTGGCCAGATCAAGAGCCAGAAAGTCAGGACATCCTCGCCTTC 1166
DB 1 AGGAAGGCGGGTGTGGCCAGATCAAGAGCCAGAAAGTCAGGACATCCTCGCCTTC 60
QY 1167 TATCTGGGCGCGCTGGAGACACCAACAGAGGTGA 1200
DB 61 TATCTGGGCGCGCTGGAGACACCAACAGAGGTGA 94

RESULT 26
AAS73137
ID AAS73137 standard; cDNA; 1239 BP.
XX AC AAS73137;
XX XX
XX DT 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #8941.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
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XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Dmanac RT, Liu C, Tang YT;
XX DR WPI: 2001-639362/73.
XX DR P-PSDB; ABG08950.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 1; SEQ ID No 8941; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. AAS64197-AAS94564 represent novel human
XX CC diagnostic coding sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 1239 BP; 281 A; 298 C; 360 G; 300 T; 0 other;

Query Match 5.0%; Score 94; DB 23; Length 1239;
Best Local Similarity 100.0%; Pred. No. 3.5e-31;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1360 GGTTCGCAACGCGTGGAGCTGCAGGCTTCAGCTCGCTTCAACTGGAACGACGCGCT 1419
DB 536 GGTTCGCAACGCGTGGAGCTGCAGGCTTCAGCTCGCTTCAACTGGAACGACGCGCT 595
QY 1420 GCAAAACCCGAAACCGTTACATCTGCCAGTTTGC 1453
DB 596 GCAAAACCCGAAACCGTTACATCTGCCAGTTTGC 629

RESULT 27
AAS76345
ID AAS76345 standard; cDNA; 792 BP.
XX AC AAS76345;
XX XX
XX DT 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #12149.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
```


XX	Homo sapiens.
OS	WO200175067-A2.
PN	11-OCT-2001.
XX	30-MAR-2001; 2001WO-US08631.
PD	31-MAR-2000; 2000US-0540217.
PX	23-AUG-2000; 2000US-0649167.
XX	(HYSE-) HYSEQ INC.
PA	Dzmanac RT, Liu C, Tang YT;
PI	WPI; 2001-639362/73.
XX	P-PSDB; ABG12158.
DR	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
XX	Claim 1; SEQ ID No 12149; 103pp; English.
PS	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (I) is useful in gene therapy techniques
CC	to restore normal activity of (II) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. AAS64197-AAS94564 represent novel human
CC	diagnostic coding sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	Sequence 792 BP; 176 A; 226 C; 239 G; 151 T; 0 other;
SQ	
Query Match	4.6%; Score 86; DB 23; Length 792;
Best Local Similarity	100.0%; Pred. No. 1.le-23;
Matches	86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	414 TC CGCGCCTGTGGGCACCCCTGCAAGTGGCTGGAACATGCAGCTGCCCGGGCTTG 473
Db	
Db	235 TC CGCGCCTGTGGGCACCCCTGCAAGTGGCTGGAACATGCAGCTGCCCGGGCTTG 294
QY	474 GC GTCTCTTTTGAAGTGGTCAGCCT 499
Db	
Db	295 GC GTCTCTTTTGAAGTGGTCAGCCT 320
RESULT 28	
AAS88505/c	
ID	AAS88505 standard; cDNA; 3660 BP.
XX	
XX	AAS88505;
XX	
DT	13-FEB-2002 (first entry)
DE	DNA encoding novel human diagnostic protein #24309.
XX	

KW	Human; chromosome mapping; gene therapy; forensic;
KW	food supplement; medical imaging; diagnostic; genetic disorder; ss.
OS	Homo sapiens.
XX	WO200175067-A2.
PN	11-OCT-2001.
XX	30-MAR-2001; 2001WO-US08631.
PF	31-MAR-2000; 2000US-0540217.
XX	23-AUG-2000; 2000US-0649167.
PR	(HYSE-) HYSEQ INC.
FA	Dzmanac RT, Liu C, Tang YT;
XX	WPI; 2001-639362/73.
PI	P-PSDB; ABG24318.
DR	New isolated polynucleotide and encoded polypeptides, useful in
DR	diagnostics, forensics, gene mapping, identification of mutations
XX	responsible for genetic disorders or other traits and to assess
PT	biodiversity
PT	Claim 1; SEQ ID No 24309; 103pp; English.
PS	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (I) is useful in gene therapy techniques
CC	to restore normal activity of (II) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. AAS64197-AAS94564 represent novel human
CC	diagnostic coding sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	Sequence 3660 BP; 901 A; 903 C; 1053 G; 803 T; 0 other;
SQ	
Query Match	4.2%; Score 79; DB 23; Length 3660;
Best Local Similarity	99.2%; Pred. No. 1.2e-24;
Matches	129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	430 CCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCCGGGCTTGGCGTCTTTGTTGAAG 489
Db	
Db	211 CCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCCGGGCTTGGCGTCTTTGTTGAAG 152
QY	490 TGCTCAGCCTATGTTTGCAGAGGGGACGGTACAGCCAGCGGAGAGTGTGCTC 549
Db	
Db	151 TGCTCAGCCTATGTTTGCAGAGGGGACGGTACAGCCAGCGGAGAGTGTGCTC 92
QY	550 GCAACGCCAC 559
Db	
Db	91 GCAACGCCAC 82
RESULT 29	
AAS89242/c	
ID	AAS89242 standard; cDNA; 3660 BP.
XX	

AC AAS89242;
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #25046.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX
XX P-PSDB: ABG25055.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 1; SEQ ID No 25046; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human
XX diagnostic coding sequences of the invention.
XX Note: the sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 3660 BP; 901 A; 903 C; 1053 G; 803 T; 0 other;
XX
XX Query Match 4.2%; Score 79; DB 23; Length 3660;
XX Best Local Similarity 99.2%; Pred. No. 1.2e-24;
XX Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 430 CCTGCAAGTGGCTGGAACATGCTGCTGCGCGGGTGGCGTTCCTTTGTTGAAG 489
DB 211 CCTGCAAGTGGCTGGAACATGCTGCTGCGCGGGTGGCGTTCCTTTGTTGAAG 152
QY 490 TGGTCAAGCTTATGTTTGCAGAGGGGCGGTTACAGCCAGCGGCGAGAGGTGTC 549
DB 151 TGGTCAAGCTTATGTTTGCAGAGGGGCGGTTACAGCCAGCGGCGAGAGGTGTC 92
QY 550 GCAACGCCAC 559
DB 91 GCAACGCCAC 82

RESULT 30
AAS81206
ID AAS81206 standard; cDNA; 915 BP.
XX
XX AAS81206;
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #17010.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX
XX P-PSDB: ABG17019.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 1; SEQ ID No 17010; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human
XX diagnostic coding sequences of the invention.
XX Note: the sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 915 BP; 212 A; 244 C; 264 G; 195 T; 0 other;
XX
XX Query Match 3.8%; Score 72; DB 23; Length 915;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-21;
XX Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1260 GACTCCTTCCTGGGCGGACAGGGGAGCACCAGGCGCTTACACGTTTTCCTTTGGGCGAG 1319
DB 118 GACTCCTTCCTGGGCGGACAGGGGAGCACCAGGCGCTTTCCTTTGGGCGAG 177
QY 1320 CCTGACACAC 1331

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Db 178 CCTGACACAC 189
|||||
RESULT 31
AAX80091
ID AAX80091 standard; DNA; 45 BP.
XX
AC AAX80091;
XX
XX 12-AUG-1999 (first entry)
XX
DE Human PRO347 probe.
XX
XX Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
KW secreted protein; transmembrane protein; inflammation disorder;
KW probe; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9928462-A2.
XX
PD 10-JUN-1999.
XX
PF 01-DEC-1998; 98WO-US25108.
XX
PR 25-FEB-1998; 98US-0075945.
PR 03-DEC-1997; 97US-0067411.
PR 11-DEC-1997; 97US-0069278.
PR 11-DEC-1997; 97US-0069334.
PR 11-DEC-1997; 97US-0069335.
PR 12-DEC-1997; 97US-0069425.
PR 16-DEC-1997; 97US-0069694.
PR 16-DEC-1997; 97US-0069702.
PR 17-DEC-1997; 97US-0069873.
PR 18-DEC-1997; 97US-0068017.
PR 05-JAN-1998; 98US-0070440.
PR 09-FEB-1998; 98US-0074086.
PR 09-FEB-1998; 98US-0074092.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;
PI Yuan J;
XX
XX WPI; 1999-371118/31.
XX
PT Nucleic acids encoding PRO secreted and transmembrane proteins
XX
PS Example 11; Page 57; 123pp; English.
XX
CC The present invention describes nucleic acids encoding PRO secreted and
CC transmembrane proteins used therapeutically. The PRO proteins have
CC cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive
CC activity. The proteins and polynucleotides can be used in therapy.
CC identification of homologues, raising antibodies and design of probes
CC and primers. They can be used in a range of diseases related to proteins
CC that they have homology with, e.g. a PRO protein having homology to
CC complement proteins may be used in inflammatory responses. The present
CC sequence represents a probe used in an example from the present
CC invention.
XX
SQ Sequence 45 BP; 8 A; 17 C; 14 G; 6 T; 0 other;
Query Match 2.4%; Score 45; DB 20; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1254 GCCAAGGACTCCTTCGCTGGGCCACAGGGGAGCACCAGGCCTTC 1298
|||||
RESULT 32
AAX46921
ID AAX46921 standard; CDNA; 45 BP.
XX
AC AAX46921;
XX
XX 03-OCT-2000 (first entry)
XX
DE Probe used to screen for cDNA encoding novel polypeptide PRO347.
XX
XX PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357;
KW PRO15; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell; probe;
KW tumorigenesis; cancer; neoplastic cell growth; cell proliferation; ss.
XX
OS Homo sapiens.
XX
PN WO200037640-A2.
XX
PD 29-JUN-2000.
XX
PF 16-DEC-1999; 99WO-US30095.
XX
PR 22-DEC-1998; 98US-0113296.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28565.
XX
PA (GETH ) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
PI Wood WI;
XX
XX WPI; 2000-452188/39.
XX
PT New anti-polypeptide antibody useful in the treatment and diagnosis of
PT neoplastic cell growth and proliferation.
XX
PS Example 9; Page 101; 220pp; English.
XX
CC The present sequence represents a probe used to screen for cDNA
CC encoding a novel human polypeptide. The specification describes
CC novel polypeptides designated PRO201, PRO292, PRO327, PRO1265,
CC PRO344, PRO343, PRO347, PRO357, PRO715, PRO1017, PRO1112, PRO509,
CC PRO853 and PRO882. These genes are amplified in the genome of
CC tumour cells. The polypeptides are believed to contribute
CC to tumorigenesis. The polypeptides are useful target for the
CC identification of certain cancers, and may act as predictors of the
CC prognosis of tumour treatment. Antibodies against these polypeptides
CC are useful in the treatment and diagnosis of neoplastic cell growth
CC and proliferation in mammals.
XX
SQ Sequence 45 BP; 8 A; 17 C; 14 G; 6 T; 0 other;
Query Match 2.4%; Score 45; DB 21; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1254 GCCAAGGACTCCTTCGCTGGGCCACAGGGGAGCACCAGGCCTTC 1298
|||||
Db 1 GCCAAGGACTCCTTCGCTGGGCCACAGGGGAGCACCAGGCCTTC 45
|||||
RESULT 33
AAA49497
ID AAA49497 standard; DNA; 45 BP.

```


CC are used in gene therapy. The present sequence is a PCR primer used in
 CC the invention.

XX Sequence 30 BP; 3 A; 8 C; 11 G; 8 T; 0 other;

Query Match 1.6%; Score 30; DB 24; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0047;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 GGGCCACACAGCCCATGCTGCATCCAGAG 137
 Db 30 GGGCCACACAGCCCATGCTGCATCCAGAG 1

RESULT 35

AAx87290/c
 ID AAX87290 standard; DNA; 27 BP.

XX AAX87290;

DT 27-SEP-1999 (first entry)

DE PRO347 probe 44176.Lm.pl.

KW PRO347; cancer; tumour; diagnosis; therapy; human; probe; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9935170-A2.

PN 15-JUL-1999.

PD 05-JAN-1999; 99WO-US00106.

PF 20-NOV-1998; 98US-0109304.

PR 05-JAN-1998; 98US-0070440.

PR 29-APR-1998; 98US-0083500.

PR 22-MAY-1998; 98US-0086414.

PR 10-JUN-1998; 98US-0088742.

PR 10-NOV-1998; 98US-0107783.

XX (GETH) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;

PI Roy MA, Wood WI;

XX WPI; 1999-430385/36.

DR Antibody against proteins expressed in neoplastic cells, useful for

PT tumor diagnosis and treatment

XX Example 2; Page 54; 162pp; English.

CC This is the nucleotide sequence of hybridisation probe 44176.Lm.pl
 CC that can be used in the identification of DNA44176 (see AAX87260)
 CC nucleic acids coding for PRO347 (see AAY06483). This gene is
 CC amplified in various tumour lines. The invention identifies 14
 CC genes (see AAX87254-67) that are amplified in the genome of certain
 CC human lung, colon and/or breast cancers and/or cell lines. This
 CC gene amplification is expected to be associated with overexpression
 CC of the gene product and to contribute to tumorigenesis. The
 CC encoded proteins (see AAY06477-90) may be useful targets for the
 CC diagnosis and/or treatment of certain cancers, and may act as
 CC predictors of the prognosis of tumour treatment.

XX Sequence 27 BP; 7 A; 10 C; 3 G; 7 T; 0 other;

Query Match 1.4%; Score 27; DB 20; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.098;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1714 TGGGAAGATGGGCTTCAATTAGATGCC 1740

Db 27 TGGGAAGATGGGCTTCAATTAGATGCC 1

RESULT 36

AAA46958/c

ID AAA46958 standard; cDNA; 27 BP.

XX AAA46958;

XX 03-OCT-2000 (first entry)

DE PCR primer used to amplify cDNA encoding novel polypeptide PRO347.

XX PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357;

KW PRO15; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell; probe;

KW tumorigenesis; cancer; neoplastic cell growth; cell proliferation;

XX PCR primer; ss.

XX Homo sapiens.

XX WO200037640-A2.

PN 29-JUN-2000.

PD 16-DEC-1999; 99WO-US30095.

PF 22-DEC-1998; 98US-0113296.

PR 08-MAR-1999; 99WO-US05028.

PR 02-JUN-1999; 99WO-US12252.

PR 01-SEP-1999; 99WO-US20111.

PR 15-SEP-1999; 99WO-US21090.

PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28409.

PR 02-DEC-1999; 99WO-US28301.

XX (GETH) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;

PI Wood WI;

XX WPI; 2000-452188/39.

DR New anti-polypeptide antibody useful in the treatment and diagnosis of

PT neoplastic cell growth and proliferation -

XX Example 17; Page 110; 220pp; English.

CC PCR primers AAA46957-58 and probe AAA46959 were used to isolate cDNA
 CC encoding a novel human polypeptide. The specification describes novel
 CC polypeptides designated PRO201, PRO292, PRO327, PRO1265, PRO344, PRO343,
 CC PRO347, PRO357, PRO1017, PRO1112, PRO509, PRO853 and PRO882.
 CC These genes are amplified in the genome of tumour cells. The
 CC polypeptides are believed to contribute to tumorigenesis. The
 CC polypeptides are useful target for the identification of certain cancers,
 CC and may act as predictors of the prognosis of tumour treatment.
 CC Antibodies against these polypeptides are useful in the treatment and
 CC diagnosis of neoplastic cell growth and proliferation in mammals.

XX Sequence 27 BP; 7 A; 10 C; 3 G; 7 T; 0 other;

Query Match 1.4%; Score 27; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.098;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1714 TGGGAAGATGGGCTTCAATTAGATGCC 1740

Db 27 TGGGAAGATGGGCTTCAATTAGATGCC 1

RESULT 37

AAA49533/c

ID AAA49533 standard; DNA; 27 BP.
 AC AAA49533;
 XX
 DT 25-SEP-2000 (first entry)
 XX
 DE Probe for analysing human PRO347.
 XX
 KW PRO: membrane bound protein; secreted protein; PRO357; PRO327;
 KW PRO243; PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347;
 KW PRO355; PRO353; PRO361; PRO363; transmembrane polypeptide;
 KW antibody; screening; detection; inhibition; probe; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200032776-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 01-DEC-1999; 99WO-US28301.
 XX
 PR 01-DEC-1998; 98WO-US25108.
 PR 16-DEC-1998; 98US-0112850.
 PR 22-DEC-1998; 98US-0113296.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
 PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
 PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
 XX
 DR WPI; 2000-412324/35.
 XX
 PT New human nucleic acids encoding secreted and transmembrane
 PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
 PT and diagnostic agents
 XX
 PS Example 28; Page 120; 187pp; English.
 XX
 CC New human nucleic acids encoding secreted and transmembrane
 CC polypeptides which are designated as PRO polypeptides are described
 CC The membrane-bound proteins have various industrial applications,
 CC including as pharmaceutical and diagnostic agents. The membrane-bound
 CC proteins can also be employed for screening of potential peptide or
 CC small molecule inhibitors of the relevant receptor/ligand interaction.
 CC Anti-PRO antibodies are useful for the affinity purification of PRO
 CC from recombinant cell culture or natural sources. Two primers
 CC (AAA49532, AAA49534) were used for gene amplification analysis of the
 CC sequence encoding human PRO347. A hybridisation probe also used in
 CC the analysis is described (AAA49533).
 XX
 SQ Sequence 27 BP; 7 A; 10 C; 3 G; 7 T; 0 other;
 Query Match 1.4%; Score 27; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1714 TGGGAGATGGGCTTCAATTAGATGGC 1740
 |||||
 DB 27 TGGGAGATGGGCTTCAATTAGATGGC 1
 RESULT 38
 AAX80090/c
 ID AAX80090 standard; DNA; 24 BP.
 XX
 AC AAX80090;
 XX
 DT 12-AUG-1999 (first entry)
 XX
 DE Human PRO347 PCR primer #2.
 XX
 KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;

KW secreted protein; transmembrane protein; inflammation disorder;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN WO9928462-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US25108.
 XX
 PR 25-FEB-1998; 98US-0075945.
 PR 03-DEC-1997; 97US-0067411.
 PR 11-DEC-1997; 97US-0069278.
 PR 11-DEC-1997; 97US-0069334.
 PR 11-DEC-1997; 97US-0069335.
 PR 12-DEC-1997; 97US-0069425.
 PR 16-DEC-1997; 97US-0069694.
 PR 16-DEC-1997; 97US-0069696.
 PR 17-DEC-1997; 97US-0069702.
 PR 17-DEC-1997; 97US-0069873.
 PR 18-DEC-1997; 97US-0068017.
 PR 05-JAN-1998; 98US-0070440.
 PR 09-FEB-1998; 98US-0074086.
 PR 09-FEB-1998; 98US-0074092.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;
 PI Yuan J;
 XX
 DR WPI; 1999-371118/31.
 XX
 PT Nucleic acids encoding PRO secreted and transmembrane proteins
 PT
 PS Example 11; Page 57; 123pp; English.
 XX
 CC The present invention describes nucleic acids encoding PRO secreted and
 CC transmembrane proteins used therapeutically. The PRO proteins have
 CC cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive
 CC activity. The proteins and polynucleotides can be used in therapy,
 CC identification of homologues, raising antibodies and design of probes
 CC and primers. They can be used in a range of diseases related to proteins
 CC that they have homology with, e.g. a PRO protein having homology to
 CC complement proteins may be used in inflammatory responses. The present
 CC invention represents a PCR primer used in an example from the present
 CC invention.
 XX
 SQ Sequence 24 BP; 5 A; 3 C; 13 G; 3 T; 0 other;
 Query Match 1.3%; Score 24; DB 20; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1777 CTCCTTCCACCTGCCGACGCC 1800
 |||||
 DB 24 CTCCTTCCACCTGCCGACGCC 1
 RESULT 39
 AAX80089
 ID AAX80089 standard; DNA; 24 BP.
 XX
 AC AAX80089;
 XX
 DT 12-AUG-1999 (first entry)
 XX
 DE Human PRO347 PCR primer #1.
 XX
 KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
 KW secreted protein; transmembrane protein; inflammation disorder;

KW PCR primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9928462-A2.
 PN 10-JUN-1999.
 XX 01-DEC-1998; 98WO-US25108.
 XX 25-FEB-1998; 98US-0075945.
 PR 03-DEC-1997; 97US-0067411.
 PR 11-DEC-1997; 97US-0069278.
 PR 11-DEC-1997; 97US-0069334.
 PR 11-DEC-1997; 97US-0069335.
 PR 12-DEC-1997; 97US-0069425.
 PR 16-DEC-1997; 97US-0069634.
 PR 16-DEC-1997; 97US-0069656.
 PR 16-DEC-1997; 97US-0069702.
 PR 17-DEC-1997; 97US-0069870.
 PR 17-DEC-1997; 97US-0069873.
 PR 18-DEC-1997; 97US-0068017.
 PR 05-JAN-1998; 98US-0070440.
 PR 09-FEB-1998; 98US-0074086.
 PR 09-FEB-1998; 98US-0074092.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;
 PI Yuan J;
 XX WPI; 1999-371118/31.
 XX Nucleic acids encoding PRO secreted and transmembrane proteins
 XX Example 11; Page 57; 123pp; English.
 XX The present invention describes nucleic acids encoding PRO secreted and
 CC transmembrane proteins used therapeutically. The PRO proteins have
 CC cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive
 CC activity. The proteins and polynucleotides can be used in therapy,
 CC identification of homologues, raising antibodies and design of probes
 CC and primers. They can be used in a range of diseases related to proteins
 CC that they have homology with, e.g. a PRO protein having homology to
 CC complement proteins may be used in inflammatory responses. The present
 CC sequence represents a PCR primer used in an example from the present
 CC invention.
 XX Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 other;
 SQ Query Match 1.3%; Score 24; DB 20; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1221 AGGAACCTCTGGATCGGCTCACC 1244
 Db 1 AGGAACCTCTGGATCGGCTCACC 24
 RESULT 40
 AAA46919
 ID AAA46919 standard; cDNA; 24 BP.
 XX AA46919;
 AC AA46919;
 XX 03-OCT-2000 (first entry)
 DT PCR primer used to amplify cDNA encoding novel polypeptide PRO347.
 DE PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357;
 XX PRO715; PRO1017; PRO1112; PRO853; PRO882; tumour cell;
 KW tumorigenesis; cancer; neoplastic cell growth; cell proliferation;
 KW PCR primer; ss.
 XX Homo sapiens.
 OS WO200037640-A2.

KW PCR primer; ss.
 XX Homo sapiens.
 XX WO200037640-A2.
 PN 29-JUN-2000.
 XX 16-DEC-1999; 99WO-US30095.
 XX 22-DEC-1998; 98US-0113296.
 PR 08-MAR-1999; 99WO-US05028.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 15-SEP-1999; 99WO-US21090.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28565.
 XX (GETH) GENENTECH INC.
 PA Rotstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
 PI Wood WI;
 XX WPI; 2000-452188/39.
 XX New anti-polypeptide antibody useful in the treatment and diagnosis of
 PT neoplastic cell growth and proliferation -
 XX Example 9; Page 101; 220pp; English.
 XX PCR primers AAA46919-20 were used to amplify cDNA encoding a novel
 CC human polypeptide. The specification describes novel polypeptides
 CC designated PRO201, PRO292, PRO327, PRO1265, PRO344, PRO343, PRO347,
 CC PRO357, PRO715, PRO1017, PRO1112, PRO509, PRO853 and PRO882. These
 CC genes are amplified in the genome of tumour cells. The polypeptides
 CC are believed to contribute to tumorigenesis. The polypeptides are
 CC useful target for the identification of certain cancers, and may act
 CC as predictors of the prognosis of tumour treatment. Antibodies against
 CC these polypeptides are useful in the treatment and diagnosis of
 CC neoplastic cell growth and proliferation in mammals.
 XX Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 other;
 SQ Query Match 1.3%; Score 24; DB 21; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1221 AGGAACCTCTGGATCGGCTCACC 1244
 Db 1 AGGAACCTCTGGATCGGCTCACC 24
 RESULT 41
 AAA46920/C
 ID AAA46920 standard; cDNA; 24 BP.
 XX AA46920;
 AC AA46920;
 XX 03-OCT-2000 (first entry)
 DT PCR primer used to amplify cDNA encoding novel polypeptide PRO347.
 DE PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357;
 XX PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;
 KW tumorigenesis; cancer; neoplastic cell growth; cell proliferation;
 KW PCR primer; ss.
 XX Homo sapiens.
 OS WO200037640-A2.

PD 29-JUN-2000.
 XX 16-DEC-1999; 99WO-US30095.
 PF 22-DEC-1998; 98US-0113296.
 XX 08-MAR-1999; 99WO-US05028.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 15-SEP-1999; 99WO-US21090.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28565.
 XX (GETH) GENENTECH INC.
 XX Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
 PI Wood WI;
 DR WPI; 2000-452188/39.
 XX New anti-polypeptide antibody useful in the treatment and diagnosis of
 PT neoplastic cell growth and proliferation -
 XX Example 9; Page 101; 220pp; English.
 XX PCR primers AAA46919-20 were used to amplify cDNA encoding a novel
 CC human polypeptide. The specification describes novel polypeptides
 CC designated PRO201, PRO282, PRO327, PRO343, PRO347, PRO347,
 CC PRO357, PRO117, PRO112, PRO509, PRO853 and PRO882. These
 CC genes are amplified in the genome of tumour cells. The polypeptides
 CC are believed to contribute to tumourigenesis. The polypeptides are
 CC useful target for the identification of certain cancers, and may act
 CC as predictors of the prognosis of tumour treatment. Antibodies against
 CC these polypeptides are useful in the treatment and diagnosis of
 CC neoplastic cell growth and proliferation in mammals.
 XX Sequence 24 BP; 5 A; 3 C; 13 G; 3 T; 0 other;
 SQ
 Query Match 1.3%; Score 24; DB 21; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1777 CTCCTCTCCACCTGGCCGACGCC 1800
 DB 24 CTCCTCTCCACCTGGCCGACGCC 1
 RESULT 42
 AAA49495
 ID AAA49495 standard; DNA; 24 BP.
 XX
 AC AAA49495;
 XX 25-SEP-2000 (first entry)
 XX Primer for isolating cDNA clones encoding human PRO347.
 DE PRO; membrane bound protein; secreted protein; PRO357; PRO327;
 DE PRO243; PRO115; PRO241; PRO299; PRO233; PRO344; PRO347;
 KW PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;
 KW antibody; screening; detection; inhibition; probe; primer; ss.
 XX Synthetic.
 OS WO200032776-A2.
 PN 08-JUN-2000.
 XX 01-DEC-1999; 99WO-US28301.
 PF 01-DEC-1998; 98WO-US25108.
 PR 16-DEC-1998; 98US-0112850.
 PR 22-DEC-1998; 98US-0113296.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
 PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
 PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
 XX WPI; 2000-412324/35.

PR 22-DEC-1998; 98US-0113296.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
 PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
 PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
 XX WPI; 2000-412324/35.
 XX New human nucleic acids encoding secreted and transmembrane
 PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
 PT and diagnostic agents
 XX Example 11; Page 103; 187pp; English.
 XX New human nucleic acids encoding secreted and transmembrane
 CC polypeptides which are designated as PRO polypeptides are described
 CC The membrane-bound proteins have various industrial applications,
 CC including as pharmaceutical and diagnostic agents. The membrane-bound
 CC proteins can also be employed for screening of potential peptide or
 CC small molecule inhibitors of the relevant receptor/ligand interaction.
 CC Anti-PRO antibodies are useful for the affinity purification of PRO
 CC from recombinant cell culture or natural sources. Two primers
 CC (AAA49495, AAA49496) were used to isolate the cDNA sequence encoding
 CC human PRO347. A hybridisation probe for human PRO347 is also
 CC described (AAA49497).
 XX Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 other;
 SQ
 Query Match 1.3%; Score 24; DB 21; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1221 AGGAACCTCTGGATCGGCTCACC 1244
 DB 1 AGGAACCTCTGGATCGGCTCACC 24
 RESULT 43
 AAA49496/C
 ID AAA49496 standard; DNA; 24 BP.
 XX
 AC AAA49496;
 XX 25-SEP-2000 (first entry)
 XX Primer for isolating cDNA clones encoding human PRO347.
 DE PRO; membrane bound protein; secreted protein; PRO357; PRO327;
 DE PRO243; PRO115; PRO241; PRO299; PRO233; PRO344; PRO347;
 KW PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;
 KW antibody; screening; detection; inhibition; probe; primer; ss.
 XX Synthetic.
 OS WO200032776-A2.
 PN 08-JUN-2000.
 XX 01-DEC-1999; 99WO-US28301.
 PF 01-DEC-1998; 98WO-US25108.
 PR 16-DEC-1998; 98US-0112850.
 PR 22-DEC-1998; 98US-0113296.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
 PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
 PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
 XX WPI; 2000-412324/35.

XX New human nucleic acids encoding secreted and transmembrane
PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
PT and diagnostic agents
XX
XX Example 11; Page 103; 187pp; English.
XX
CC New human nucleic acids encoding secreted and transmembrane
CC polypeptides which are designated as PRO polypeptides are described
CC The membrane-bound proteins have various industrial applications,
CC including as pharmaceutical and diagnostic agents. The membrane-bound
CC proteins can also be employed for screening of potential peptide or
CC small molecule inhibitors of the relevant receptor/ligand interaction.
CC Anti-PRO antibodies are useful for the affinity purification of PRO
CC from recombinant cell culture or natural sources. Two primers
CC (AAA49495, AAA49496) were used to isolate the cDNA sequence encoding
CC human PRO347. A hybridisation probe for human PRO347 is also
CC described (AAA49497).
XX
XX Sequence 24 BP; 5 A; 3 C; 13 G; 3 T; 0 other;
SQ

Query Match 1.3%; Score 24; DB 21; Length 24;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1777 CTCTCTCCACCTGGCCGACACCC 1800
|||||
DB 24 CTCTCTCCACCTGGCCGACACCC 1

RESULT 44
AAT12249/c
ID AAT12249 standard; DNA; 7216 BP.
XX
AC AAT12249;
XX
DT 08-APR-1996 (first entry)
XX
DE Cytochrome P450 isoenzyme mutant CYP2A6v2 genomic DNA.
XX
KW CYP2A6v2; cytochrome P450 isoenzyme; drug metabolism; gene therapy;
KW polymorphism; genotyping; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_difference 2019
FT /*tag= a
FT /*note= "base n at position 2019 is not identified
FT in the specification"
XX
PN W09534679-A2.
XX
PD 21-DEC-1995.
XX
PF 16-JUN-1995; 95WO-US07605.
XX
PR 12-APR-1995; 95GB-0007640.
PR 16-JUN-1994; 94GB-0012054.
PR 13-FEB-1995; 95GB-0002728.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Gonzalez FU, Idle JR;
XX
DR WPI; 1996-049706/05.
XX
PT Cytochrome P450 isoenzyme mutant genes - used for developing prods.
PT for detecting or treating sensitivity to drugs or carcinogens
XX
PS Claim 2; Fig 12; 65pp; English.
XX
CC cDNA (AAT12248) and genomic (AAT12249) sequences were detected for

CC a new mutant variant, designated CYP2A6v2, of cytochrome P450
CC isoenzyme CYP2A6, an allele associated with drug sensitivity and
CC carcinogen metabolism. Alterations in sequence from the wild-type
CC CYP2A6 gene occur within exons 3, 6 and 8, and are attributed to
CC gene conversion. The nucleic acid sequences can be used to
CC determine a patient's sensitivity to drugs or to chemical or
CC environmental carcinogens, and can also be used in gene therapy,
CC in gene polymorphism detection and in genotyping.
XX
SQ Sequence 7216 BP; 1646 A; 2195 C; 1747 G; 1627 T; 1 other;
Query Match 1.1%; Score 21; DB 17; Length 7216;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1634 GGGCAGAGAGAGCGCAGGAGG 1654
|||||
DB 1605 GGGCAGAGAGAGCGCAGGAGG 1585

RESULT 45
ABK84266/c
ID ABK84266 standard; cDNA; 8778 BP.
XX
AC ABK84266;
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #837.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
PN W0200228999-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US30821.
XX
PR 03-OCT-2000; 2000US-237189p.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR WPI; 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
PS Claim 1; SEQ ID No 837; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs. (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially

chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, renal glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

Query Match 1.1%; Score 21; DB 24; Length 8778;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1634 GGCAGAGAGAGGAGGAGG 1654
|||||
Db 1492 GGCAGAGAGAGGAGGAGG 1472

RESULT 46
ABK12674
ID ABK12674 standard; DNA; 27780 BP.
XX AC ABK12674;
XX 18-JUN-2002 (first entry)
XX Selectin L Lymphocyte Adhesion Molecule 1 (SELL) gene.
DE Human; Selectin L Lymphocyte Adhesion Molecule 1 (SELL) gene.
KW neonatal pertussis; whooping cough; haplotyping; ds;
KW single nucleotide polymorphism.
XX Homo sapiens.
XX Key Location/Qualifiers
FH variation replace (3349,G)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism"
FT replace (3444,C)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism"
FT CDS 4067..23781
FT /*tag= c
FT /product= "Selectin L Lymphocyte Adhesion Molecule 1"
FT replace (4260,T)
FT /*tag= d
FT /standard_name= "Single nucleotide polymorphism"
FT replace (5153,A)
FT /*tag= e
FT /standard_name= "Single nucleotide polymorphism"
FT replace (6682,G)
FT /*tag= f
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace (6783,G)

FT /*tag= g
FT /standard_name= "Single nucleotide polymorphism"
FT replace (6784,T)
FT /*tag= h
FT /standard_name= "Single nucleotide polymorphism"
FT replace (6997,C)
FT /*tag= i
FT /standard_name= "Single nucleotide polymorphism"
FT replace (7027,C)
FT /*tag= j
FT /standard_name= "Single nucleotide polymorphism"
FT replace (8220,C)
FT /*tag= k
FT /standard_name= "Single nucleotide polymorphism"
FT replace (10868,T)
FT /*tag= l
FT /standard_name= "Single nucleotide polymorphism"
FT replace (12363,A)
FT /*tag= m
FT /standard_name= "Single nucleotide polymorphism"
FT replace (13838,A)
FT /*tag= n
FT /standard_name= "Single nucleotide polymorphism"
FT replace (18851,G)
FT /*tag= o
FT /standard_name= "Single nucleotide polymorphism"
FT replace (19074,G)
FT /*tag= p
FT /standard_name= "Single nucleotide polymorphism"
FT replace (19155,A)
FT /*tag= q
FT /standard_name= "Single nucleotide polymorphism"
FT replace (23767,T)
FT /*tag= r
FT /standard_name= "Single nucleotide polymorphism"
FT replace (23925,C)
FT /*tag= s
FT /standard_name= "Single nucleotide polymorphism"
FT replace (24041,C)
FT /*tag= t
FT /standard_name= "Single nucleotide polymorphism"
FT replace (24122,T)
FT /*tag= u
FT /standard_name= "Single nucleotide polymorphism"
FT WO200216654-A1.
XX 28-FEB-2002.
XX 27-AUG-2001; 2001WO-US266675.
XX 25-AUG-2000; 2000US-228262P.
XX (GENA-) GENAISSANCE PHARM INC.
XX Anastasio AE, Bieglecki KM, Kliem SE, Koshy B, Kumar AM;
XX WPI: 2002-292071/33.
XX P-PSDB; AAU76539.
XX Novel genetic variants of selectin L lymphocyte adhesion molecule 1 (SELL) gene useful for therapeutic purposes and for expressing SELL protein useful in identifying drugs to treat whooping cough -
XX Claim 1; Fig 1; 137pp; English.

The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence which is a polymorphic variant of a reference sequence for Selectin L Lymphocyte Adhesion Molecule 1 (SELL) gene. SELL polypeptide is useful for screening for drugs targeting the polypeptide. Oligonucleotides derived from (I) are used to target SELL and a haplotype or haplotype pair of SELL gene. These are useful in developing diagnostic tests and therapeutic treatments for neonatal

CC pertussis (whooping cough). (1) is useful for studying the expression and
 CC function of SELL and expressing SELL protein for use in screening for
 CC candidate drugs to treat diseases related to SELL activity. The
 CC polymorphism and haplotype data are useful for validating whether SELL is
 CC a suitable target for drugs to treat whooping cough, screening for such
 CC drugs and reducing bias in clinical trials of such drugs. Establishing
 CC the SELL haplotype or haplotype pair in clinical trials is useful for
 CC improving the efficiency and reliability of several steps in the
 CC discovery and development of drugs for treating diseases associated with
 CC SELL activity e.g. neonatal pertussis (whooping cough). The haplotyping
 CC method is useful to validate SELL as a candidate target for treating a
 CC specific condition or disease predicted to be associated with SELL
 CC activity. The method is also useful in screening for compounds
 CC targeting SELL to treat a specific condition or disease predicted to be
 CC associated with SELL activity, e.g. detecting which of the SELL
 CC haplotypes or haplotype pairs present in individual members of a
 CC population with the specific disease of interest enables one to screen
 CC for compounds that display the highest desired agonist or antagonist
 CC activity for each of the most frequent SELL isoforms present in the
 CC disease population. A polymorphic variant of SELL is useful in studying
 CC the effect of the variation on the biological activity of SELL, on the
 CC binding affinity of candidate drugs targeting SELL for the treatment of
 CC neonatal pertussis (whooping cough) and in assays to measure the
 CC binding affinities of one or more candidate drugs targeting the SELL
 CC protein. The present sequence represents the SELL gene.

XX SQ Sequence 27780 BP; 8061 A; 5257 C; 5581 G; 8860 T; 21 other;

Query Match 1.1%; Score 21; DB 24; Length 27780;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1636 GCAGAGAGGCGGAGGCC 1656

Db 12949 GCAGAGAGGCGGAGGCC 12969

RESULT 47

AAA34791/c
 ID AAA34791 standard; DNA; 138169 BP.

AC AAA34791;

XX 28-JUL-2000 (first entry)

DE Human adenosine receptor related polynucleotide SEQ ID NO:2480.

DE Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; hypotensive; cytotatic;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; impaired airway;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.

XX WO200009525-A2.

PN 24-FEB-2000.

XX 03-AUG-1999; 99WO-US17712.

XX 03-AUG-1998; 98US-0095212.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT

PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -

PS Disclosure; Page 613-645; 1343pp; English.

XX The present invention describes a new composition comprising an
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers which may metastasize to the lungs, including
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC the breast and prostate cancer. The reduction of the adenosine content of
 CC the ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680
 CC (AAA32323 to AAA3992) are specifically claimed ONs from the present
 CC invention. N.B. Sequences given in the disclosure of the present
 CC invention do not match up with their corresponding SEQ ID NO: sequences
 CC given in the sequence listing.

XX SQ Sequence 138169 BP; 41766 A; 28262 C; 26273 G; 41868 T; 0 other;

Query Match 1.1%; Score 21; DB 21; Length 138169;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1636 GCAGAGAGGCGGAGGCC 1656

Db 31241 GCAGAGAGGCGGAGGCC 31221

RESULT 48

AAF20913/c
 ID AAF20913 standard; DNA; 141589 BP.

XX AC AAF20913;

XX 14-MAR-2001 (first entry)

XX Human ELAM-1 polynucleotide fragment #2480.

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; ROS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.

XX Homo sapiens.

XX WO2000062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US08020.

XX 06-APR-1999; 99US-0127958.

XX (UYEC-) UNIV EAST CAROLINA.
XX PPA (NYCE/) NYCE J W.
XX NYCE JW;
XX WP1; 2000-679539/66.
XX
XX Low adenosine (A) content antisense oligonucleotides which do not
XX trigger adenosine receptors during metabolism, useful e.g. for treating
XX cancers and respiratory obstructions -
XX
XX Disclosure; Page 178-205; 1592pp; English.
XX
XX The present invention describes low adenosine (A) content antisense
XX oligonucleotides and compositions (I) comprising them. In the antisense
XX oligonucleotides the A is replaced by a 'Universal' or alternative base.
XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
XX immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
XX The antisense oligonucleotides and (I) can be used to down-regulate the
XX expression and/or activity of target polypeptides associated with
XX lung/respiratory disorders and malignancies, such as stimulating and
XX activating peptide factors and transmitters, transcription factors,
XX immunoglobulins and antibodies, antibody receptors, cytokines and
XX chemokines, endogenously produced specific and non-specific enzymes,
XX binding proteins, adhesion molecules and their receptors, cytokine and
XX chemokine receptors, adenosine receptors, bradykinin receptors, central
XX nervous system (CNS) and peripheral nervous and non-nervous system
XX receptors, CNS and peripheral nervous and non-nervous system peptide
XX transmitters, defensins, growth factors, vasoactive peptides and
XX receptors, binding proteins and malignancy associated proteins. The
XX antisense oligonucleotides may be used in this way to treat disorders
XX including respiratory obstruction (especially pulmonary obstruction
XX and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
XX and/or bronchoconstriction and/or lung inflammation, allergy(ies)
XX condition selected from pulmonary vasoconstriction, inflammation,
XX allergies, asthma, impeded respiration, respiratory distress syndrome
XX (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
XX hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
XX pulmonary transplantation rejection, pulmonary infections, bronchitis,
XX and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
XX fragments and antisense oligonucleotides used in the exemplification of
XX the present invention.
XX
XX Sequence 141589 BP; 42856 A; 28938 C; 26863 G; 42932 T; 0 other;
XX
XX Query Match 1.1%; Score 21; DB 21; Length 141589;
XX Best Local Similarity 100.0%; Pred. No. 25;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1636 GCAGAGAGCGCAGGAGGCC 1656
XX |||||||
XX Db 31241 GCAGAGAGCGCAGGAGGCC 31221
XX
XX RESULT 49
XX AAF21127/c
XX ID AAF21127 standard; DNA; 141589 BP.
XX AC
XX AAF21127;
XX
XX 14-MAR-2001 (first entry)
XX
XX Human low adenosine antisense oligonucleotide related sequence #2694.
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX human; airway disorder; bronchoconstriction; lung inflammation;
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;
XX immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
XX respiratory obstruction; pulmonary obstruction; impeded respiration;
XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
XX pulmonary hypertension; emphysema; pulmonary transplantation rejection;
XX

DT 14-MAR-2001 (first entry)
 XX Human low adenosine antisense oligonucleotide related sequence #2719.
 DE Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 XX human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO2000062736-A2.
 PN
 XX
 PD 26-OCT-2000.
 XX
 XX 24-MAR-2000; 2000WO-US08020.
 PF
 XX 06-APR-1999; 99US-0127958.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 PA
 XX Nyce JW;
 XX
 XX WPI; 2000-679539/66.
 DR
 XX
 XX Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Disclosure; Page 1049-1081; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 XX
 XX Sequence 141589 BP; 42855 A; 28938 C; 26864 G; 42932 T; 0 other;
 Query Match 1.1%; Score 21; DB 21; Length 141589;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1636 GCAGAGAGAGCGAGGAGGCC 1656
 |||||
 Db 31241 GCAGAGAGAGCGAGGAGGCC 31221

Search completed: December 28, 2002, 23:25:31
 Job time : 1264 secs

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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 23:04:38 ; search time 85 Seconds
(without alignments)
6768.537 Million cell updates/sec

Title: US-09-944-896-49

Perfect score: 1876

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 10

Total number of hits satisfying chosen parameters: 164122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	21	1.1	8779	US-08-750-703-4	Sequence 4, Appli
4	19	1.0	1329	US-09-152-060-25	Sequence 25, Appl
5	19	1.0	2260	US-08-788-750-1	Sequence 1, Appli
6	19	1.0	3475	US-07-960-389-1	Sequence 1, Appli
7	19	1.0	35100	US-08-770-379-19	Sequence 19, Appl
8	19	1.0	35100	US-08-757-669A-19	Sequence 19, Appl
9	19	1.0	35100	US-09-230-371A-19	Sequence 19, Appl
10	18	1.0	562	US-08-329-704-3	Sequence 3, Appli
11	18	1.0	562	US-08-472-604-3	Sequence 3, Appli
12	18	1.0	562	US-08-486-117-3	Sequence 3, Appli
13	18	1.0	562	US-08-477-537-3	Sequence 3, Appli
14	18	1.0	629	US-09-149-476-232	Sequence 232, App
15	18	1.0	669	US-09-328-111-342	Sequence 342, App
16	18	1.0	759	US-09-276-531-71	Sequence 71, Appl
17	18	1.0	768	US-08-567-816A-1	Sequence 1, Appli
18	18	1.0	979	US-09-288-143-52	Sequence 52, Appl
19	18	1.0	1261	US-09-724-864-34	Sequence 34, Appl
20	18	1.0	1568	US-09-247-155-68	Sequence 68, Appl
21	18	1.0	1676	US-08-117-965-27	Sequence 27, Appl
22	18	1.0	1766	PCT-US92-06532-2	Sequence 2, Appli
23	18	1.0	1797	US-09-364-230-19	Sequence 19, Appl
24	18	1.0	1844	US-09-123-912-88	Sequence 88, Appl
25	18	1.0	1844	US-09-643-597-88	Sequence 88, Appl
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27	18	1.0	1927	US-08-837-199A-40	Sequence 40, Appl

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0.9	5086	2	US-08-365-486A-14	Sequence 14, Appl
0.9	5086	3	US-09-080-285-19	Sequence 19, Appl
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c 102	17	0.9	5086	5	PCT-US93-06251-2	Sequence 2, Appli	c 175	16	0.9	536	4	US-09-397-787-67	Sequence 67, Appl
c 103	17	0.9	5094	4	US-09-234-186-7	Sequence 7, Appli	c 176	16	0.9	538	4	US-09-020-956-105	Sequence 105, App
c 104	17	0.9	5104	6	5506344-1	Patent No. 5506344	c 177	16	0.9	538	4	US-09-607-607-105	Sequence 105, App
105	17	0.9	7881	2	US-08-751-189-1	Sequence 1, Appli	c 178	16	0.9	538	4	US-09-603-785-105	Sequence 105, App
106	17	0.9	7881	2	US-09-060-836-1	Sequence 1, Appli	c 179	16	0.9	538	4	US-09-439-313-105	Sequence 105, App
107	17	0.9	7881	4	US-09-184-445-1	Sequence 1, Appli	c 180	16	0.9	538	4	US-09-352-616A-105	Sequence 105, App
108	17	0.9	8241	6	517844-1	Patent No. 517844	c 181	16	0.9	538	4	US-09-232-149A-105	Sequence 105, App
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110	17	0.9	8409	4	US-09-167-681-37	Sequence 37, Appl	183	16	0.9	550	4	US-09-221-017B-740	Sequence 740, App
111	17	0.9	8967	1	US-08-366-851A-1	Sequence 1, Appli	184	16	0.9	574	4	US-09-605-785-356	Sequence 356, App
112	17	0.9	9009	1	US-07-864-004B-3	Sequence 3, Appli	c 185	16	0.9	574	4	US-09-439-313-356	Sequence 356, App
113	17	0.9	9009	1	US-08-351-937A-3	Sequence 3, Appli	c 186	16	0.9	574	4	US-09-352-616A-356	Sequence 356, App
114	17	0.9	9009	1	US-08-212-133A-1	Sequence 1, Appli	187	16	0.9	582	4	US-09-149-476-197	Sequence 197, App
115	17	0.9	9009	1	US-08-474-503-1	Sequence 1, Appli	188	16	0.9	586	4	US-08-906-156A-20	Sequence 20, Appl
116	17	0.9	9009	2	US-08-630-707A-1	Sequence 1, Appli	189	16	0.9	587	4	US-08-906-156A-68	Sequence 68, Appl
117	17	0.9	9009	4	US-09-037-601-1	Sequence 1, Appli	190	16	0.9	590	2	US-08-485-778-44	Sequence 44, Appl
118	17	0.9	9009	4	US-09-315-179-1	Sequence 1, Appli	c 191	16	0.9	590	4	US-09-026-601-41	Sequence 41, Appl
119	17	0.9	9009	4	US-09-523-656-1	Sequence 1, Appli	192	16	0.9	591	4	US-09-247-155-59	Sequence 59, Appl
120	17	0.9	9009	5	PCT-US93-03273-3	Sequence 3, Appli	c 193	16	0.9	661	4	US-09-328-111-69	Sequence 69, Appl
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c 123	17	0.9	11770	4	US-08-961-527-172	Sequence 172, App	c 196	16	0.9	686	4	US-09-372-422A-45	Sequence 45, Appl
c 124	17	0.9	4403765	4	US-09-103-840A-2	Sequence 2, Appli	197	16	0.9	700	4	US-09-152-060-26	Sequence 26, Appl
c 125	16	0.9	30	3	US-08-771-781-2	Sequence 2, Appli	198	16	0.9	725	4	US-09-352-990-19	Sequence 19, Appl
c 126	16	0.9	30	4	US-09-244-794A-16	Sequence 16, Appl	199	16	0.9	738	4	US-09-392-184-13	Sequence 13, Appl
c 127	16	0.9	30	4	US-09-247-190-16	Sequence 16, Appl	c 200	16	0.9	749	4	US-09-469-242-5	Sequence 5, Appli
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c 140	16	0.9	75	4	US-09-605-192-2	Sequence 2, Appli	213	16	0.9	913	3	US-08-651-136C-13	Sequence 13, Appl
c 141	16	0.9	97	1	US-08-120-827-87	Sequence 87, Appl	214	16	0.9	913	4	US-09-229-911A-13	Sequence 13, Appl
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c 143	16	0.9	97	3	US-08-952-664-15	Sequence 15, Appl	216	16	0.9	917	4	US-09-368-951-1	Sequence 1, Appli
c 144	16	0.9	97	4	US-09-487-874-15	Sequence 15, Appl	c 217	16	0.9	943	1	US-07-807-043B-12	Sequence 12, Appl
c 145	16	0.9	195	4	US-09-189-060B-50	Sequence 50, Appl	c 218	16	0.9	943	1	US-08-299-849B-12	Sequence 12, Appl
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c 148	16	0.9	279	4	US-09-040-984-43	Sequence 43, Appl	c 221	16	0.9	947	4	US-08-037-230D-12	Sequence 12, Appl
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c 150	16	0.9	279	4	US-09-643-597-43	Sequence 43, Appl	c 223	16	0.9	974	3	US-08-675-885-3	Sequence 3, Appli
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c 152	16	0.9	309	3	US-08-581-148C-2	Sequence 2, Appli	c 225	16	0.9	991	3	US-09-258-367-2	Sequence 2, Appli
c 153	16	0.9	369	4	US-09-643-597-148	Sequence 148, App	c 226	16	0.9	991	4	US-09-546-550-2	Sequence 2, Appli
c 154	16	0.9	395	4	US-09-195-106-21	Sequence 21, Appl	c 227	16	0.9	991	4	US-09-431-414-2	Sequence 2, Appli
c 155	16	0.9	395	4	US-09-370-838-164	Sequence 164, App	c 228	16	0.9	991	4	US-09-225-670-2	Sequence 2, Appli
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c 160	16	0.9	433	4	US-09-123-912-58	Sequence 58, Appl	c 233	16	0.9	1033	4	US-08-961-527-290	Sequence 290, App
c 161	16	0.9	433	4	US-09-643-597-58	Sequence 58, Appl	c 234	16	0.9	1032	4	US-09-227-357-134	Sequence 134, App
c 162	16	0.9	443	4	US-09-149-476-60	Sequence 60, Appl	c 235	16	0.9	1034	4	US-09-227-357-15	Sequence 15, Appl
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c 167	16	0.9	491	4	US-09-370-838-90	Sequence 90, Appl	c 240	16	0.9	1054	5	PCT-US94-12904-1	Sequence 1, Appli
c 168	16	0.9	493	4	US-09-280-116-166	Sequence 166, App	c 241	16	0.9	1073	3	US-08-911-423-1	Sequence 1, Appli
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c 319	16	0.9	1953	1			c 392	16	0.9	2885	4		

393	16	0.9	2885	4	US-09-232-200-56	Sequence 56, Appl	456	16	0.9	5948	2	US-08-662-227-1	Sequence 1, Appl
394	16	0.9	2885	4	US-09-232-197-36	Sequence 36, Appl	467	16	0.9	5948	4	US-09-017-947-1	Sequence 1, Appl
395	16	0.9	2885	4	US-09-232-197-56	Sequence 56, Appl	468	16	0.9	6671	1	US-08-280-443-1	Sequence 1, Appl
396	16	0.9	2885	4	US-09-232-201-36	Sequence 36, Appl	469	16	0.9	6671	1	US-08-457-459-1	Sequence 1, Appl
397	16	0.9	2885	4	US-09-232-201-56	Sequence 56, Appl	470	16	0.9	6671	1	US-08-555-678-1	Sequence 1, Appl
398	16	0.9	2899	4	US-08-981-392-24	Sequence 24, Appl	471	16	0.9	6671	5	PCT-US95-02275-1	Sequence 1, Appl
399	16	0.9	2904	4	US-09-221-294-3	Sequence 3, Appl	472	16	0.9	7498	2	US-08-816-693A-1	Sequence 1, Appl
400	16	0.9	2953	2	US-08-859-201-1	Sequence 1, Appl	473	16	0.9	7498	3	US-08-885-291-1	Sequence 1, Appl
c 401	16	0.9	3016	2	US-08-344-155C-97	Sequence 97, Appl	474	16	0.9	7498	4	US-09-496-672-1	Sequence 1, Appl
c 402	16	0.9	3017	4	US-09-009-490A-86	Sequence 86, Appl	475	16	0.9	7610	4	US-09-659-791A-12	Sequence 12, Appl
c 403	16	0.9	3018	1	US-08-347-718B-3	Sequence 3, Appl	476	16	0.9	8257	4	US-09-368-590-1	Sequence 1, Appl
c 404	16	0.9	3018	6	US-08-482-262-3	Sequence 3, Appl	477	16	0.9	8257	4	US-09-484-970B-65	Sequence 65, Appl
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c 406	16	0.9	3138	1	5284931-1	Patent No. 5284931	479	16	0.9	9934	4	US-09-167-681-45	Sequence 45, Appl
c 407	16	0.9	3138	1	US-07-867-106-4	Sequence 4, Appl	c 480	16	0.9	11495	4	US-09-056-105-9	Sequence 2, Appl
c 408	16	0.9	3156	2	US-08-887-518-1	Sequence 1, Appl	c 481	16	0.9	13011	2	US-09-056-105-9	Sequence 2, Appl
c 409	16	0.9	3156	2	US-09-023-321-1	Sequence 1, Appl	c 482	16	0.9	13977	4	US-08-791-849A-14	Sequence 14, Appl
c 410	16	0.9	3156	2	US-09-032-475-1	Sequence 1, Appl	c 483	16	0.9	15297	4	US-09-484-970B-60	Sequence 60, Appl
c 411	16	0.9	3195	2	US-08-951-648-5	Sequence 5, Appl	c 484	16	0.9	19307	3	US-08-836-022A-10	Sequence 3, Appl
c 412	16	0.9	3195	2	US-09-174-437-5	Sequence 5, Appl	c 485	16	0.9	19307	3	US-09-427-048A-10	Sequence 10, Appl
c 413	16	0.9	3364	2	US-08-735-609-9	Sequence 9, Appl	c 486	16	0.9	35060	3	US-08-814-095-7	Sequence 7, Appl
c 414	16	0.9	3364	2	US-08-735-609-9	Sequence 9, Appl	c 487	16	0.9	35060	3	US-08-814-095-7	Sequence 7, Appl
c 415	16	0.9	3364	2	US-08-735-609-9	Sequence 9, Appl	c 488	16	0.9	36651	4	US-09-738-894A-3	Sequence 3, Appl
c 416	16	0.9	3364	2	US-08-735-609-9	Sequence 9, Appl	c 489	16	0.9	38564	4	US-09-738-894A-3	Sequence 3, Appl
c 417	16	0.9	3364	2	US-09-244-752-9	Sequence 9, Appl	c 490	16	0.9	49136	4	US-09-738-894A-3	Sequence 3, Appl
c 418	16	0.9	3364	2	US-09-244-752-9	Sequence 9, Appl	c 491	16	0.9	49136	4	US-09-738-894A-3	Sequence 3, Appl
c 419	16	0.9	3364	2	US-09-244-752-9	Sequence 9, Appl	c 492	16	0.9	49272	1	US-09-738-894A-3	Sequence 3, Appl
c 420	16	0.9	3394	4	US-09-562-919-9	Sequence 9, Appl	c 493	16	0.9	50341	2	US-09-738-894A-3	Sequence 3, Appl
c 421	16	0.9	3441	2	US-08-159-784-4	Sequence 4, Appl	c 494	16	0.9	50341	2	US-09-738-894A-3	Sequence 3, Appl
c 422	16	0.9	3441	2	US-08-159-784-4	Sequence 4, Appl	c 495	16	0.9	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 423	16	0.9	3494	4	US-09-453-702B-164	Sequence 164, Appl	c 496	16	0.9	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 424	16	0.9	3494	4	US-09-453-702B-164	Sequence 164, Appl	c 497	16	0.9	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 425	16	0.9	3871	2	US-08-595-455B-3	Sequence 3, Appl	c 498	16	0.9	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 426	16	0.9	3871	2	US-08-595-455B-3	Sequence 3, Appl	c 499	16	0.9	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 427	16	0.9	3871	2	US-08-595-455B-3	Sequence 3, Appl	c 500	16	0.9	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 428	16	0.9	3871	2	US-08-595-455B-3	Sequence 3, Appl	c 501	16	0.9	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 429	16	0.9	3894	4	US-09-094-410-3	Sequence 3, Appl	c 502	16	0.9	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 430	16	0.9	4047	2	US-09-511-625B-3	Sequence 3, Appl	c 503	15	0.8	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 431	16	0.9	4047	2	US-09-511-625B-3	Sequence 3, Appl	c 504	15	0.8	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 432	16	0.9	4168	3	US-08-612-734B-1	Sequence 1, Appl	c 505	15	0.8	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 433	16	0.9	4190	3	US-08-836-567-11	Sequence 11, Appl	c 506	15	0.8	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 434	16	0.9	4204	2	US-08-938-251A-2	Sequence 2, Appl	c 507	15	0.8	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 435	16	0.9	4204	2	US-08-938-251A-2	Sequence 2, Appl	c 508	15	0.8	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 436	16	0.9	4204	2	US-08-938-251A-2	Sequence 2, Appl	c 509	15	0.8	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 437	16	0.9	4204	2	US-08-938-251A-2	Sequence 2, Appl	c 510	15	0.8	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 438	16	0.9	4237	1	US-07-844-298B-1	Sequence 1, Appl	c 511	15	0.8	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 439	16	0.9	4237	1	US-07-844-298B-1	Sequence 1, Appl	c 512	15	0.8	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 440	16	0.9	4237	1	US-07-844-298B-1	Sequence 1, Appl	c 513	15	0.8	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 441	16	0.9	4237	1	US-07-844-298B-1	Sequence 1, Appl	c 514	15	0.8	52297	4	US-09-738-894A-3	Sequence 3, Appl
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c 456	16	0.9	4237	1	US-07-844-298B-1	Sequence 1, Appl	c 529	15	0.8	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 457	16	0.9	4237	1	US-07-844-298B-1	Sequence 1, Appl	c 530	15	0.8	52297	4	US-09-738-894A-3	Sequence 3, Appl
c 458	16	0.9	4237	1	US-07-844-298B-1	Sequence 1, Appl	c 531	15	0.8	52297	4	US-09-738-894A-3	Sequence 3, Appl
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539	15	0.8	159	6	5486462-1	Patent No. 5486462	612	15	0.8	469	4	US-09-328-111-436	Sequence 436, App
540	15	0.8	171	5	PCT-US93-06251-62	Sequence 62, Appl	613	15	0.8	473	4	US-09-615-192A-184	Sequence 184, App
541	15	0.8	183	5	PCT-US93-06251-56	Sequence 56, Appl	614	15	0.8	474	4	US-09-227-357-129	Sequence 129, App
542	15	0.8	199	1	US-08-330-108-4	Sequence 4, Appl	615	15	0.8	475	4	US-09-105-542A-13	Sequence 13, Appl
543	15	0.8	199	5	PCT-US92-10087-4	Sequence 4, Appl	616	15	0.8	496	4	US-09-328-111-125	Sequence 125, App
544	15	0.8	200	2	US-08-454-557C-80	Sequence 80, Appl	617	15	0.8	498	1	US-07-885-970A-8	Sequence 8, Appl
545	15	0.8	200	2	US-08-340-426D-80	Sequence 80, Appl	618	15	0.8	498	1	US-08-298-687A-8	Sequence 8, Appl
546	15	0.8	200	2	US-08-450-673C-80	Sequence 80, Appl	619	15	0.8	498	1	US-08-530-797-7	Sequence 7, Appl
547	15	0.8	200	5	PCT-US95-17111A-80	Sequence 80, Appl	620	15	0.8	498	1	US-08-298-829-8	Sequence 8, Appl
548	15	0.8	216	1	US-07-973-321B-1	Sequence 1, Appl	621	15	0.8	498	2	US-08-787-335-7	Sequence 7, Appl
549	15	0.8	216	1	US-08-090-527A-1	Sequence 1, Appl	622	15	0.8	507	1	US-08-686-878A-22	Sequence 22, Appl
550	15	0.8	222	6	5274075-1	Patent No. 5274075	623	15	0.8	507	4	US-09-175-928-22	Sequence 22, Appl
551	15	0.8	225	1	US-07-603-716-40	Sequence 40, Appl	624	15	0.8	511	4	US-09-404-879A-64	Sequence 64, Appl
552	15	0.8	225	3	US-08-475-411A-40	Sequence 40, Appl	625	15	0.8	518	1	US-08-485-284A-2	Sequence 2, Appl
553	15	0.8	225	4	US-08-478-029A-40	Sequence 40, Appl	626	15	0.8	518	1	US-09-221-017B-186	Sequence 186, App
554	15	0.8	239	5	PCT-US93-06251-50	Sequence 50, Appl	627	15	0.8	527	4	US-09-370-838-281	Sequence 281, App
555	15	0.8	246	4	US-09-276-531-58	Sequence 58, Appl	628	15	0.8	529	3	US-08-545-809A-44	Sequence 44, Appl
556	15	0.8	257	4	US-09-040-984-48	Sequence 48, Appl	629	15	0.8	530	2	US-08-346-429-5	Sequence 5, Appl
557	15	0.8	257	4	US-09-123-912-48	Sequence 48, Appl	630	15	0.8	536	1	US-08-329-704-1	Sequence 1, Appl
558	15	0.8	257	4	US-09-643-597-48	Sequence 48, Appl	631	15	0.8	536	2	US-08-472-604-1	Sequence 1, Appl
559	15	0.8	262	4	US-09-117-121-21	Sequence 21, Appl	632	15	0.8	536	2	US-08-486-117-1	Sequence 1, Appl
560	15	0.8	275	1	US-08-215-084A-2	Sequence 2, Appl	633	15	0.8	536	4	US-08-477-537-1	Sequence 1, Appl
561	15	0.8	275	1	US-08-463-212-2	Sequence 2, Appl	634	15	0.8	546	4	US-09-643-597-129	Sequence 129, App
562	15	0.8	275	1	US-08-463-211-2	Sequence 2, Appl	635	15	0.8	548	4	US-09-036-355A-1	Sequence 1, Appl
563	15	0.8	284	4	US-09-040-984-80	Sequence 80, Appl	636	15	0.8	559	4	US-09-280-116-5	Sequence 5, Appl
564	15	0.8	284	4	US-09-123-912-80	Sequence 80, Appl	637	15	0.8	566	4	US-09-105-542A-1	Sequence 1, Appl
565	15	0.8	284	4	US-09-643-597-80	Sequence 80, Appl	638	15	0.8	570	2	US-08-633-682-1	Sequence 1, Appl
566	15	0.8	285	2	US-08-630-822A-85	Sequence 85, Appl	639	15	0.8	570	3	US-08-936-772-1	Sequence 1, Appl
567	15	0.8	285	2	US-09-005-069-85	Sequence 85, Appl	640	15	0.8	570	4	US-09-395-918-1	Sequence 1, Appl
568	15	0.8	285	4	US-09-171-156A-34	Sequence 34, Appl	641	15	0.8	570	4	US-09-385-982-124	Sequence 124, App
569	15	0.8	297	1	US-08-244-626-9	Sequence 9, Appl	642	15	0.8	572	1	US-09-328-111-644	Sequence 644, App
570	15	0.8	298	4	US-09-060-756-78	Sequence 78, Appl	643	15	0.8	591	1	US-07-973-321B-3	Sequence 3, Appl
571	15	0.8	302	4	US-09-608-785-255	Sequence 255, App	644	15	0.8	591	1	US-08-090-527A-3	Sequence 3, Appl
572	15	0.8	302	4	US-09-439-313-255	Sequence 255, App	645	15	0.8	593	4	US-09-385-982-132	Sequence 132, App
573	15	0.8	302	4	US-09-352-616A-255	Sequence 255, App	646	15	0.8	594	1	US-08-289-458-1	Sequence 1, Appl
574	15	0.8	309	1	US-09-232-149A-255	Sequence 255, App	647	15	0.8	594	2	US-08-761-549-1	Sequence 1, Appl
575	15	0.8	309	1	US-08-086-410-24	Sequence 24, Appl	648	15	0.8	594	4	US-09-127-646-1	Sequence 1, Appl
576	15	0.8	315	4	US-09-040-984-1	Sequence 1, Appl	649	15	0.8	595	4	US-09-171-156A-52	Sequence 52, Appl
577	15	0.8	315	4	US-09-123-912-1	Sequence 1, Appl	650	15	0.8	595	4	US-09-171-156A-54	Sequence 54, Appl
578	15	0.8	315	4	US-09-643-597-1	Sequence 1, Appl	651	15	0.8	603	4	US-08-998-416-1152	Sequence 1152, App
579	15	0.8	326	4	US-09-629-645A-17	Sequence 17, Appl	652	15	0.8	603	4	US-09-385-982-251	Sequence 251, App
580	15	0.8	328	4	US-09-280-116-2	Sequence 2, Appl	653	15	0.8	604	4	US-09-342-653-3	Sequence 3, Appl
581	15	0.8	332	4	US-08-991-789A-153	Sequence 153, App	654	15	0.8	610	4	US-09-149-476-121	Sequence 121, App
582	15	0.8	332	4	US-09-062-451-153	Sequence 153, App	655	15	0.8	614	4	US-09-844-525A-12	Sequence 12, App
583	15	0.8	332	4	US-09-598-326-153	Sequence 153, App	656	15	0.8	614	4	US-09-105-542A-2	Sequence 2, Appl
584	15	0.8	336	4	US-09-060-756-243	Sequence 243, App	657	15	0.8	620	4	US-09-385-982-153	Sequence 153, App
585	15	0.8	347	4	US-09-060-756-192	Sequence 192, App	658	15	0.8	622	4	US-09-040-984-57	Sequence 57, Appl
586	15	0.8	347	4	US-09-328-111-848	Sequence 848, App	659	15	0.8	622	4	US-09-123-912-57	Sequence 57, Appl
587	15	0.8	349	4	US-08-943-731-119	Sequence 119, App	660	15	0.8	622	4	US-09-643-597-57	Sequence 57, Appl
588	15	0.8	354	4	US-09-480-921B-21	Sequence 21, Appl	661	15	0.8	624	4	US-09-257-580-3	Sequence 3, Appl
589	15	0.8	360	1	US-07-920-519-28	Sequence 28, Appl	662	15	0.8	631	4	US-09-328-111-126	Sequence 126, App
590	15	0.8	360	1	US-08-086-410-21	Sequence 21, Appl	663	15	0.8	633	3	US-09-050-603A-36	Sequence 36, Appl
591	15	0.8	360	1	US-08-314-586-28	Sequence 28, Appl	664	15	0.8	633	3	US-09-102-420B-36	Sequence 36, Appl
592	15	0.8	360	1	US-09-227-357-121	Sequence 121, App	665	15	0.8	633	4	US-09-352-990-15	Sequence 15, Appl
593	15	0.8	362	4	US-09-060-756-381	Sequence 381, App	666	15	0.8	633	4	US-09-497-698-36	Sequence 36, Appl
594	15	0.8	363	4	US-08-905-223-206	Sequence 206, App	667	15	0.8	639	4	US-09-328-111-180	Sequence 180, App
595	15	0.8	363	4	US-09-276-599-20	Sequence 20, Appl	668	15	0.8	641	2	US-08-522-421-6	Sequence 6, Appl
596	15	0.8	367	4	US-09-328-111-446	Sequence 446, App	669	15	0.8	642	4	US-09-280-116-255	Sequence 255, App
597	15	0.8	367	4	US-09-219-983A-13	Sequence 13, Appl	670	15	0.8	642	4	US-09-370-838-119	Sequence 119, App
598	15	0.8	378	6	5274075-3	Patent No. 5274075	671	15	0.8	643	4	US-08-861-774E-43	Sequence 43, Appl
599	15	0.8	384	1	US-08-259-372A-13	Sequence 13, Appl	672	15	0.8	649	4	US-08-861-774E-61	Sequence 61, Appl
600	15	0.8	384	1	US-08-642-671D-13	Sequence 13, Appl	673	15	0.8	649	4	US-09-230-670C-2	Sequence 2, Appl
601	15	0.8	388	4	US-08-642-274D-13	Sequence 13, Appl	674	15	0.8	655	3	US-09-188-930-119	Sequence 119, App
602	15	0.8	388	4	US-08-952-014C-13	Sequence 13, Appl	675	15	0.8	672	4	US-09-161-241-78	Sequence 78, App
603	15	0.8	407	4	US-09-280-116-105	Sequence 105, App	676	15	0.8	675	4	US-08-998-416-179	Sequence 179, App
604	15	0.8	412	4	US-09-200-934-7	Sequence 7, Appl	677	15	0.8	681	4	US-09-134-001C-2410	Sequence 2410, App
605	15	0.8	423	1	US-08-470-179-163	Sequence 163, App	678	15	0.8	685	4	US-08-998-416-951	Sequence 151, App
606	15	0.8	426	4	US-09-060-756-124	Sequence 124, App	679	15	0.8	686	1	US-08-591-498-15	Sequence 15, App
607	15	0.8	436	4	US-09-060-756-100	Sequence 100, App	680	15	0.8	691	6	5175255-3	Patent No. 5175255
608	15	0.8	452	1	US-07-662-198B-1	Sequence 1, Appl	681	15	0.8	693	4	US-09-280-116-36	Sequence 36, Appl
609	15	0.8	452	1	US-08-322-742-1	Sequence 1, Appl	682	15	0.8	700	1	US-08-037-579A-4	Sequence 4, Appl
610	15	0.8	461	2	US-08-467-046-24	Sequence 24, Appl	683	15	0.8	700	1	US-07-846-992-1	Sequence 1, Appl
611	15	0.8	462	4	US-09-712-016-68	Sequence 68, Appl	684	15	0.8	700	1	US-08-469-555-1	Sequence 1, Appl

685	15	0.8	700	3	US-08-601-184-4	Sequence 4, Appli	758	15	0.8	861	2	US-08-924-759-15	Sequence 15, Appli
686	15	0.8	704	2	US-08-874-186-43	Sequence 43, Appl	759	15	0.8	861	3	US-09-248-335-15	Sequence 15, Appl
687	15	0.8	707	2	US-08-850-910A-40	Sequence 40, Appl	760	15	0.8	863	1	US-07-940-861-11	Sequence 11, Appl
c 688	15	0.8	711	4	US-08-943-731-108	Sequence 108, App	761	15	0.8	863	1	US-08-459-512-11	Sequence 11, Appl
689	15	0.8	720	3	US-08-946-026-14	Sequence 14, Appl	762	15	0.8	863	2	US-08-459-657-11	Sequence 11, Appl
690	15	0.8	720	4	US-08-998-416-582	Sequence 582, App	763	15	0.8	863	2	US-08-460-132-11	Sequence 11, Appl
c 691	15	0.8	724	4	US-09-221-017B-719	Sequence 719, App	764	15	0.8	863	5	PCT-US92-02050-11	Sequence 11, Appl
c 692	15	0.8	725	4	US-08-998-416-829	Sequence 829, App	765	15	0.8	863	6	5185441-35	Patent No. 5185441
693	15	0.8	731	4	US-09-043-646-1	Sequence 1, Appli	766	15	0.8	863	6	5223394-5	Patent No. 5223394
c 694	15	0.8	731	4	US-09-641-638-87	Sequence 87, Appl	767	15	0.8	867	4	US-09-473-316A-22	Sequence 22, Appl
695	15	0.8	735	4	US-09-149-476-269	Sequence 269, App	768	15	0.8	868	1	US-08-387-845-3	Sequence 3, Appli
696	15	0.8	739	1	US-08-156-383-3	Sequence 3, Appli	769	15	0.8	868	2	US-08-778-275-3	Sequence 3, Appli
697	15	0.8	739	5	US-08-340-136-3	Sequence 3, Appli	770	15	0.8	868	3	US-08-867-352-3	Sequence 3, Appli
698	15	0.8	739	5	PCT-US92-10866-3	Sequence 3, Appli	771	15	0.8	880	1	US-08-616-368A-7	Sequence 7, Appli
699	15	0.8	740	4	US-09-020-956-17	Sequence 17, Appl	772	15	0.8	880	3	US-09-054-298-7	Sequence 7, Appli
700	15	0.8	740	4	US-09-030-607-17	Sequence 17, Appl	773	15	0.8	880	4	US-08-818-653-7	Sequence 7, Appli
701	15	0.8	740	4	US-09-605-785-17	Sequence 17, Appl	774	15	0.8	882	2	US-08-909-965C-9	Sequence 9, Appli
702	15	0.8	740	4	US-09-439-313-17	Sequence 17, Appl	775	15	0.8	884	1	US-08-178-708-7	Sequence 7, Appli
703	15	0.8	740	4	US-09-352-616A-17	Sequence 17, Appl	776	15	0.8	894	1	US-08-457-552-7	Sequence 7, Appli
704	15	0.8	740	4	US-09-232-149A-17	Sequence 17, Appl	777	15	0.8	894	1	US-08-456-430-7	Sequence 7, Appli
705	15	0.8	751	1	US-08-592-936B-10	Sequence 10, Appl	778	15	0.8	894	2	US-08-994-418-7	Sequence 7, Appli
706	15	0.8	751	1	US-08-788-928A-16	Sequence 16, Appl	779	15	0.8	894	5	PCT-US95-00432-7	Sequence 7, Appli
707	15	0.8	751	2	US-09-111-573-10	Sequence 10, Appl	780	15	0.8	897	2	US-08-630-822A-59	Sequence 59, Appl
708	15	0.8	752	4	US-09-247-155-47	Sequence 47, Appl	781	15	0.8	897	2	US-09-005-069-59	Sequence 59, Appl
709	15	0.8	765	1	US-08-173-510B-102	Sequence 102, App	782	15	0.8	897	2	US-09-171-156A-17	Sequence 17, Appl
710	15	0.8	765	2	US-08-458-218-100	Sequence 100, App	783	15	0.8	901	4	US-09-475-316A-12	Sequence 12, Appl
711	15	0.8	765	2	US-08-450-497-102	Sequence 102, App	784	15	0.8	905	2	US-08-941-263-2	Sequence 2, Appli
712	15	0.8	771	4	US-09-040-984-85	Sequence 85, Appl	785	15	0.8	905	3	US-09-227-178-2	Sequence 2, Appli
713	15	0.8	771	4	US-09-123-912-85	Sequence 85, Appl	786	15	0.8	905	4	US-08-470-449-2	Sequence 2, Appli
714	15	0.8	771	4	US-09-643-597-85	Sequence 85, Appl	787	15	0.8	912	2	US-08-993-228-7	Sequence 7, Appli
715	15	0.8	775	3	US-09-361-434-6	Sequence 85, Appl	788	15	0.8	921	1	US-08-722-001-17	Sequence 17, Appl
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Db 1605 GGCAGAGAGAGCGGAGG 1585

RESULT 3
US-08-750-703-4/c
; Sequence 4, Application US/08750703
; Patent No. 5891633
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Frank J.; Idle, Jeffrey R.
; TITLE OF INVENTION: DEFECTS IN DRUG
; TITLE OF INVENTION: METABOLISM
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 345 Park Ave.
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,703
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07605
; FILING DATE: 16-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dorothy R. Auth
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4196PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8779 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: CYP2A13
; LOCATION:
; OTHER INFORMATION:
US-08-750-703-4

Query Match 1.1%; Score 21; DB 2; Length 8779;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-152-060-25/c
; Sequence 25, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003Pl.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11

; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
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; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
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; LOCATION: (1140)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-152-060-25

Query Match 1.0%; Score 19; DB 4; Length 1329;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1645 GGCAGGGGCGGAGG 1663
| | | | | | | | | | | | | | | |
Db 152 GGCAGGGGCGGAGG 134

RESULT 5
US-08-788-750-1/c
; Sequence 1, Application US/08788750
; Patent No. 5910430
; GENERAL INFORMATION:
; APPLICANT: Ellis, Catherine
; APPLICANT: Bergsma, Derk
; TITLE OF INVENTION: No 5910430el G-Protein Coupled Receptor
; TITLE OF INVENTION: (HTADX50)
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,750
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

```

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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-788-750-1

Query Match 1.0%; Score 19; DB 2; Length 2260;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1645 GGCAGGAGGCGCAGTGAGG 1663
| | | | | | | | | | | | | | | |
DB 771 GGCAGGAGGCGCAGTGAGG 753

RESULT 6
US-07-960-389-1
; Sequence 1, Application US/07960389
; Patent No. 5705611
; GENERAL INFORMATION:
; APPLICANT: HAYASHIDA, Kasuhiro;
; TITLE OF INVENTION: Human GM-CSF Receptor Component
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disc
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System Software 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/960,389
; FILING DATE: 07-JAN-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 554,745
; FILING DATE: 18-JUL-1990
; APPLICATION NUMBER: PCT/US 91/04846
; FILING DATE: 16-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Blasdale, John H. C.
; REGISTRATION NUMBER: 31,895
; REFERENCE/DOCKET NUMBER: DX0143Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2902
; TELEFAX: (908) 298-5388
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3475 base pairs
; TYPE: nucleotides
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: DNA sequence encoding Human GM-CSF receptor
; US-07-960-389-1
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Query Match 1.0%; Score 19; DB 1; Length 3475;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 GCTGTGCTCTGGCCCTCC 183
| | | | | | | | | | | | | | | |
DB 1563 GCTGTGCTCTGGCCCTCC 1581

RESULT 7
US-08-770-379-19/c
; Sequence 19, Application US/08770379
; Patent No. 5849564
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
; TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,379
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 52342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-770-379-19

Query Match 1.0%; Score 19; DB 2; Length 35100;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1351 CTGCCATGGGTTGGCAA 1369
| | | | | | | | | | | | | | | |
DB 13366 CTGCCATGGGTTGGCAA 13348

RESULT 8
US-08-757-669A-19/c
; Sequence 19, Application US/08757669A
; Patent No. 6183751
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
```

APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/757,669A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-669A-19

Query Match 1.0%; Score 19; DB 4; Length 35100;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1351 CTGCCATGGGGTTTGGCAA 1369
|||||
DB 13366 CTGCCATGGGGTTTGGCAA 13348

RESULT 9

US-09-230-371A-19/c
Sequence 19, Application US/09230371A
Patent No. 6348586
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A
APPLICANT: Russo, James J
APPLICANT: Edelman, Isidore S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
USES THEREOF
FILE REFERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US97/13346
PRIOR FILING DATE: 1997-07-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 35100
TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-19

Query Match 1.0%; Score 19; DB 4; Length 35100;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1351 CTGCCATGGGGTTTGGCAA 1369
|||||
DB 13366 CTGCCATGGGGTTTGGCAA 13348

RESULT 10

US-08-329-704-3
Sequence 3, Application US/08329704
Patent No. 5786210
GENERAL INFORMATION:
APPLICANT: Kelnner, Gregory S.
APPLICANT: Kennedy, Jacqueline L.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN THYMOKINE GENES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/329,704
FILING DATE: 25-OCT-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/193,483
FILING DATE: 08-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,421
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0430K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 562 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 15..356
US-08-329-704-3

Query Match 1.0%; Score 18; DB 1; Length 562;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 TCCTGGCCCTCCTTGGCA 189
|||||
DB 28 TCCTGGCCCTCCTTGGCA 45

RESULT 11

US-08-472-604-3
Sequence 3, Application US/08472604
Patent No. 5677285
GENERAL INFORMATION:
APPLICANT: Kelnner, Gregory S.
APPLICANT: Kennedy, Jacqueline L.

APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN THYMOKINE GENES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,604
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,704
FILING DATE: 25-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,421
FILING DATE: 22-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/193,483
FILING DATE: 08-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0430K1GB
TELEPHONE: 415-852-9196
TELEFAX: 415-852-9196
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 562 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 15..356
US-08-472-604-3

Query Match 1.0%; Score 18; DB 2; Length 562;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 TCCTGGCCCTCCTTGGCA 189
|||||
DB 28 TCCTGGCCCTCCTTGGCA 45

RESULT 12
US-08-486-117-3
Sequence 3, Application US/08486117
Patent No. 5985580
GENERAL INFORMATION:
APPLICANT: Keiner, Gregory S.
APPLICANT: Kennedy, Jacqueline L.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN THYMOKINE GENES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,117
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,704
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,421
FILING DATE: 22-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/193,483
FILING DATE: 08-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0430K1GC
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 562 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 15..356
US-08-486-117-3

Query Match 1.0%; Score 18; DB 2; Length 562;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 TCCTGGCCCTCCTTGGCA 189
|||||
DB 28 TCCTGGCCCTCCTTGGCA 45

RESULT 13
US-08-477-537-3
Sequence 3, Application US/08477537
Patent No. 6245329
GENERAL INFORMATION:
APPLICANT: Keiner, Gregory S.
APPLICANT: Kennedy, Jacqueline L.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN THYMOKINE GENES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,537
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

us-09-944-896-49.olilo.rni

Mon Dec 30 09:16:08 2002

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APPLICATION NUMBER: US 08/329,704
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,421
FILING DATE: 22-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/193,483
FILING DATE: 08-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0430K1CD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 562 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 15..356
US-08-477-537-3

Query Match 1.0% Score 18; DB 4; Length 562;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 TCCTGGCCCTCTCTGGCA 189
    |||||
Db 28 TCCTGGCCCTCTCTGGCA 45

RESULT 14
US-09-149-476-232
; Sequence 232, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22

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; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
```

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
```

Query Match 1.0%; Score 18; DB 4; Length 629;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1859 AGCTGAAAAA 1876
      |||
Db 569 AGCTGAAAAA 586
```

RESULT 15

```
US-09-328-111-342/c
; Sequence 342, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Rushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(669)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-342
```

Query Match 1.0%; Score 18; DB 4; Length 669;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1859 AGCTGAAAAA 1876
      |||
Db 43 AGCTGAAAAA 26
```

us-09-944-896-49.oli10.rni

```

RESULT 16
US-09-276-531-71/c
; Sequence 71, Application US/09276531
; Patent No. 6183968
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Reddy, Roopa
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
; TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,531
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/079,677
; FILING DATE: March 27, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lynn E. Murry, Ph.D.
; REGISTRATION NUMBER: 42,918
; REFERENCE/DOCKET NUMBER: PA-0008 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 853-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT07
; CLONE: 1506088
;
US-09-276-531-71

Query Match 1.0%; Score 18; DB 4; Length 759;
Best Local Similarity 100.0%; Pred.No. 83;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1855 AATCAGCTGAAAAA 1872
Db 641 AATCAGCTGAAAAA 624
|||||
|||||

RESULT 17
US-08-567-816A-1
; Sequence 1, Application US/08567816A
; Patent No. 5780268
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Guegler, Karl P.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: A NEW CHEMOKINE EXPRESSED IN A MIXED
; TITLE OF INVENTION: LYMPHOCYTE REACTION

```


100

RESULT 22
 PCT-US92-06532-2
 ; Sequence 2, Application PC/TUS9206532
 ; GENERAL INFORMATION:
 ; APPLICANT: Krause, James E.
 ; TITLE OF INVENTION: Human Substance P Receptor
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SD
 ; STREET: 800 N. Lindbergh Blvd.
 ; CITY: St. Louis
 ; STATE: Missouri
 ; COUNTRY: U.S.A.
 ; ZIP: 63167
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/06532
 ; FILING DATE: 19920805
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meyer, Scott J.
 ; REGISTRATION NUMBER: 25,275
 ; REFERENCE/DOCKET NUMBER: 07-24(776)A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (314)694-3117
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1766 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 211..1431
 PCT-US92-06532-2

Query Match 1.0%; Score 18; DB 5; Length 1766;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1174 GCCGCTGGAGACCA 1191
 |||||
 DB 1265 GCCGCTGGAGACCA 1282

RESULT 23
 US-09-364-230-19
 ; Sequence 19, Application US/09364230
 ; Patent No. 6348339
 ; GENERAL INFORMATION:
 ; APPLICANT: Cahoon, Rebecca E.
 ; APPLICANT: Hitz, William D.
 ; APPLICANT: Kinney, Anthony J.
 ; APPLICANT: Rafalski, J. Antoni
 ; TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
 ; FILE REFERENCE: BB-1178
 ; CURRENT APPLICATION NUMBER: US/09/364,230
 ; CURRENT FILING DATE: 1999-07-29
 ; EARLIER APPLICATION NUMBER: 60/094,990
 ; EARLIER FILING DATE: July 31, 1998
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 19
 ; LENGTH: 1797
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa

US-09-364-230-19
 Query Match 1.0%; Score 18; DB 4; Length 1797;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1859 AGCTGAAAAA 1876
 |||||
 DB 1770 AGCTGAAAAA 1787
 RESULT 24
 US-09-123-912-88
 ; Sequence 88, Application US/09123912A
 ; Patent No. 6312695
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Wang, Tongtong
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
 ; FILE REFERENCE: 210121.455C1
 ; CURRENT APPLICATION NUMBER: US/09/123,912A
 ; CURRENT FILING DATE: 1998-07-27
 ; PRIOR APPLICATION NUMBER: 09/040,802
 ; PRIOR FILING DATE: 1998-03-18
 ; NUMBER OF SEQ ID NOS: 114
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 88
 ; LENGTH: 1844
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-123-912-88

Query Match 1.0%; Score 18; DB 4; Length 1844;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1859 AGCTGAAAAA 1876
 |||||
 DB 1816 AGCTGAAAAA 1833

RESULT 25
 US-09-643-597-88
 ; Sequence 88, Application US/09643597
 ; Patent No. 6426072
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, AiJun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: McNeill, Patricia D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.455C11
 ; CURRENT APPLICATION NUMBER: US/09/643,597
 ; CURRENT FILING DATE: 2000-08-21
 ; NUMBER OF SEQ ID NOS: 369
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 88
 ; LENGTH: 1844
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-643-597-88

Query Match 1.0%; Score 18; DB 4; Length 1844;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1859 ACCTGAAAAA 1876
Db 1816 AGCTGAAAAA 1833

RESULT 26

US-08-837-199A-9
; Sequence 9, Application US/08837199A
; Patent No. 6455277
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/08/837,199A
; CURRENT FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1927
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (538)..(1926)
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (1)..(537)
; OTHER INFORMATION: No. 6455277e= "1 to 537 is -235 to 301 of Figure 5 2lacon"
; LOCATION: (538)..(1926)
; NAME/KEY: misc_feature
; LOCATION: (550)..(550)
; OTHER INFORMATION: N in position 550 indicates any nucleic acid
US-08-837-199A-9

Query Match 1.0%; Score 18; DB 4; Length 1927;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 AGCTGGCATCCGGCCTG 422
Db 718 AGCTGGCATCCGGCCTG 735

RESULT 27

US-08-837-199A-40
; Sequence 40, Application US/08837199A
; Patent No. 6455277
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/08/837,199A
; CURRENT FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 1927
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (550)..(550)
; OTHER INFORMATION: N in position 550 indicates any nucleic acid
US-08-837-199A-40

Query Match 1.0%; Score 18; DB 4; Length 1927;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 AGCTGGCATCCGGCCTG 422
Db 718 AGCTGGCATCCGGCCTG 735

RESULT 28

US-08-837-199A-11
; Sequence 11, Application US/08837199A
; Patent No. 6455277
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/08/837,199A
; CURRENT FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1929
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (540)..(1928)
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (1)..(539)
; OTHER INFORMATION: No. 6455277e= "1 to 539 is -237 to 301 of Figure 5 2lbccon"
US-08-837-199A-11

Query Match 1.0%; Score 18; DB 4; Length 1929;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 AGCTGGCATCCGGCCTG 422
Db 720 AGCTGGCATCCGGCCTG 737

RESULT 29

US-08-837-199A-41
; Sequence 41, Application US/08837199A
; Patent No. 6455277
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/08/837,199A
; CURRENT FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 1929

; TYPE: DNA
; ORGANISM: HUMAN
US-08-837-199A-41

Query Match 1.0%; Score 18; DB 4; Length 1929;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 405 AGCCTGGCATCCGGCCTG 422
|||||

Db 720 AGCCTGGCATCCGGCCTG 737

RESULT 30

US-08-837-199A-1
; Sequence 1, Application US/08837199A

; Patent No. 6455277

; GENERAL INFORMATION:

; APPLICANT: FOX, GARY M.

; APPLICANT: JING, SHUOIAN

; APPLICANT: WEN, DUANZHI

; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR

; FILE REFERENCE: A-401C

; CURRENT APPLICATION NUMBER: US/08/837,199A

; CURRENT FILING DATE: 1997-04-14

; PRIOR APPLICATION NUMBER: US 60/015,907

; PRIOR FILING DATE: 1996-04-22

; PRIOR APPLICATION NUMBER: US 60/017,221

; PRIOR FILING DATE: 1996-05-09

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 2568

; TYPE: DNA

; ORGANISM: HUMAN

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (540)..(1934)

; OTHER INFORMATION:

; NAME/KEY: misc_feature

; LOCATION: (2078)..(2078)

; OTHER INFORMATION: N in position 2078 indicates a position of divergence between dif

; OTHER INFORMATION: ferent receptor clones

; NAME/KEY: misc_feature

; LOCATION: (2107)..(2107)

; OTHER INFORMATION: N in position 2107 indicates a position of divergence between dif

; OTHER INFORMATION: ferent receptor clones

; NAME/KEY: misc_feature

; LOCATION: (2241)..(2241)

; OTHER INFORMATION: N in position 2241 indicates a position of divergence between dif

; OTHER INFORMATION: ferent receptor clones

; NAME/KEY: misc_feature

; LOCATION: (2250)..(2250)

; OTHER INFORMATION: N in position 2250 indicates a position of divergence between dif

; OTHER INFORMATION: ferent receptor clones

; NAME/KEY: misc_feature

; LOCATION: (2256)..(2294)

; OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence be

; OTHER INFORMATION: tween different receptor clones

US-08-837-199A-1

Query Match

Best Local Similarity 100.0%; Score 18; DB 4; Length 2568;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 405 AGCCTGGCATCCGGCCTG 422
|||||

Db 720 AGCCTGGCATCCGGCCTG 737

RESULT 31

US-08-837-199A-5

; Sequence 5, Application US/08837199A

; Patent No. 6455277

; GENERAL INFORMATION:

; APPLICANT: FOX, GARY M.

; APPLICANT: JING, SHUOIAN

; APPLICANT: WEN, DUANZHI

; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR

; FILE REFERENCE: A-401C

; CURRENT APPLICATION NUMBER: US/08/837,199A

; CURRENT FILING DATE: 1997-04-14

; PRIOR APPLICATION NUMBER: US 60/015,907

; PRIOR FILING DATE: 1996-04-22

; PRIOR APPLICATION NUMBER: US 60/017,221

; PRIOR FILING DATE: 1996-05-09

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 3209

; TYPE: DNA

; ORGANISM: HUMAN

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (540)..(1937)

; OTHER INFORMATION:

; NAME/KEY: misc_feature

; LOCATION: (1)..(510)

; OTHER INFORMATION: note="1 to 510 is -237 to 272 of Fig 5 Hsgr-21bf"

; NAME/KEY: misc_feature

; LOCATION: (1)..(539)

; OTHER INFORMATION: note="1 to 539 is -237 to 301 of Fig 5 Gdnfr"

; NAME/KEY: misc_feature

; LOCATION: (2078)..(2078)

; OTHER INFORMATION: N in position 2078 indicates a position of divergence between

; OTHER INFORMATION: ferent receptor clones

; NAME/KEY: misc_feature

; LOCATION: (2256)..(2294)

; OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence

; OTHER INFORMATION: tween different receptor clones

; NAME/KEY: misc_feature

; LOCATION: (1091)..(1091)

; OTHER INFORMATION: N in position 1091 indicates any nucleic acid

US-08-837-199A-5

Query Match

Best Local Similarity 100.0%; Score 18; DB 4; Length 3209;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 405 AGCCTGGCATCCGGCCTG 422
|||||

Db 720 AGCCTGGCATCCGGCCTG 737

RESULT 32

US-08-837-199A-37

; Sequence 37, Application US/08837199A

; Patent No. 6455277

; GENERAL INFORMATION:

; APPLICANT: FOX, GARY M.

; APPLICANT: JING, SHUOIAN

; APPLICANT: WEN, DUANZHI

; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR

; FILE REFERENCE: A-401C

; CURRENT APPLICATION NUMBER: US/08/837,199A

; CURRENT FILING DATE: 1997-04-14

; PRIOR APPLICATION NUMBER: US 60/015,907

; PRIOR FILING DATE: 1996-04-22

; PRIOR APPLICATION NUMBER: US 60/017,221

; PRIOR FILING DATE: 1996-05-09

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 37

; LENGTH: 3209

; TYPE: DNA

; ORGANISM: HUMAN

FEATURE:
NAME/KEY: misc.feature
LOCATION: (1091)..(1091)
OTHER INFORMATION: N in position 1091 indicates any nucleic acid.
NAME/KEY: misc.feature
LOCATION: (2078)..(2078)
OTHER INFORMATION: N in position 2078 indicates a position of divergence between dif
OTHER INFORMATION: ferent receptor clones.
NAME/KEY: misc.feature
LOCATION: (2256)..(2294)
OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence bet
OTHER INFORMATION: ween different receptor clones.
US-08-837-199A-37

Query Match 1.0%; Score 18; DB 4; Length 3209;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 AGCCTGGCATCGGCGCTG 422
|||||
Db 720 AGCCTGGCATCGGCGCTG 737

RESULT 33

US-09-651-011A-3
Sequence 3, Application US/09651011A
Patent No. 6346416

GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
TITLE OF INVENTION: ANTISENSE MODULATION OF HPK/GCK-LIKE KINASE EXPRESSION
FILE REFERENCE: RFS-0168
CURRENT APPLICATION NUMBER: US/09/651,011A
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 3
LENGTH: 4266
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(3528)
US-09-651-011A-3

Query Match 1.0%; Score 18; DB 4; Length 4266;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 248 CCTGAACAGGAGGAGAG 265
|||||
Db 889 CCTGAACAGGAGGAGAG 906

RESULT 34

US-09-513-057C-26
Sequence 26, Application US/09513057C
Patent No. 6433251

GENERAL INFORMATION:
APPLICANT: Wagner, et al.
TITLE OF INVENTION: GENES REGULATING CIRCADIAN CLOCK FUNCTION AND PHOTOPERIODISM
FILE REFERENCE: 1505-54357
CURRENT APPLICATION NUMBER: US/09/513,057C
CURRENT FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 4478
TYPE: DNA
ORGANISM: Oryza sativa

FEATURE:
NAME/KEY: exon
LOCATION: (1)..(261)
OTHER INFORMATION:

NAME/KEY: exon
LOCATION: (1660)..(2645)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (3330)..(3381)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (3495)..(4478)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (262)..(1659)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (2646)..(3329)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (3382)..(3494)
OTHER INFORMATION:
US-09-513-057C-26

Query Match 1.0%; Score 18; DB 4; Length 4478;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 GTGCTCCTGGCCCTCCTT 185
|||||
Db 4033 GTGCTCCTGGCCCTCCTT 4050

RESULT 35

US-09-484-970B-106
Sequence 106, Application US/09484970B
Patent No. 6426186

GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Volkmut, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 106
LENGTH: 4822
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1
NAME/KEY: unsure
LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,
OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-106

Query Match 1.0%; Score 18; DB 4; Length 4822;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1294 CCTTCACAGTTTGCCCT 1311
|||||
Db 2073 CCTTCACAGTTTGCCCT 2090

RESULT 36

US-09-415-946-2

Sequence 2, Application US/09415946
Patent No. 6376751

GENERAL INFORMATION:
APPLICANT: Sung, Z. Renee
APPLICANT: Aubert, Dominique
APPLICANT: Chen, Lingjing
APPLICANT: The Regents of the University of California

;; TITLE OF INVENTION: Nucleic Acids That Control Reproductive Development in
;; TITLE OF INVENTION: Plants
;; FILE REFERENCE: 018941-000110US
;; CURRENT APPLICATION NUMBER: US/09/415,946
;; CURRENT FILING DATE: 1999-10-08
;; PRIOR APPLICATION NUMBER: US 09/169,696
;; PRIOR FILING DATE: 1998-10-09
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 8648
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
;; FEATURE:
;; OTHER INFORMATION: EMF1 gene and its promoter region
;; NAME/KEY: promoter
;; LOCATION: (1)..(3201)
;; NAME/KEY: CDS
;; LOCATION: join(4241..4335, 4448..4623, 4704..4823, 4903..4956,
;; OTHER INFORMATION: EMBRYONIC FLOWER 1 (EMF1)
;; NAME/KEY: exon
;; LOCATION: (3202)..(3265)
;; OTHER INFORMATION: exon 1
;; NAME/KEY: intron
;; LOCATION: (3266)..(4159)
;; NAME/KEY: exon
;; LOCATION: (4160)..(4335)
;; OTHER INFORMATION: exon 2
;; NAME/KEY: intron
;; LOCATION: (4336)..(4447)
;; NAME/KEY: exon
;; LOCATION: (4448)..(4623)
;; OTHER INFORMATION: exon 3
;; NAME/KEY: intron
;; LOCATION: (4624)..(4703)
;; NAME/KEY: exon
;; LOCATION: (4704)..(4823)
;; OTHER INFORMATION: exon 4
;; NAME/KEY: intron
;; LOCATION: (4824)..(4902)
;; NAME/KEY: exon
;; LOCATION: (4903)..(4956)
;; OTHER INFORMATION: exon 5
;; NAME/KEY: intron
;; LOCATION: (4957)..(5045)
;; NAME/KEY: exon
;; LOCATION: (5046)..(6307)
;; OTHER INFORMATION: exon 6
;; NAME/KEY: intron
;; LOCATION: (6308)..(6447)
;; NAME/KEY: exon
;; LOCATION: (6448)..(8065)
;; OTHER INFORMATION: exon 7
;; NAME/KEY: intron
;; LOCATION: (8066)..(8300)
;; NAME/KEY: exon
;; LOCATION: (8301)..(8648)
;; OTHER INFORMATION: exon 8
;;
US-09-415-946-2

Query Match 1.0%; Score 18; DB 4; Length 8648;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1840 GGGTATTAAATATGAAT 1957
|||||
Db 1130 GGGTATTAAATATGAAT 1147

RESULT 37
US-08-476-866-20
; Sequence 20, Application US/08476866
; Patent No. 5994339

;; GENERAL INFORMATION:
;; APPLICANT: CRAPO, JAMES D.
;; APPLICANT: FRIDOVICH, IRWIN
;; APPLICANT: OURY, TIM
;; APPLICANT: DAY, BRIAN J.
;; APPLICANT: FOLZ, RODNEY J.
;; APPLICANT: FREEMAN, BRUCE A.
;; TITLE OF INVENTION: SUPEROXIDE DISMUTASE AND MIMETICS THEREOF
;; NUMBER OF SEQUENCES: 24
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NIXON & VANDERHYE P.C.
;; STREET: 1100 NORTH GLEBE ROAD
;; CITY: ARLINGTON
;; STATE: VIRGINIA
;; COUNTRY: U.S.A.
;; ZIP: 22201-4714
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/476,866
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/322,766
;; FILING DATE: 13-OCT-1994
;; APPLICATION NUMBER: US 08/136,207
;; FILING DATE: 15-OCT-1993
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WILSON, MARY J.
;; REGISTRATION NUMBER: 32,955
;; REFERENCE/DOCKET NUMBER: 1579-74
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 816-4000
;; TELEFAX: (703) 816-4100
;; TELEX: 200797 NIXN UR
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10079 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 5086..5803
;;
US-08-476-866-20

Query Match 1.0%; Score 18; DB 2; Length 10079;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1543 CTGCTGTGCCACCTGTCT 1560
|||||
Db 3808 CTGCTGTGCCACCTGTCT 3825

RESULT 38
US-09-415-946-1
; Sequence 1, Application US/09415946
; Patent No. 6376751
;; GENERAL INFORMATION:
;; APPLICANT: Sung, Z. Renee
;; APPLICANT: Aubert, Dominique
;; APPLICANT: Chen, Lingjing
;; APPLICANT: The Regents of the University of California
;; TITLE OF INVENTION: Nucleic Acids That Control Reproductive Development in
;; TITLE OF INVENTION: Plants
;; FILE REFERENCE: 018941-000110US
;; CURRENT APPLICATION NUMBER: US/09/415,946

```
; CURRENT FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,696
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17341
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: genomic DNA (Ecotype Columbia) from CD82 clone
; NAME/KEY: promoter
; LOCATION: (1)..(3201)
; NAME/KEY: CDS
; LOCATION: join(4241..4335, 4448..4623, 4704..4823, 4903..4956,
; OTHER INFORMATION: EMBRYONIC FLOWER 1 (EMF1)
; NAME/KEY: exon
; LOCATION: (3202)..(3265)
; OTHER INFORMATION: exon 1
; NAME/KEY: intron
; LOCATION: (3266)..(4159)
; NAME/KEY: exon
; LOCATION: (4160)..(4335)
; OTHER INFORMATION: exon 2
; NAME/KEY: intron
; LOCATION: (4336)..(4447)
; NAME/KEY: exon
; LOCATION: (4448)..(4623)
; OTHER INFORMATION: exon 3
; NAME/KEY: intron
; LOCATION: (4624)..(4703)
; NAME/KEY: exon
; LOCATION: (4704)..(4823)
; OTHER INFORMATION: exon 4
; NAME/KEY: intron
; LOCATION: (4824)..(4902)
; NAME/KEY: exon
; LOCATION: (4903)..(4956)
; OTHER INFORMATION: exon 5
; NAME/KEY: intron
; LOCATION: (4957)..(5045)
; NAME/KEY: exon
; LOCATION: (5046)..(6307)
; OTHER INFORMATION: exon 6
; NAME/KEY: intron
; LOCATION: (6308)..(6447)
; NAME/KEY: exon
; LOCATION: (6448)..(8065)
; OTHER INFORMATION: exon 7
; NAME/KEY: intron
; LOCATION: (8066)..(8300)
; NAME/KEY: exon
; LOCATION: (8301)..(8648)
; OTHER INFORMATION: exon 8
; US-09-415-946-1
```

```
Query Match
Best Local Similarity 100.0%; Score 18; DB 4; Length 17341;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1840 GGGTATTAAATATGAAT 1857
Db 1130 GGGTATTAAATATGAAT 1147
|||||
```

```
RESULT 39
US-09-797-906-3
; Sequence 3, Application US/09797906
; Patent No. 6329188
```

```
; GENERAL INFORMATION:
; APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
```

```
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: C1001151CIP
; CURRENT APPLICATION NUMBER: US/09/797,906
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 84495
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(84495)
; OTHER INFORMATION: n = A,T,C or G
; US-09-797-906-3

Query Match
Best Local Similarity 100.0%; Score 18; DB 4; Length 84495;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1859 AGCTGAAAAA 1876
Db 4080 AGCTGAAAAA 4097
|||||
```

```
RESULT 40
US-08-342-411A-32
; Sequence 32, Application US/08342411A
; Patent No. 5639616
; GENERAL INFORMATION:
; APPLICANT: LIAO, Shutsung
; APPLICANT: SONG, Ching
; TITLE OF INVENTION: UBIQUITOUS NUCLEAR RECEPTOR:
; COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342.411A
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KITCHELL, BARBARA S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-342-411A-32
```

```
Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1024 CCCTGACCTGAGATC 1040
|||||
```


; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-588-258B-21

Query Match 0.9%; Score 17; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1451 TGCCAGGAGCACATCT 1467
Db 174 TGCCAGGAGCACATCT 190

RESULT 44

US-08-460-505-21
; Sequence 21, Application US/08460505
; Patent No. 6069296

GENERAL INFORMATION:

; APPLICANT: Horvitz, Robert H.

; APPLICANT: Koelle, Michael

; TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/460,505

; FILING DATE: 02-JUN-1995

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Bieker-Brady, Kristina

; REGISTRATION NUMBER: 39,109

; REFERENCE/DOCKET NUMBER: 01997/214001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 198 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-460-505-21

Query Match 0.9%; Score 17; DB 3; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1451 TGCCAGGAGCACATCT 1467
Db 174 TGCCAGGAGCACATCT 190

RESULT 45

PCT-US96-08295-21

; Sequence 21, Application PC/TUS9608295

; GENERAL INFORMATION:

; APPLICANT: Massachusetts Institute of Technology

; TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING

; NUMBER OF SEQUENCES: 41

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/08295
; FILING DATE: 31-MAY-1996
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/588,258
; FILING DATE: 12-JAN-96
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 01997/216001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 198 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

PCT-US96-08295-21

Query Match 0.9%; Score 17; DB 5; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1451 TGCCAGGAGCACATCT 1467
Db 174 TGCCAGGAGCACATCT 190

RESULT 46

US-08-518-878B-34
; Sequence 34, Application US/08518878B
; Patent No. 5702902

; GENERAL INFORMATION:

; APPLICANT: Tartaglia, Louis A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/518,878B

; FILING DATE: 23-AUG-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7853-036

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 457 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 US-08-518-878B-34

Query Match 0.9%; Score 17; DB 1; Length 457;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1860 GCTGAAAAA 1876
 |||||
 Db 441 GCTGAAAAA 457

RESULT 47
 US-08-294-522B-35
 Sequence 35, Application US/08294522B
 Patent No. 5741666
 GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.
 TITLE OF INVENTION: Compositions and Methods for the
 TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/294,522B
 FILING DATE: 23-AUG-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-015

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864/9741
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 457 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:

NAME/KEY: CDS
 LOCATION: 25...315
 US-08-294-522B-35

Query Match 0.9%; Score 17; DB 1; Length 457;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1860 GCTGAAAAA 1876
 |||||
 Db 441 GCTGAAAAA 457

RESULT 48
 US-08-807-861A-34
 Sequence 34, Application US/08807861A
 Patent No. 5853975
 GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
 TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/807,861A
 FILING DATE: 26-FEB-1997
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/518,878
 FILING DATE: 23-AUG-1995
 APPLICATION NUMBER: US 08/470,868
 FILING DATE: 06-JUN-1995
 APPLICATION NUMBER: US 08/294,522
 FILING DATE: 23-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-066

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 457 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 US-08-807-861A-34

Query Match 0.9%; Score 17; DB 2; Length 457;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1860 GCTGAAAAA 1876
 |||||
 Db 441 GCTGAAAAA 457

RESULT 49
 US-08-470-868A-34
 Sequence 34, Application US/08470868A
 Patent No. 5861485
 GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis C.
 TITLE OF INVENTION: Compositions and Methods for the
 TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie and Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864/9741
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 457 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:

NAME/KEY: CDS
 LOCATION: 25...315
 US-08-470-868A-34

Query Match 0.9%; Score 17; DB 1; Length 457;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1860 GCTGAAAAA 1876
 |||||
 Db 441 GCTGAAAAA 457

```

; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,868A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-0031-999
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
US-08-470-868A-34

```

```

Query Match 0.9%; Score 17; DB 2; Length 457;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1860 GCTGAAAAA 1876
Db 441 GCTGAAAAA 457

```

```

RESULT 50
US-09-210-681-34
; Sequence 34, Application US/09210681
; Patent No. 6057109
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITILE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/807,861
; FILING DATE: 26-FEB-1997
; APPLICATION NUMBER: US 08/518,878
; FILING DATE: 23-AUG-1995
; APPLICATION NUMBER: US 08/470,868
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/294,522
; FILING DATE: 23-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742

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; REFERENCE/DOCKET NUMBER: 7853-066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
US-09-210-681-34

Query Match 0.9%; Score 17; DB 3; Length 457;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1860 GCTGAAAAA 1876
Db 441 GCTGAAAAA 457

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Search completed: December 29, 2002, 01:15:08
Job time : 282 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2002, 01:11:38 ; Search time 129 Seconds
(without alignments)
5907.719 Million cell updates/sec

Title: US-09-944-896-49
Perfect score: 1876
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 363474 seqs, 203117208 residues

Word size : 10

Total number of hits satisfying chosen parameters: 300621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	1876	100.0	1876	9	US-09-944-403-49
3	1876	100.0	1876	9	US-09-944-896-49
4	1876	100.0	1876	9	US-09-944-944-49
5	1876	100.0	1876	10	US-09-866-028-49
6	1876	100.0	1876	10	US-09-944-449-49
7	1876	100.0	1876	10	US-09-944-457-49
8	1876	100.0	1876	10	US-09-945-587-49
9	1876	100.0	1876	10	US-09-945-015-49
10	1876	100.0	1876	10	US-09-944-396-49
11	1876	100.0	1876	10	US-09-944-097-49
12	1876	100.0	1876	10	US-09-944-432-49
13	1876	100.0	1876	10	US-09-943-762-49
14	1876	100.0	1876	10	US-09-944-896-104
15	1876	100.0	1876	10	US-09-943-851A-49
16	1029	54.9	1876	10	US-09-790-264-1
17	1029	54.9	1923	9	US-10-042-141-12
18	1029	54.9	1923	10	US-09-726-843-12
19	1008	53.7	1338	10	US-09-790-264-3

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45	2.4	45	9	US-09-944-896-53	Sequence 53, Appl
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37	1.4	27	9	US-09-944-413-103	Sequence 103, App
38	1.4	27	9	US-09-944-403-103	Sequence 103, App
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40	1.4	27	9	US-09-944-944-103	Sequence 103, App
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47	1.4	27	10	US-09-944-097-103	Sequence 103, App
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56	1.3	24	9	US-09-866-028-51	Sequence 51, Appl
57	1.3	24	9	US-09-944-449-51	Sequence 51, Appl
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65	1.3	24	10	US-09-943-851A-51	Sequence 51, Appl
66	1.3	24	10	US-09-790-264-8	Sequence 5183, Ap
67	1.3	24	10	US-09-944-413-104	Sequence 104, App
68	1.3	24	10	US-09-944-403-104	Sequence 104, App
69	1.3	24	10	US-09-944-896-104	Sequence 104, App
70	1.3	24	10	US-09-944-944-104	Sequence 104, App
71	1.3	24	10	US-09-866-028-104	Sequence 104, App
72	1.3	24	10	US-09-944-449-104	Sequence 104, App
73	1.3	24	10	US-09-944-457-104	Sequence 104, App
74	1.3	24	10	US-09-944-432-104	Sequence 104, App
75	1.3	24	10	US-09-943-762-104	Sequence 104, App
76	1.3	24	10	US-09-944-654-104	Sequence 104, App
77	1.3	24	10	US-09-943-851A-104	Sequence 104, App
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79	1.3	24	10	US-09-790-264-8	Sequence 8, Appl1
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81	1.3	24	10	US-09-944-403-104	Sequence 104, App
82	1.3	24	10	US-09-944-896-104	Sequence 104, App
83	1.3	24	10	US-09-944-944-104	Sequence 104, App
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86	1.3	24	10	US-09-944-457-104	Sequence 104, App
87	1.3	24	10	US-09-943-762-104	Sequence 104, App
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93	1.3	24	10	US-09-944-403-104	Sequence 104, App
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99	1.3	24	10	US-09-943-762-104	Sequence 104, App
100	1.3	24	10	US-09-944-654-104	Sequence 104, App

c 93	19	1.0	10	US-09-945-015-104	Sequence 104, App	166	18	1.0	1332	9	US-09-992-598-269	Sequence 269, App
c 94	19	1.0	10	US-09-944-396-104	Sequence 104, App	167	18	1.0	1332	9	US-09-989-293A-269	Sequence 269, App
c 95	19	1.0	10	US-09-944-097-104	Sequence 104, App	168	18	1.0	1332	9	US-09-989-735-269	Sequence 269, App
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c 97	19	1.0	10	US-09-943-762-104	Sequence 104, App	170	18	1.0	1332	10	US-09-989-722-269	Sequence 269, App
c 98	19	1.0	10	US-09-944-654-104	Sequence 104, App	171	18	1.0	1332	10	US-09-989-723-269	Sequence 269, App
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c 101	19	1.0	1060	US-09-925-301-116	Sequence 116, App	174	18	1.0	1332	10	US-09-989-731-269	Sequence 269, App
c 102	19	1.0	1329	US-09-852-797-25	Sequence 25, Appl	175	18	1.0	1332	10	US-09-989-732-269	Sequence 269, App
c 103	19	1.0	1329	US-09-853-161-25	Sequence 25, Appl	176	18	1.0	1332	10	US-09-989-732-269	Sequence 269, App
c 104	19	1.0	1329	US-09-852-659A-25	Sequence 25, Appl	177	18	1.0	1332	10	US-09-991-073-269	Sequence 269, App
c 105	19	1.0	1356	US-09-808-602-20	Sequence 20, Appl	178	18	1.0	1332	10	US-09-990-442-269	Sequence 269, App
c 106	19	1.0	1667	US-09-808-602-16	Sequence 16, Appl	179	18	1.0	1332	10	US-09-991-163-269	Sequence 269, App
c 107	19	1.0	1691	US-09-808-602-18	Sequence 18, Appl	180	18	1.0	1332	10	US-09-993-604-269	Sequence 269, App
c 108	19	1.0	1835	US-09-925-302-32	Sequence 32, Appl	181	18	1.0	1332	10	US-09-990-456-269	Sequence 269, App
c 109	19	1.0	3230	US-09-764-878-358	Sequence 358, App	182	18	1.0	1332	10	US-09-989-721-269	Sequence 269, App
c 110	19	1.0	3318	US-09-808-602-91	Sequence 91, Appl	183	18	1.0	1400	10	US-09-796-858-29	Sequence 29, Appl
c 111	19	1.0	3439	US-10-044-090-546	Sequence 546, App	184	18	1.0	1678	10	US-09-731-872-182	Sequence 182, App
c 112	19	1.0	155074	US-10-026-188-6	Sequence 6, Appl	185	18	1.0	1724	10	US-09-832-616-1	Sequence 1, Appl
c 113	19	1.0	155074	US-10-026-188-6	Sequence 6, Appl	186	18	1.0	1815	10	US-09-832-496-1	Sequence 1, Appl
c 114	18	1.0	18	US-09-944-413-102	Sequence 102, App	187	18	1.0	1844	10	US-09-735-705-88	Sequence 88, Appl
c 115	18	1.0	18	US-09-944-403-102	Sequence 102, App	188	18	1.0	1844	10	US-09-850-716A-88	Sequence 88, Appl
c 116	18	1.0	18	US-09-944-896-102	Sequence 102, App	189	18	1.0	1844	10	US-09-897-778-88	Sequence 88, Appl
c 117	18	1.0	18	US-09-944-944-102	Sequence 102, App	190	18	1.0	1859	10	US-09-764-864-740	Sequence 740, App
c 118	18	1.0	18	US-09-866-028-102	Sequence 102, App	191	18	1.0	1893	9	US-10-063-547-149	Sequence 149, App
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c 126	18	1.0	18	US-09-943-762-102	Sequence 102, App	199	18	1.0	2397	9	US-09-902-853-324	Sequence 324, App
c 127	18	1.0	18	US-09-943-762-102	Sequence 102, App	200	18	1.0	2397	10	US-09-909-320-324	Sequence 324, App
c 128	18	1.0	18	US-09-943-851A-102	Sequence 102, App	201	18	1.0	2397	12	US-10-052-586-29	Sequence 29, Appl
c 129	18	1.0	77	US-09-933-797-765	Sequence 765, App	202	18	1.0	2397	9	US-09-759-056-1	Sequence 1, Appl
c 130	18	1.0	229	US-09-864-761-25170	Sequence 25170, A	203	18	1.0	2732	9	US-09-901-812-1	Sequence 1, Appl
c 131	18	1.0	229	US-09-864-761-26170	Sequence 26170, A	204	18	1.0	2732	9	US-09-901-812-1	Sequence 1, Appl
c 132	18	1.0	291	US-09-923-876-3910	Sequence 3910, Ap	205	18	1.0	2777	9	US-09-759-056-4	Sequence 4, Appl
c 133	18	1.0	431	US-09-864-761-4145	Sequence 4145, Ap	206	18	1.0	2777	9	US-09-901-812-4	Sequence 4, Appl
c 134	18	1.0	474	US-09-867-701-9902	Sequence 9902, Ap	207	18	1.0	2777	9	US-09-992-598-288	Sequence 288, App
c 135	18	1.0	494	US-10-063-547-29	Sequence 29, Appl	208	18	1.0	3334	9	US-09-989-735-288	Sequence 288, App
c 136	18	1.0	494	US-10-006-867-29	Sequence 29, Appl	209	18	1.0	3334	9	US-10-063-547-57	Sequence 57, Appl
c 137	18	1.0	496	US-09-783-590-3813	Sequence 3813, Ap	210	18	1.0	3334	9	US-09-989-735-288	Sequence 288, App
c 138	18	1.0	540	US-09-864-761-9434	Sequence 9434, Ap	211	18	1.0	3334	9	US-09-990-444-288	Sequence 288, App
c 139	18	1.0	559	US-09-864-761-9804	Sequence 9804, Ap	212	18	1.0	3334	10	US-09-989-722-288	Sequence 288, App
c 140	18	1.0	593	US-09-764-868-192	Sequence 192, App	213	18	1.0	3334	10	US-09-989-723-288	Sequence 288, App
c 141	18	1.0	635	US-09-983-965-563	Sequence 563, App	214	18	1.0	3334	10	US-09-989-279-288	Sequence 288, App
c 142	18	1.0	654	US-09-814-122-31	Sequence 31, Appl	215	18	1.0	3334	10	US-09-989-727-288	Sequence 288, App
c 143	18	1.0	669	US-09-879-536-342	Sequence 342, App	216	18	1.0	3334	10	US-09-989-731-288	Sequence 288, App
c 144	18	1.0	730	US-09-950-933A-1	Sequence 1, Appl	217	18	1.0	3334	10	US-09-989-732-288	Sequence 288, App
c 145	18	1.0	929	US-09-814-122-16	Sequence 16, Appl	218	18	1.0	3334	10	US-09-991-073-288	Sequence 288, App
c 146	18	1.0	936	US-09-925-301-83	Sequence 83, Appl	219	18	1.0	3334	10	US-09-990-442-288	Sequence 288, App
c 147	18	1.0	963	US-09-992-598-423	Sequence 423, App	220	18	1.0	3334	10	US-09-991-163-288	Sequence 288, App
c 148	18	1.0	963	US-09-989-293A-423	Sequence 423, App	221	18	1.0	3334	10	US-09-993-604-288	Sequence 288, App
c 149	18	1.0	963	US-09-989-735-423	Sequence 423, App	222	18	1.0	3334	10	US-09-990-456-288	Sequence 288, App
c 150	18	1.0	963	US-09-990-444-423	Sequence 423, App	223	18	1.0	3334	12	US-10-006-867-57	Sequence 57, Appl
c 151	18	1.0	963	US-09-989-722-423	Sequence 423, App	224	18	1.0	3379	10	US-09-789-386-1	Sequence 1, Appl
c 152	18	1.0	963	US-09-989-723-423	Sequence 423, App	225	18	1.0	3579	10	US-09-893-348-22	Sequence 22, Appl
c 153	18	1.0	963	US-09-989-279-423	Sequence 423, App	226	18	1.0	3611	9	US-09-836-392-3	Sequence 3, Appl
c 154	18	1.0	963	US-09-989-727-423	Sequence 423, App	227	18	1.0	4053	10	US-09-758-140-5	Sequence 5, Appl
c 155	18	1.0	963	US-09-989-731-423	Sequence 423, App	228	18	1.0	4053	10	US-09-972-599A-5	Sequence 5, Appl
c 156	18	1.0	963	US-09-989-732-423	Sequence 423, App	229	18	1.0	4165	10	US-09-864-864-274	Sequence 274, App
c 157	18	1.0	963	US-09-991-073-423	Sequence 423, App	230	18	1.0	4166	10	US-09-960-253-155	Sequence 155, App
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c 161	18	1.0	963	US-09-990-456-423	Sequence 423, App	234	18	1.0	110096	10	US-09-880-107-1542	Sequence 1542, Ap
c 162	18	1.0	963	US-09-989-721-423	Sequence 423, App	235	18	1.0	0.9	17	US-09-790-264-7	Sequence 7, Appl
c 163	18	1.0	1030	US-09-764-864-739	Sequence 739, App	236	17	0.9	131	10	US-09-867-701-8701	Sequence 8701, Ap
c 164	18	1.0	1040	US-09-764-864-319	Sequence 319, App	237	17	0.9	160	10	US-09-867-701-6283	Sequence 6283, Ap
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c 242	17	0.9	210	10	US-09-867-701-9070	Sequence 9070, Ap	c 315	17	0.9	2181	9	US-09-978-295A-51	Sequence 51, Appl
c 243	17	0.9	222	10	US-09-783-590-636	Sequence 636, App	c 316	17	0.9	2181	9	US-09-978-697-51	Sequence 51, Appl
c 244	17	0.9	253	10	US-09-923-596-2007	Sequence 2007, Ap	c 317	17	0.9	2181	9	US-09-978-192A-51	Sequence 51, Appl
c 245	17	0.9	257	10	US-09-964-824A-41	Sequence 41, Appl	c 318	17	0.9	2181	9	US-09-953-499-7	Sequence 7, Appl
c 246	17	0.9	257	10	US-09-964-824A-448	Sequence 448, App	c 319	17	0.9	2181	9	US-09-953-499-11	Sequence 11, Appl
c 247	17	0.9	257	10	US-09-880-107-965	Sequence 965, App	c 320	17	0.9	2181	9	US-09-999-832A-51	Sequence 51, Appl
c 248	17	0.9	257	10	US-09-967-768A-78	Sequence 78, Appl	c 321	17	0.9	2181	9	US-09-822-849A-49	Sequence 49, Appl
c 249	17	0.9	265	10	US-09-764-846-24	Sequence 24, Appl	c 322	17	0.9	2261	10	US-09-891-216-7	Sequence 7, Appl
c 250	17	0.9	284	10	US-09-250-883-13	Sequence 13, Appl	c 323	17	0.9	2332	9	US-09-764-904-136	Sequence 136, App
c 251	17	0.9	301	10	US-09-960-352-4747	Sequence 4747, Ap	c 324	17	0.9	2332	10	US-09-764-860-1197	Sequence 1197, Ap
c 252	17	0.9	309	10	US-09-925-302-387	Sequence 387, App	c 325	17	0.9	2346	10	US-09-925-297-32	Sequence 32, Appl
c 253	17	0.9	330	10	US-09-917-800A-671	Sequence 671, App	c 326	17	0.9	2362	10	US-09-866-582-7	Sequence 7, Appl
c 254	17	0.9	347	10	US-09-880-107-364	Sequence 364, App	c 327	17	0.9	2502	10	US-09-891-216-8	Sequence 8, Appl
c 255	17	0.9	349	10	US-09-983-965-2319	Sequence 2319, Ap	c 328	17	0.9	2663	10	US-09-995-593A-8	Sequence 8, Appl
c 256	17	0.9	356	10	US-09-960-352-125	Sequence 125, App	c 329	17	0.9	2935	9	US-09-828-366-20	Sequence 20, Appl
c 257	17	0.9	380	9	US-09-954-531-621	Sequence 621, App	c 330	17	0.9	3010	9	US-09-764-868-242	Sequence 242, App
c 258	17	0.9	380	10	US-09-969-708-585	Sequence 585, App	c 331	17	0.9	3010	9	US-09-989-293A-313	Sequence 313, App
c 259	17	0.9	380	10	US-09-917-800A-179	Sequence 179, App	c 332	17	0.9	3010	9	US-09-989-735-313	Sequence 313, App
c 260	17	0.9	381	10	US-09-878-574-1427	Sequence 1427, Ap	c 333	17	0.9	3010	9	US-09-989-735-313	Sequence 313, App
c 261	17	0.9	404	9	US-09-946-807-1469	Sequence 1469, Ap	c 334	17	0.9	3010	9	US-09-989-722-313	Sequence 313, App
c 262	17	0.9	404	10	US-09-795-668-1469	Sequence 1469, Ap	c 335	17	0.9	3010	10	US-09-989-723-313	Sequence 313, App
c 263	17	0.9	404	10	US-09-795-686-1469	Sequence 1469, Ap	c 336	17	0.9	3010	10	US-09-989-723-313	Sequence 313, App
c 264	17	0.9	411	10	US-09-969-708-125	Sequence 125, App	c 337	17	0.9	3010	10	US-09-989-727-313	Sequence 313, App
c 265	17	0.9	449	10	US-09-924-035A-239	Sequence 239, App	c 338	17	0.9	3010	10	US-09-989-727-313	Sequence 313, App
c 266	17	0.9	473	10	US-09-864-761-10846	Sequence 10846, A	c 339	17	0.9	3010	10	US-09-989-731-313	Sequence 313, App
c 267	17	0.9	478	10	US-09-864-761-568	Sequence 568, App	c 340	17	0.9	3010	10	US-09-989-732-313	Sequence 313, App
c 268	17	0.9	494	9	US-09-954-531-675	Sequence 675, App	c 341	17	0.9	3010	10	US-09-991-073-313	Sequence 313, App
c 269	17	0.9	516	9	US-09-954-531-633	Sequence 633, App	c 342	17	0.9	3010	10	US-09-991-073-313	Sequence 313, App
c 270	17	0.9	516	9	US-09-954-531-1042	Sequence 1042, Ap	c 343	17	0.9	3010	10	US-09-991-163-313	Sequence 313, App
c 271	17	0.9	516	10	US-09-962-436-348	Sequence 348, App	c 344	17	0.9	3010	10	US-09-993-604-313	Sequence 313, App
c 272	17	0.9	516	10	US-09-954-456-834	Sequence 834, App	c 345	17	0.9	3010	10	US-09-990-456-313	Sequence 313, App
c 273	17	0.9	516	10	US-09-954-456-1259	Sequence 1259, Ap	c 346	17	0.9	3010	10	US-09-989-721-313	Sequence 313, App
c 274	17	0.9	516	10	US-09-880-107-114	Sequence 114, App	c 347	17	0.9	3010	10	US-09-887-576-459	Sequence 459, App
c 275	17	0.9	564	9	US-09-894-844-124	Sequence 124, App	c 348	17	0.9	3770	9	US-09-924-366B-19	Sequence 19, Appl
c 276	17	0.9	583	10	US-09-864-761-7403	Sequence 7403, Ap	c 349	17	0.9	3923	10	US-09-910-087-20	Sequence 20, Appl
c 277	17	0.9	598	10	US-09-864-761-13298	Sequence 13298, A	c 350	17	0.9	3923	10	US-09-880-107-3935	Sequence 3935, Ap
c 278	17	0.9	645	10	US-09-770-149-582	Sequence 582, App	c 351	17	0.9	3923	10	US-09-967-768A-222	Sequence 222, App
c 279	17	0.9	730	10	US-09-867-580-677	Sequence 677, App	c 352	17	0.9	4101	9	US-09-981-353-28	Sequence 28, Appl
c 280	17	0.9	903	10	US-09-974-300-4731	Sequence 4731, Ap	c 353	17	0.9	4629	10	US-09-150-811-7	GENERAL INFORMA
c 281	17	0.9	978	10	US-09-886-055-234	Sequence 234, App	c 354	17	0.9	4839	10	US-09-764-867-476	Sequence 476, App
c 282	17	0.9	997	10	US-09-800-729-14	Sequence 14, Appl	c 355	17	0.9	5640	10	US-09-774-434-3	Sequence 3, Appl
c 283	17	0.9	1017	10	US-09-800-528-7	Sequence 7, Appl	c 356	17	0.9	9009	9	US-09-957-641-1	Sequence 1, Appl
c 284	17	0.9	1021	10	US-09-789-561-61	Sequence 61, Appl	c 357	17	0.9	11617	9	US-09-860-670-265	Sequence 265, App
c 285	17	0.9	1050	10	US-09-800-729-46	Sequence 46, Appl	c 358	17	0.9	17764	10	US-09-070-927A-301	Sequence 301, App
c 286	17	0.9	1071	10	US-09-800-729-45	Sequence 45, Appl	c 359	17	0.9	32132	10	US-09-764-877-2308	Sequence 2308, Ap
c 287	17	0.9	1086	10	US-09-789-561-82	Sequence 82, Appl	c 360	17	0.9	45845	10	US-09-927-091-6	Sequence 6, Appl
c 288	17	0.9	1086	10	US-09-800-729-48	Sequence 48, Appl	c 361	17	0.9	180216	10	US-09-835-232-6	Sequence 6, Appl
c 289	17	0.9	1092	10	US-09-867-550-1055	Sequence 1055, Ap	c 362	17	0.9	465237	10	US-09-933-267A-1	Sequence 1, Appl
c 290	17	0.9	1125	9	US-09-938-842A-5081	Sequence 5081, Ap	c 363	17	0.9	659158	9	US-09-771-208-20	Sequence 20, Appl
c 291	17	0.9	1138	10	US-09-800-729-44	Sequence 44, Appl	c 364	16	0.9	24	10	US-09-216-393-356	Sequence 356, App
c 292	17	0.9	1149	10	US-09-800-729-47	Sequence 47, Appl	c 365	16	0.9	77	10	US-09-919-580-319	Sequence 319, App
c 293	17	0.9	1189	10	US-09-770-445-49	Sequence 49, Appl	c 366	16	0.9	101	10	US-09-834-975-712	Sequence 712, App
c 294	17	0.9	1297	10	US-09-770-445-17	Sequence 17, Appl	c 367	16	0.9	112	10	US-09-925-300-880	Sequence 880, App
c 295	17	0.9	1332	10	US-09-250-883-14	Sequence 14, Appl	c 368	16	0.9	118	10	US-09-974-300-7727	Sequence 7727, Ap
c 296	17	0.9	1350	9	US-09-984-245-115	Sequence 115, App	c 369	16	0.9	133	10	US-09-925-299-701	Sequence 701, App
c 297	17	0.9	1351	9	US-09-984-245-85	Sequence 85, Appl	c 370	16	0.9	135	10	US-09-895-828-108	Sequence 108, App
c 298	17	0.9	1400	10	US-09-774-490-5	Sequence 5, Appl	c 371	16	0.9	140	10	US-09-867-701-3127	Sequence 3127, Ap
c 299	17	0.9	1465	10	US-09-864-761-13828	Sequence 13828, A	c 372	16	0.9	142	9	US-09-954-531-608	Sequence 608, App
c 300	17	0.9	1501	10	US-09-925-302-41	Sequence 41, Appl	c 373	16	0.9	142	10	US-09-954-456-22	Sequence 22, Appl
c 301	17	0.9	1521	10	US-09-864-761-30395	Sequence 30395, A	c 374	16	0.9	142	10	US-09-954-456-549	Sequence 549, App
c 302	17	0.9	1572	12	US-10-062-254-267	Sequence 267, App	c 375	16	0.9	142	10	US-09-954-456-1614	Sequence 1614, Ap
c 303	17	0.9	1641	10	US-09-731-816-3	Sequence 3, Appl	c 376	16	0.9	147	10	US-09-924-035A-247	Sequence 247, App
c 304	17	0.9	1660	9	US-09-764-868-244	Sequence 244, App	c 377	16	0.9	148	10	US-09-880-107-386	Sequence 386, App
c 305	17	0.9	1737	10	US-09-925-301-186	Sequence 186, App	c 378	16	0.9	152	9	US-09-736-457-436	Sequence 436, App
c 306	17	0.9	1758	10	US-09-815-242-7035	Sequence 7035, Ap	c 379	16	0.9	152	9	US-09-736-457-924	Sequence 924, App
c 307	17	0.9	1793	10	US-09-925-301-343	Sequence 343, App	c 380	16	0.9	152	9	US-09-902-941-436	Sequence 924, App
c 308	17	0.9	1860	10	US-09-880-107-1618	Sequence 1618, Ap	c 381	16	0.9	152	9	US-09-902-941-924	Sequence 924, App
c 309	17	0.9	1892	12	US-10-078-929-105	Sequence 105, App	c 382	16	0.9	161	10	US-09-867-701-9144	Sequence 9144, Ap
c 310	17	0.9	1925	10	US-09-938-842A-4067	Sequence 4067, Ap	c 383	16	0.9	161	10	US-09-728-445-550	Sequence 550, App
c 311	17	0.9	1981	10	US-09-908-322-26	Sequence 26, Appl	c 384	16	0.9	164	10	US-09-783-590-5195	Sequence 5195, Ap

c 385	16	0.9	165	10	US-09-983-965-5149	Sequence 5149, Ap	458	16	0.9	327	10	US-09-867-701-8374	Sequence 8374, Ap
c 386	16	0.9	175	10	US-09-770-696-319	Sequence 319, App	c 459	16	0.9	327	10	US-09-960-352-4646	Sequence 4646, Ap
c 387	16	0.9	181	10	US-09-764-877-20	Sequence 20, Appl	c 460	16	0.9	328	10	US-09-924-035A-534	Sequence 534, App
c 388	16	0.9	188	10	US-09-917-800A-602	Sequence 602, App	c 461	16	0.9	331	10	US-09-783-590-5221	Sequence 5221, Ap
c 389	16	0.9	196	10	US-09-895-828-310	Sequence 310, App	c 462	16	0.9	332	10	US-09-867-701-7441	Sequence 7441, Ap
c 390	16	0.9	197	10	US-09-783-590-2899	Sequence 2899, Ap	c 463	16	0.9	334	10	US-09-867-701-343	Sequence 343, App
c 391	16	0.9	200	10	US-09-960-352-14582	Sequence 14582, A	c 464	16	0.9	334	10	US-09-867-701-8380	Sequence 8380, Ap
c 392	16	0.9	207	10	US-09-764-847-402	Sequence 402, App	c 465	16	0.9	334	10	US-09-880-107-508	Sequence 508, App
c 393	16	0.9	209	10	US-09-764-846-63	Sequence 63, Appl	c 466	16	0.9	335	10	US-09-964-824A-403	Sequence 403, App
c 394	16	0.9	211	10	US-09-867-701-9752	Sequence 9752, Ap	c 467	16	0.9	338	10	US-09-983-965-5112	Sequence 5112, Ap
c 395	16	0.9	211	10	US-09-960-352-6835	Sequence 6836, Ap	c 468	16	0.9	339	10	US-09-919-580-744	Sequence 744, App
c 396	16	0.9	211	10	US-09-880-107-1535	Sequence 1515, Ap	c 469	16	0.9	340	10	US-09-574-2254	Sequence 2254, Ap
c 397	16	0.9	213	10	US-09-864-761-25096	Sequence 25096, A	c 470	16	0.9	340	10	US-09-867-701-8308	Sequence 8308, Ap
c 398	16	0.9	216	10	US-09-864-761-20049	Sequence 20049, A	c 471	16	0.9	341	10	US-09-815-343-717	Sequence 717, App
c 399	16	0.9	217	10	US-09-867-701-9498	Sequence 9498, Ap	c 472	16	0.9	346	10	US-09-770-791-763	Sequence 763, App
c 400	16	0.9	219	9	US-09-728-444-916	Sequence 916, App	c 473	16	0.9	348	10	US-09-960-352-12770	Sequence 12770, A
c 401	16	0.9	221	10	US-09-867-701-10386	Sequence 10386, A	c 474	16	0.9	350	10	US-09-960-352-7303	Sequence 7303, Ap
c 402	16	0.9	225	10	US-09-867-701-7438	Sequence 7438, Ap	c 475	16	0.9	352	10	US-09-867-701-8585	Sequence 8585, Ap
c 403	16	0.9	234	10	US-09-867-701-9928	Sequence 9928, Ap	c 476	16	0.9	356	10	US-09-867-701-10595	Sequence 10595, A
c 404	16	0.9	235	10	US-09-998-598-2601	Sequence 2601, Ap	c 477	16	0.9	359	10	US-09-960-352-12234	Sequence 12234, A
c 405	16	0.9	239	10	US-09-777-564-1554	Sequence 1554, Ap	c 478	16	0.9	360	9	US-09-938-842A-164	Sequence 164, App
c 406	16	0.9	241	10	US-09-880-107-3113	Sequence 3113, Ap	c 479	16	0.9	361	10	US-09-960-352-12770	Sequence 12770, A
c 407	16	0.9	243	9	US-10-079-623-305	Sequence 305, App	c 480	16	0.9	362	10	US-09-917-800A-678	Sequence 678, App
c 408	16	0.9	243	9	US-10-040-739-1020	Sequence 1020, Ap	c 481	16	0.9	362	10	US-09-867-701-7143	Sequence 7143, Ap
c 409	16	0.9	245	10	US-09-777-564-1543	Sequence 1543, Ap	c 482	16	0.9	367	10	US-09-867-701-892	Sequence 892, App
c 410	16	0.9	247	10	US-09-919-580-685	Sequence 685, App	c 483	16	0.9	369	10	US-09-735-705-148	Sequence 148, App
c 411	16	0.9	252	10	US-09-864-761-21981	Sequence 21981, A	c 484	16	0.9	369	10	US-09-850-716A-148	Sequence 148, App
c 412	16	0.9	252	10	US-09-960-352-2480	Sequence 2480, Ap	c 485	16	0.9	369	10	US-09-897-778-148	Sequence 148, App
c 413	16	0.9	261	10	US-09-864-761-26238	Sequence 26238, A	c 486	16	0.9	371	10	US-09-925-299-16	Sequence 16, Appl
c 414	16	0.9	261	10	US-09-783-590-7039	Sequence 7039, Ap	c 487	16	0.9	371	10	US-09-770-791-351	Sequence 351, App
c 415	16	0.9	269	10	US-09-960-352-10807	Sequence 10807, A	c 488	16	0.9	373	10	US-09-764-877-960	Sequence 960, App
c 416	16	0.9	270	10	US-09-895-828-209	Sequence 209, App	c 489	16	0.9	375	10	US-09-867-701-8960	Sequence 8960, Ap
c 417	16	0.9	270	10	US-09-867-701-7636	Sequence 7636, Ap	c 490	16	0.9	375	10	US-09-764-877-891	Sequence 891, App
c 418	16	0.9	271	10	US-09-923-876-4367	Sequence 4367, Ap	c 491	16	0.9	378	10	US-09-864-761-3801	Sequence 3801, Ap
c 419	16	0.9	272	10	US-09-925-302-139	Sequence 139, App	c 492	16	0.9	384	10	US-09-880-107-346	Sequence 346, App
c 420	16	0.9	275	10	US-09-925-299-609	Sequence 609, App	c 493	16	0.9	387	10	US-09-919-580-793	Sequence 793, App
c 421	16	0.9	277	10	US-09-895-828-275	Sequence 275, App	c 494	16	0.9	388	10	US-09-867-701-5772	Sequence 5772, Ap
c 422	16	0.9	278	10	US-09-777-564-1623	Sequence 1623, Ap	c 495	16	0.9	388	10	US-09-880-107-1378	Sequence 1378, Ap
c 423	16	0.9	278	10	US-09-895-828-263	Sequence 263, Ap	c 496	16	0.9	392	10	US-09-960-352-14021	Sequence 14021, A
c 424	16	0.9	279	10	US-09-735-705-43	Sequence 43, Appl	c 497	16	0.9	392	10	US-09-960-352-5105	Sequence 5105, Ap
c 425	16	0.9	279	10	US-09-895-828-387	Sequence 387, App	c 498	16	0.9	393	10	US-09-960-352-5187	Sequence 5187, Ap
c 426	16	0.9	279	10	US-09-895-828-387	Sequence 387, App	c 499	16	0.9	395	9	US-09-854-133-144	Sequence 164, App
c 427	16	0.9	279	10	US-09-897-778-43	Sequence 43, Appl	c 500	16	0.9	395	10	US-09-738-973-164	Sequence 164, App
c 428	16	0.9	280	10	US-09-895-828-360	Sequence 360, App	c 501	16	0.9	395	12	US-10-114-482-21	Sequence 21, Appl
c 429	16	0.9	282	10	US-09-895-828-166	Sequence 166, App	c 502	16	0.9	396	9	US-09-970-966-51	Sequence 51, Appl
c 430	16	0.9	282	10	US-09-895-828-262	Sequence 262, App	c 503	16	0.9	396	9	US-09-970-966-59	Sequence 59, Appl
c 431	16	0.9	283	10	US-09-895-828-395	Sequence 395, App	c 504	16	0.9	396	9	US-09-970-966-131	Sequence 131, App
c 432	16	0.9	285	10	US-09-895-828-359	Sequence 359, App	c 505	16	0.9	396	10	US-09-825-294-51	Sequence 51, Appl
c 433	16	0.9	285	10	US-09-867-701-9394	Sequence 9394, Ap	c 506	16	0.9	396	10	US-09-825-294-59	Sequence 59, Appl
c 434	16	0.9	287	9	US-09-933-797-348	Sequence 348, App	c 507	16	0.9	396	10	US-09-825-294-131	Sequence 131, App
c 435	16	0.9	287	10	US-09-783-590-11346	Sequence 11346, A	c 508	16	0.9	396	10	US-09-864-761-26657	Sequence 26657, A
c 436	16	0.9	290	9	US-09-728-444-1155	Sequence 1155, Ap	c 509	16	0.9	396	10	US-09-880-107-2059	Sequence 2059, Ap
c 437	16	0.9	299	10	US-09-919-580-544	Sequence 544, App	c 510	16	0.9	397	10	US-09-960-253-112	Sequence 112, App
c 438	16	0.9	300	9	US-10-025-380-882	Sequence 882, App	c 511	16	0.9	397	10	US-09-983-965-5216	Sequence 5216, Ap
c 439	16	0.9	300	10	US-09-922-217-882	Sequence 882, App	c 512	16	0.9	404	10	US-09-878-574-5158	Sequence 5158, Ap
c 440	16	0.9	303	10	US-09-833-263-882	Sequence 882, App	c 513	16	0.9	406	10	US-09-864-761-1075	Sequence 1075, Ap
c 441	16	0.9	303	10	US-09-998-598-77	Sequence 77, Appl	c 514	16	0.9	406	10	US-09-960-352-1542	Sequence 1542, Ap
c 442	16	0.9	305	10	US-09-969-708-361	Sequence 361, App	c 515	16	0.9	407	10	US-09-960-352-4585	Sequence 4585, Ap
c 443	16	0.9	305	10	US-09-954-456-2104	Sequence 2104, Ap	c 516	16	0.9	408	10	US-09-960-352-12948	Sequence 12948, A
c 444	16	0.9	311	10	US-09-925-299-734	Sequence 734, App	c 517	16	0.9	411	10	US-09-960-352-14278	Sequence 14278, A
c 445	16	0.9	314	10	US-09-880-107-1027	Sequence 1027, Ap	c 518	16	0.9	411	10	US-09-960-352-3551	Sequence 3551, Ap
c 446	16	0.9	315	10	US-09-867-701-7731	Sequence 7731, Ap	c 519	16	0.9	415	10	US-09-867-701-4385	Sequence 4385, Ap
c 447	16	0.9	317	10	US-09-960-352-14196	Sequence 14196, A	c 520	16	0.9	415	10	US-09-919-580-50	Sequence 50, Appl
c 448	16	0.9	318	10	US-09-867-701-7761	Sequence 7761, Ap	c 521	16	0.9	418	12	US-09-920-300A-527	Sequence 527, App
c 449	16	0.9	319	9	US-09-920-455-198	Sequence 198, App	c 522	16	0.9	418	12	US-10-033-528-527	Sequence 527, App
c 450	16	0.9	320	10	US-09-820-089A-27	Sequence 27, Appl	c 523	16	0.9	420	10	US-09-964-761-3950	Sequence 3950, Ap
c 451	16	0.9	320	10	US-09-969-708-434	Sequence 434, App	c 524	16	0.9	420	10	US-09-735-705-65	Sequence 65, Appl
c 452	16	0.9	321	9	US-09-954-456-1091	Sequence 1091, Ap	c 525	16	0.9	420	10	US-09-850-716A-65	Sequence 65, Appl
c 453	16	0.9	322	9	US-09-989-920-140	Sequence 140, App	c 526	16	0.9	420	10	US-09-924-035A-514	Sequence 514, App
c 454	16	0.9	322	9	US-09-954-531-595	Sequence 595, App	c 527	16	0.9	425	10	US-09-897-778-65	Sequence 65, Appl
c 455	16	0.9	322	10	US-09-962-436-236	Sequence 296, App	c 528	16	0.9	425	10	US-09-764-846-49	Sequence 49, Appl
c 456	16	0.9	324	10	US-09-960-352-9118	Sequence 9118, Ap	c 529	16	0.9	425	10	US-09-969-347-302	Sequence 302, App
c 457	16	0.9	326	10	US-09-813-358-129	Sequence 129, App	c 530	16	0.9	425	10	US-09-917-800A-406	Sequence 406, App

531	16	0.9	426	10	US-09-813-358-190	Sequence 190, App	604	16	0.9	491	10	US-09-738-973-90	Sequence 90, Appl
532	16	0.9	426	10	US-09-960-352-556	Sequence 556, App	c 605	16	0.9	491	10	US-09-917-800A-452	Sequence 452, App
533	16	0.9	428	10	US-09-895-828-45	Sequence 556, App	c 606	16	0.9	494	9	US-09-954-531-105	Sequence 105, App
534	16	0.9	431	10	US-09-783-590-5592	Sequence 5592, App	c 607	16	0.9	494	10	US-09-867-701-3275	Sequence 3275, App
535	16	0.9	432	10	US-09-954-456-2110	Sequence 2110, App	c 608	16	0.9	495	10	US-09-924-038A-678	Sequence 678, App
536	16	0.9	432	10	US-09-917-800A-463	Sequence 463, App	c 609	16	0.9	498	10	US-09-920-300A-1622	Sequence 1622, App
537	16	0.9	433	10	US-09-735-705-58	Sequence 58, Appl	610	16	0.9	498	12	US-10-033-528-1622	Sequence 1622, App
538	16	0.9	433	10	US-09-850-716A-58	Sequence 58, Appl	611	16	0.9	499	9	US-09-232-880-73	Sequence 73, Appl
539	16	0.9	433	10	US-09-897-778-58	Sequence 58, Appl	612	16	0.9	499	9	US-10-012-896-73	Sequence 73, Appl
540	16	0.9	434	10	US-09-864-761-3274	Sequence 3274, App	613	16	0.9	499	9	US-09-895-793-73	Sequence 73, Appl
541	16	0.9	434	10	US-09-919-580-133	Sequence 133, App	614	16	0.9	499	9	US-09-895-814-73	Sequence 73, Appl
542	16	0.9	434	10	US-09-919-580-133	Sequence 133, App	615	16	0.9	499	10	US-09-759-143-73	Sequence 73, Appl
543	16	0.9	436	9	US-09-960-352-12424	Sequence 12424, A	616	16	0.9	499	10	US-09-780-669-73	Sequence 73, Appl
544	16	0.9	436	10	US-09-623-19	Sequence 19, Appl	617	16	0.9	499	10	US-09-030-606-73	Sequence 73, Appl
545	16	0.9	436	10	US-09-867-701-1890	Sequence 1890, App	618	16	0.9	499	10	US-09-822-827-73	Sequence 73, Appl
546	16	0.9	436	10	US-09-924-038A-193	Sequence 193, App	619	16	0.9	499	10	US-09-115-453-73	Sequence 73, Appl
547	16	0.9	437	10	US-09-770-444-992	Sequence 992, App	620	16	0.9	499	10	US-09-864-761-8727	Sequence 8727, App
548	16	0.9	439	10	US-09-917-800A-626	Sequence 626, App	621	16	0.9	509	10	US-09-864-761-14830	Sequence 14830, A
549	16	0.9	439	10	US-09-917-800A-829	Sequence 829, App	622	16	0.9	509	10	US-09-864-761-13011	Sequence 13011, A
550	16	0.9	440	10	US-09-770-444-929	Sequence 929, App	623	16	0.9	517	10	US-09-867-701-872	Sequence 872, App
551	16	0.9	444	10	US-09-983-965-2350	Sequence 2350, App	624	16	0.9	520	10	US-09-864-761-8365	Sequence 8365, App
552	16	0.9	445	10	US-09-919-172-78	Sequence 78, Appl	625	16	0.9	520	10	US-09-867-701-1380	Sequence 1380, App
553	16	0.9	445	10	US-09-960-352-12164	Sequence 12164, A	626	16	0.9	520	10	US-09-933-797-764	Sequence 764, App
554	16	0.9	445	10	US-09-924-038A-744	Sequence 744, App	627	16	0.9	524	9	US-09-934-531-476	Sequence 476, App
555	16	0.9	447	10	US-09-867-701-4517	Sequence 4517, App	628	16	0.9	526	9	US-09-919-580-791	Sequence 791, App
556	16	0.9	448	10	US-09-728-445-285	Sequence 285, App	629	16	0.9	531	10	US-09-764-898-46	Sequence 46, Appl
557	16	0.9	449	10	US-09-864-761-1920	Sequence 1920, App	630	16	0.9	533	10	US-09-876-889-67	Sequence 67, Appl
558	16	0.9	450	10	US-09-983-965-2936	Sequence 2936, App	631	16	0.9	536	9	US-09-876-889-67	Sequence 105, Appl
559	16	0.9	451	10	US-09-884-441-51	Sequence 51, Appl	632	16	0.9	538	9	US-09-232-880-105	Sequence 105, App
560	16	0.9	453	10	US-09-969-347-78	Sequence 78, Appl	633	16	0.9	538	9	US-10-012-896-105	Sequence 105, App
561	16	0.9	454	9	US-09-764-868-516	Sequence 516, App	634	16	0.9	538	9	US-09-895-793-105	Sequence 105, App
562	16	0.9	454	10	US-09-770-444-589	Sequence 589, App	635	16	0.9	538	9	US-09-895-814-105	Sequence 105, App
563	16	0.9	455	10	US-09-864-761-10104	Sequence 10104, A	636	16	0.9	538	10	US-09-759-143-105	Sequence 105, App
564	16	0.9	455	10	US-09-731-872-206	Sequence 206, App	637	16	0.9	538	10	US-09-780-669-105	Sequence 105, App
565	16	0.9	455	10	US-09-880-107-2531	Sequence 2531, App	638	16	0.9	538	10	US-09-030-606-105	Sequence 105, App
566	16	0.9	456	10	US-09-867-701-10799	Sequence 10799, A	639	16	0.9	538	10	US-09-822-827-105	Sequence 105, App
567	16	0.9	456	10	US-09-998-598-823	Sequence 823, App	640	16	0.9	538	10	US-09-115-453-105	Sequence 105, App
568	16	0.9	457	10	US-09-770-444-508	Sequence 508, App	641	16	0.9	541	9	US-09-852-797-37	Sequence 37, Appl
569	16	0.9	457	10	US-09-783-590-2004	Sequence 2004, App	642	16	0.9	541	10	US-09-853-161-37	Sequence 37, Appl
570	16	0.9	457	10	US-09-917-800A-322	Sequence 322, App	643	16	0.9	541	10	US-09-852-659A-37	Sequence 37, Appl
571	16	0.9	457	10	US-09-764-877-3908	Sequence 3908, App	644	16	0.9	550	10	US-09-919-580-83	Sequence 83, Appl
572	16	0.9	458	10	US-09-954-456-107	Sequence 107, App	645	16	0.9	555	10	US-09-880-192-19	Sequence 19, Appl
573	16	0.9	458	10	US-09-954-456-334	Sequence 334, App	646	16	0.9	556	10	US-09-917-800A-24	Sequence 24, Appl
574	16	0.9	458	10	US-09-764-877-825	Sequence 825, App	647	16	0.9	557	10	US-09-917-800A-45	Sequence 45, Appl
575	16	0.9	459	10	US-09-864-761-6170	Sequence 6170, App	648	16	0.9	557	10	US-09-917-800A-77	Sequence 77, Appl
576	16	0.9	459	10	US-09-864-761-17532	Sequence 17532, A	649	16	0.9	562	10	US-09-764-877-3907	Sequence 3907, App
577	16	0.9	461	9	US-10-011-445-15	Sequence 16, Appl	650	16	0.9	565	10	US-09-895-686-68	Sequence 68, Appl
578	16	0.9	463	10	US-09-770-444-377	Sequence 377, App	651	16	0.9	565	10	US-09-895-686-68	Sequence 9029, App
579	16	0.9	464	10	US-09-867-701-3272	Sequence 3272, App	652	16	0.9	568	10	US-09-864-761-9029	Sequence 7140, App
580	16	0.9	464	10	US-09-908-805B-37	Sequence 37, Appl	653	16	0.9	570	10	US-09-864-761-7140	Sequence 7140, App
581	16	0.9	465	10	US-09-867-701-5154	Sequence 5154, App	654	16	0.9	570	10	US-09-864-761-12053	Sequence 12053, A
582	16	0.9	467	10	US-09-834-975-470	Sequence 470, App	655	16	0.9	570	10	US-09-864-761-13571	Sequence 13571, A
583	16	0.9	468	10	US-09-880-107-3655	Sequence 3655, App	656	16	0.9	574	9	US-10-012-896-356	Sequence 356, App
584	16	0.9	472	10	US-09-764-869-3224	Sequence 3224, App	657	16	0.9	574	9	US-09-895-793-356	Sequence 356, App
585	16	0.9	472	10	US-09-954-456-1486	Sequence 1486, App	658	16	0.9	574	10	US-09-759-143-356	Sequence 356, App
586	16	0.9	474	10	US-09-919-580-698	Sequence 698, App	659	16	0.9	574	10	US-09-780-669-356	Sequence 356, App
587	16	0.9	475	10	US-09-864-761-14064	Sequence 14064, A	660	16	0.9	574	10	US-09-822-827-356	Sequence 356, App
588	16	0.9	477	10	US-09-917-800A-420	Sequence 420, App	661	16	0.9	579	10	US-09-864-761-9907	Sequence 9907, App
589	16	0.9	477	10	US-09-917-800A-539	Sequence 539, App	662	16	0.9	593	10	US-09-864-761-6991	Sequence 6991, App
590	16	0.9	478	10	US-09-919-580-141	Sequence 141, App	663	16	0.9	595	10	US-09-764-877-3906	Sequence 3906, App
591	16	0.9	478	10	US-09-998-598-1197	Sequence 1197, App	664	16	0.9	599	10	US-09-864-761-6635	Sequence 6635, App
592	16	0.9	479	10	US-09-917-800A-984	Sequence 984, App	665	16	0.9	599	10	US-09-864-761-13613	Sequence 13613, A
593	16	0.9	479	10	US-09-880-107-2877	Sequence 2877, App	666	16	0.9	608	10	US-09-864-761-846-88	Sequence 88, Appl
594	16	0.9	481	9	US-09-854-133-89	Sequence 89, Appl	667	16	0.9	617	10	US-09-770-449-621	Sequence 7, Appl
595	16	0.9	481	10	US-09-738-973-89	Sequence 89, Appl	668	16	0.9	634	10	US-09-907-479-7	Sequence 7, Appl
596	16	0.9	483	10	US-09-864-761-14487	Sequence 14487, A	669	16	0.9	636	10	US-09-764-877-844	Sequence 844, App
597	16	0.9	484	10	US-09-864-761-11442	Sequence 11442, A	670	16	0.9	639	10	US-09-764-853-56	Sequence 56, Appl
598	16	0.9	484	10	US-09-764-846-66	Sequence 66, Appl	671	16	0.9	647	10	US-09-216-393-338	Sequence 338, App
599	16	0.9	485	10	US-09-864-761-10491	Sequence 10491, A	672	16	0.9	647	10	US-09-216-393-339	Sequence 339, App
600	16	0.9	489	10	US-09-764-869-526	Sequence 526, App	673	16	0.9	648	10	US-09-974-300-5398	Sequence 5398, App
601	16	0.9	489	10	US-09-764-869-526	Sequence 526, App	674	16	0.9	650	10	US-09-974-300-5398	Sequence 5398, App
602	16	0.9	489	10	US-09-728-445-321	Sequence 321, App	675	16	0.9	658	10	US-09-729-674-103	Sequence 103, App
603	16	0.9	489	10	US-09-867-701-2424	Sequence 2424, App	676	16	0.9	661	10	US-09-974-300-5272	Sequence 5272, App
			491	9	US-09-854-133-90	Sequence 90, Appl	676	16	0.9	661	10	US-09-879-536-69	Sequence 69, Appl

c 677	16	0.9	666	10	US-09-764-847-1724	Sequence 1724, Ap	750	16	0.9	1085	10	US-09-731-872-169	Sequence 169, App
c 678	16	0.9	673	10	US-09-780-717-49	Sequence 49, Appl	751	16	0.9	1102	10	US-09-731-872-28	Sequence 28, Appl
c 679	16	0.9	679	10	US-09-910-943-307	Sequence 307, App	752	16	0.9	1106	9	US-09-764-868-300	Sequence 300, App
c 680	16	0.9	682	10	US-09-925-300-490	Sequence 490, App	753	16	0.9	1107	9	US-09-966-546-1	Sequence 1, Appl
c 681	16	0.9	687	9	US-09-978-235A-469	Sequence 469, App	c 754	16	0.9	1107	9	US-09-966-545-1	Sequence 1, Appl
c 682	16	0.9	687	9	US-09-978-697-469	Sequence 469, App	755	16	0.9	1117	9	US-09-981-876-54	Sequence 54, Appl
c 683	16	0.9	687	9	US-09-874-503-1	Sequence 1, Appl	756	16	0.9	1137	10	US-09-954-456-1582	Sequence 1582, Ap
c 684	16	0.9	687	9	US-09-978-192A-469	Sequence 469, App	757	16	0.9	1150	10	US-09-764-853-122	Sequence 122, App
c 685	16	0.9	687	9	US-10-000-157-1	Sequence 1, Appl	758	16	0.9	1150	10	US-09-764-898-36	Sequence 36, Appl
c 686	16	0.9	687	9	US-09-854-280-2	Sequence 2, Appl	759	16	0.9	1154	12	US-10-001-843-20	Sequence 20, Appl
c 687	16	0.9	687	10	US-09-854-280-2	Sequence 2, Appl	760	16	0.9	1185	10	US-09-886-055-342	Sequence 342, App
c 688	16	0.9	687	10	US-09-854-280-2	Sequence 2, Appl	761	16	0.9	1209	10	US-09-823-356-28	Sequence 28, Appl
c 689	16	0.9	688	9	US-09-736-457-644	Sequence 644, App	762	16	0.9	1211	9	US-09-981-876-123	Sequence 123, App
c 690	16	0.9	688	9	US-09-902-941-644	Sequence 644, App	763	16	0.9	1212	9	US-10-114-893-157	Sequence 157, App
c 691	16	0.9	691	10	US-09-864-761-19357	Sequence 19357, A	c 764	16	0.9	1227	10	US-09-815-242-6039	Sequence 6039, Ap
c 692	16	0.9	700	9	US-09-852-797-26	Sequence 26, Appl	765	16	0.9	1232	10	US-09-728-952-60	Sequence 60, Appl
c 693	16	0.9	700	10	US-09-853-161-26	Sequence 26, Appl	766	16	0.9	1240	10	US-09-925-297-259	Sequence 259, App
c 694	16	0.9	700	10	US-09-852-659A-26	Sequence 26, Appl	767	16	0.9	1244	10	US-09-764-864-101	Sequence 101, App
c 695	16	0.9	713	10	US-09-764-846-136	Sequence 136, App	768	16	0.9	1250	10	US-09-925-301-538	Sequence 538, App
c 696	16	0.9	713	10	US-09-917-800A-1717	Sequence 1717, App	769	16	0.9	1250	10	US-09-764-864-551	Sequence 551, App
c 697	16	0.9	732	9	US-09-854-133-429	Sequence 429, App	770	16	0.9	1253	10	US-09-925-301-571	Sequence 571, App
c 698	16	0.9	732	10	US-09-738-973-429	Sequence 429, App	771	16	0.9	1256	10	US-09-263-959-287	Sequence 287, App
c 699	16	0.9	736	10	US-09-925-301-548	Sequence 429, App	772	16	0.9	1265	9	US-10-102-949-6	Sequence 6, Appl
c 700	16	0.9	743	10	US-09-770-149-47	Sequence 47, Appl	773	16	0.9	1296	10	US-09-925-302-311	Sequence 311, App
c 701	16	0.9	752	10	US-09-770-445-998	Sequence 998, App	c 774	16	0.9	1325	9	US-09-989-920-85	Sequence 85, Appl
c 702	16	0.9	756	10	US-09-925-301-196	Sequence 998, App	775	16	0.9	1335	9	US-09-938-842A-2935	Sequence 2935, Ap
c 703	16	0.9	771	10	US-09-910-943-579	Sequence 579, App	776	16	0.9	1338	9	US-09-903-170C-2	Sequence 2, Appl
c 704	16	0.9	776	9	US-09-854-133-63	Sequence 63, Appl	777	16	0.9	1338	10	US-09-903-180B-2	Sequence 2, Appl
c 705	16	0.9	776	10	US-09-738-973-63	Sequence 63, Appl	778	16	0.9	1338	10	US-09-903-171A-2	Sequence 2, Appl
c 706	16	0.9	795	9	US-09-764-887-73	Sequence 73, Appl	779	16	0.9	1338	10	US-09-903-188A-2	Sequence 2, Appl
c 707	16	0.9	805	10	US-09-981-876-48	Sequence 48, Appl	780	16	0.9	1338	10	US-09-903-323A-2	Sequence 2, Appl
c 708	16	0.9	805	10	US-09-974-300-1407	Sequence 1407, Ap	781	16	0.9	1338	10	US-09-903-325A-2	Sequence 2, Appl
c 709	16	0.9	808	10	US-09-729-674-83	Sequence 83, Appl	782	16	0.9	1355	10	US-09-925-301-19	Sequence 19, Appl
c 710	16	0.9	812	10	US-09-867-550-1651	Sequence 1651, Ap	783	16	0.9	1356	10	US-09-925-301-19	Sequence 19, Appl
c 711	16	0.9	813	10	US-09-815-242-7295	Sequence 7295, Ap	784	16	0.9	1360	10	US-09-925-301-19	Sequence 19, Appl
c 712	16	0.9	813	10	US-09-969-708-502	Sequence 502, App	785	16	0.9	1390	10	US-09-915-582-18	Sequence 18, Appl
c 713	16	0.9	815	9	US-10-202-193-229	Sequence 229, App	786	16	0.9	1395	10	US-09-947-027-8	Sequence 8, Appl
c 714	16	0.9	815	12	US-10-044-090-201	Sequence 201, App	787	16	0.9	1395	12	US-10-091-009-8	Sequence 8, Appl
c 715	16	0.9	830	10	US-09-854-280-5	Sequence 5, Appl	788	16	0.9	1400	10	US-09-925-301-286	Sequence 286, App
c 716	16	0.9	830	10	US-09-854-208-5	Sequence 5, Appl	789	16	0.9	1400	10	US-09-263-959-296	Sequence 296, App
c 717	16	0.9	838	10	US-09-925-301-210	Sequence 210, App	790	16	0.9	1428	9	US-09-764-868-360	Sequence 360, App
c 718	16	0.9	843	10	US-09-764-860-1013	Sequence 1013, Ap	791	16	0.9	1438	9	US-09-989-920-141	Sequence 141, App
c 719	16	0.9	843	10	US-09-917-800A-1013	Sequence 1013, Ap	792	16	0.9	1438	9	US-09-925-302-201	Sequence 201, App
c 720	16	0.9	852	9	US-09-938-842A-1070	Sequence 1070, Ap	793	16	0.9	1441	9	US-09-989-919-60	Sequence 60, Appl
c 721	16	0.9	864	10	US-09-768-877-17	Sequence 17, Appl	794	16	0.9	1441	9	US-09-925-301-333	Sequence 333, App
c 722	16	0.9	872	12	US-10-044-090-518	Sequence 518, App	795	16	0.9	1447	10	US-09-764-864-177	Sequence 177, App
c 723	16	0.9	874	9	US-10-076-785-51	Sequence 51, Appl	796	16	0.9	1461	10	US-09-990-672B-4	Sequence 4, Appl
c 724	16	0.9	877	10	US-09-833-381-824	Sequence 824, App	797	16	0.9	1462	10	US-09-764-869-2325	Sequence 2325, Ap
c 725	16	0.9	901	10	US-09-974-300-2048	Sequence 2048, Ap	798	16	0.9	1492	10	US-09-867-550-761	Sequence 761, App
c 726	16	0.9	910	9	US-09-984-245-77	Sequence 77, Appl	799	16	0.9	1508	12	US-10-062-254-291	Sequence 291, App
c 727	16	0.9	910	10	US-09-393-634-38	Sequence 38, Appl	800	16	0.9	1533	9	US-09-978-295A-302	Sequence 302, App
c 728	16	0.9	937	10	US-09-770-445-370	Sequence 370, App	801	16	0.9	1533	9	US-09-978-692A-302	Sequence 302, App
c 729	16	0.9	939	10	US-09-886-055-230	Sequence 230, App	802	16	0.9	1533	9	US-09-999-832A-302	Sequence 302, App
c 730	16	0.9	940	10	US-09-764-860-208	Sequence 208, App	803	16	0.9	1533	12	US-10-052-586-181	Sequence 181, App
c 731	16	0.9	956	10	US-09-925-301-282	Sequence 282, App	804	16	0.9	1554	10	US-09-794-960-3	Sequence 3, Appl
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ALIGNMENTS

RESULT 1

US-09-944-413-49
; Sequence 49, Application US/09944413
; Patent No. US20020156004A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
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; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/09/944,413
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
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; PRIOR FILING DATE: December 16, 1999
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; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-413-49

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Db	1	CTCTTTTGTCCACACAGCCAGCCAGCTGACTCTCTGGAGATTGTCAATAGCTCCATCCAGCCTG	60				
QY	61	AGAAACAAGCCGGTGGCTGAGCCAGGCTGTGTCACGGAGCACCCTGACGGGCCCAACAGAC	120				
Db	61	AGAAACAAGCCGGTGGCTGAGCCAGGCTGTGTCACGGAGCACCCTGACGGGCCCAACAGAC	120				
QY	121	CCATGCTGCATCCAGAGACCTCCCTCGCGGGGGGCACTCTCTGGCTGTGCTCTCTCTGCGCC	180				
Db	121	CCATGCTGCATCCAGAGACCTCCCTCGCGGGGGGCACTCTCTGGCTGTGCTCTCTCTGCGCC	180				
QY	181	TCCTTGGCACCACTGGGACAGAGTGTGGCCACCCAGCTGCAAGGAGCAGCTCCGATGG	240				
Db	181	TCCTTGGCACCACTGGGACAGAGTGTGGCCACCCAGCTGCAAGGAGCAGCTCCGATGG	240				
QY	241	CCGGAGCCCTGAACAGGAAGAGATTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	300				
Db	241	CCGGAGCCCTGAACAGGAAGAGATTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	300				
QY	301	GCTGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGAGCTGGAGTGACAGCCTGGGCC	360				
Db	301	GCTGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGAGCTGGAGTGACAGCCTGGGCC	360				
QY	361	AACTGGCTCAAGCCAGGCGACCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCGGCC	420				
Db	361	AACTGGCTCAAGCCAGGCGACCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCGGCC	420				
QY	421	TGTTGGCCACCTGCAAGTGGGCTGGAACATGACATGCTGCTCCCGCGGGCTTGGCGTCT	480				
Db	421	TGTTGGCCACCTGCAAGTGGGCTGGAACATGACATGCTGCTCCCGCGGGCTTGGCGTCT	480				
QY	481	TTGTTGAAGTGGTCAAGCTATGTTTTCAGAGGGGCGAGCGGTACAGCCAGCGCGCAGGAG	540				
Db	481	TTGTTGAAGTGGTCAAGCTATGTTTTCAGAGGGGCGAGCGGTACAGCCAGCGCGCAGGAG	540				
QY	541	AGTGTGCTCGAAGCCACCTGACCCACCTACAGCAGCTCTGTGTGGGCCACCTCAAGCC	600				
Db	541	AGTGTGCTCGAAGCCACCTGACCCACCTACAGCAGCTCTGTGTGGGCCACCTCAAGCC	600				
QY	601	AGCTGGGCTGTGGGGCGCACTGTGCTCTGAGGCGCCAGACAGCGATAGAGCCCTTTGTCT	660				
Db	601	AGCTGGGCTGTGGGGCGCACTGTGCTCTGAGGCGCCAGACAGCGATAGAGCCCTTTGTCT	660				
QY	661	GTGCTTACTCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTTATAAGA	720				
Db	661	GTGCTTACTCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTTATAAGA	720				
QY	721	AGGGTGGCTGGTGTGCTCTGACAGCCAGTGTCTCAGGCTGCTTCAAGCCTGGGACC	780				
Db	721	AGGGTGGCTGGTGTGCTCTGACAGCCAGTGTCTCAGGCTGCTTCAAGCCTGGGACC	780				
QY	781	ATGCAGGGGGCTCTGTGAGTCCCGAGGAATCTTGTCTGATGAGCTGCAGAACCATG	840				
Db	781	ATGCAGGGGGCTCTGTGAGTCCCGAGGAATCTTGTCTGATGAGCTGCAGAACCATG	840				
QY	841	GACGTCTCAACATCAGACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACT	900				
Db	841	GACGTCTCAACATCAGACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACT	900				
QY	901	GCCAAAGTGAAGCTGACCTGCAAGTGTGTCACGGCCGGTTCGGGAGGAGAGTGTCTGT	960				
Db	901	GCCAAAGTGAAGCTGACCTGCAAGTGTGTCACGGCCGGTTCGGGAGGAGAGTGTCTGT	960				
QY	961	GCCTGTGTGACATCGGCTACGGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCC	1020				
Db	961	GCCTGTGTGACATCGGCTACGGGGGAGCCAGTGTGCCACCAAGGTGCATTTTCCCTTCC	1020				
QY	1021	ACACCTGTGACCTGAGGATCGACGAGACTGCTTTCATGGTGTCTTTCAGAGGCGACACCT	1080				

Db	1021	ACACCTGTGACCTGAGGATCGACGGAGACTGCTTTCATGGTGTCTTTCAGAGGCGACACCT	1080	
QY	1081	ATTACAGAGCCAGGATGAAATGTCTAGAGAAAGCGGGGTGCTGCCCCAGATCAAGAGCC	1140	
Db	1081	ATTACAGAGCCAGGATGAAATGTCTAGAGAAAGCGGGGTGCTGCCCCAGATCAAGAGCC	1140	
QY	1141	AGAAAGTGCAGGACATCTCGCCTTCTATCTGGGGCGCTTGAGACACCAACAGAGTGA	1200	
Db	1141	AGAAAGTGCAGGACATCTCGCCTTCTATCTGGGGCGCTTGAGACACCAACAGAGTGA	1200	
QY	1201	CTGACAGTGACTTCGAGACCAAGAACTTCTTGGATCGGGCTCACTTACAGACCGCCAGGG	1260	
Db	1201	CTGACAGTGACTTCGAGACCAAGAACTTCTTGGATCGGGCTCACTTACAGACCGCCAGGG	1260	
QY	1261	ACTCCTTCCGCTGGGCCACAGGGGAGCACAGGCGCTTCACCAAGTTTTCCTTTGGGCAGC	1320	
Db	1261	ACTCCTTCCGCTGGGCCACAGGGGAGCACAGGCGCTTCACCAAGTTTTCCTTTGGGCAGC	1320	
QY	1321	CTGCAACACACGGGTGGTGTGGCTGAGTGTGCCATGGGGTTTGGCAACTCGCTGGAGC	1380	
Db	1321	CTGCAACACACGGGTGGTGTGGCTGAGTGTGCCATGGGGTTTGGCAACTCGCTGGAGC	1380	
QY	1381	TGCAGGCTTACAGTCCCTTCAACTGGAAGCAGCAGCGCTGCAAAACCCGAAACCGTTACA	1440	
Db	1381	TGCAGGCTTACAGTCCCTTCAACTGGAAGCAGCAGCGCTGCAAAACCCGAAACCGTTACA	1440	
QY	1441	TCTGCCAGTTTCCCACAGGAGCACATCTCCCCTGGGGCCCCAGSGTCTTGAGGCCCTGACCA	1500	
Db	1441	TCTGCCAGTTTCCCACAGGAGCACATCTCCCCTGGGGCCCCAGSGTCTTGAGGCCCTGACCA	1500	
QY	1501	CATGCTCCCTCGCCTGGGAGCACCGGCTCTGTCTTACTGTCTGCCACACCTGTCT	1560	
Db	1501	CATGCTCCCTCGCCTGGGAGCACCGGCTCTGTCTTACTGTCTGCCACACCTGTCT	1560	
QY	1561	GGAAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAGAGAGTCTCAGACCTTGCAC	1620	
Db	1561	GGAAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAGAGAGTCTCAGACCTTGCAC	1620	
QY	1621	AATGCCAAGATTGGSCAGAGAGGCGAGGAGGCGAGTGAGGGCCAGGAGTGAGTGTT	1680	
Db	1621	AATGCCAAGATTGGSCAGAGAGGCGAGGAGGCGAGTGAGGGCCAGGAGTGAGTGTT	1680	
QY	1681	AGAAGAAGCTGGGGCCCTTCGCCTCTTTTGATTGGGAAGATGGGCTTCAATTAGATGCG	1740	
Db	1681	AGAAGAAGCTGGGGCCCTTCGCCTCTTTTGATTGGGAAGATGGGCTTCAATTAGATGCG	1740	
QY	1741	GAAAGAGAGGACACCGCAGTGGTCCAAAAGAGCTGCTCTCTTCCACCTTGGCCCGACGCC	1800	
Db	1741	GAAAGAGAGGACACCGCAGTGGTCCAAAAGAGCTGCTCTCTTCCACCTTGGCCCGACGCC	1800	
QY	1801	TGTGGGGCAGCGAGCTTCCCTGTGSCATGAACCCACCGGGTATTAAATTATGAATCAG	1860	
Db	1801	TGTGGGGCAGCGAGCTTCCCTGTGSCATGAACCCACCGGGTATTAAATTATGAATCAG	1860	
QY	1861	CTGAAAAAATAAAAAA 1876		
Db	1861	CTGAAAAAATAAAAAA 1876		

RESULT 2

US-09-944-403-49

; Sequence 49, Application US/09944403

; Patent No.. US20020165143A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fliviaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

RESULT 2

us-09-944-403-49

; Sequence 49, Application US/09944403

; Patent No. US20020165143A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,403
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999

PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 49
LENGTH: 1876
TYPE: DNA
ORGANISM: Homo Sapien
US-09-944-403-49

Query Match 100.0%; Score 1876; DB 9; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTTTTGTCCACACAGCCAGCCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCCTG 60
Db 1 CTCCTTTTGTCCACACAGCCAGCCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCCTG 60
QY 61 AGAACAAAGCCGGTGGCTGAGCCAGGCTGTSCAGGAGACCTGACGGGCCCCAACAGAC 120
Db 61 AGAACAAAGCCGGTGGCTGAGCCAGGCTGTSCAGGAGACCTGACGGGCCCCAACAGAC 120
QY 121 CCATGCTGCATCCAGAGACCTCCCTTGGCCGGGGGCATCTCTTGGCTGTGCTCTTGGCC 180
Db 121 CCATGCTGCATCCAGAGACCTCCCTTGGCCGGGGGCATCTCTTGGCTGTGCTCTTGGCC 180
QY 181 TCCTTTGGCACCACTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGAGGCTCCGATGG 240
Db 181 TCCTTTGGCACCACTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGAGGCTCCGATGG 240
QY 241 CCGGAGCCCTGAACAGGAAGAGAGTTTCTTGTCTCTCTCTCCCTGCACACACCCCTCGCA 300
Db 241 CCGGAGCCCTGAACAGGAAGAGAGTTTCTTGTCTCTCTCTCCCTGCACACACCCCTCGCA 300
QY 301 GCTGGTTCAGCCCTCCCTTGGCTGACATGCGGAGGCTGGAGTGCAGAGTGCAGCCCTGGCC 360
Db 301 GCTGGTTCAGCCCTCCCTTGGCTGACATGCGGAGGCTGGAGTGCAGAGTGCAGCCCTGGCC 360
QY 361 AACTGGCTCAAGCCAGGCGACCCCTCTGTGAATCCCAACCCAGCCCTGGCATCCGGCC 420
Db 361 AACTGGCTCAAGCCAGGCGACCCCTCTGTGAATCCCAACCCAGCCCTGGCATCCGGCC 420
QY 421 TGTGGCGCACCCCTGCAAGTGGGCTTGAACATGCAGCTGCTGCCCGGGGCTTGGCTCT 480
Db 421 TGTGGCGCACCCCTGCAAGTGGGCTTGAACATGCAGCTGCTGCCCGGGGCTTGGCTCT 480
QY 481 TTGTTGAAGTGTGAGCCTATGTTTGCAGAGGGGCGACGGTACAGCCACGGGCGAGGAG 540
Db 481 TTGTTGAAGTGTGAGCCTATGTTTGCAGAGGGGCGACGGTACAGCCACGGGCGAGGAG 540
QY 541 AGTGTGCTCGCAACGCCACCTGCACCCACTACAGCAGCTCTGTGTGGGCGACCTCAAGCC 600
Db 541 AGTGTGCTCGCAACGCCACCTGCACCCACTACAGCAGCTCTGTGTGGGCGACCTCAAGCC 600
QY 601 AGCTGGGCTGTGGGCGGCACTGTGCTGTGCAGGCGACAGCAGCAGATAGAGCTTTGTCT 660
Db 601 AGCTGGGCTGTGGGCGGCACTGTGCTGTGCAGGCGACAGCAGCAGATAGAGCTTTGTCT 660
QY 661 GTGCTTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACATCATCCCTTATAAGA 720
Db 661 GTGCTTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACATCATCCCTTATAAGA 720

Db 661 GTGCTACTCCCGGAGGCAACTGGAGGTCAACGGAGAGACAATCATCCCTATAAGA 720
QY 721 AGGTGCCCTGGTTCGCTGTGCACAGCCAGTGTCTCAGGCTGCTTCAAGACCTGGGACC 780
Db 721 AGGTGCCCTGGTTCGCTGTGCACAGCCAGTGTCTCAGGCTGCTTCAAGACCTGGGACC 780
QY 781 ATGCAGGGGGCTGTGAGTCCCGAGGAATCTTCTGCATGAGTGCAGAACCATG 840
Db 781 ATGCAGGGGGCTGTGAGTCCCGAGGAATCTTCTGCATGAGTGCAGAACCATG 840
QY 841 GAGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCTCCCTGTACACGGGCAGATACT 900
Db 841 GAGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCTCCCTGTACACGGGCAGATACT 900
QY 901 GCCAAGTAGGTGAGCTGCTGAGTGTGTGACGGCCGGTTCGGGAGGAGAGTGTCTGT 960
Db 901 GCCAAGTAGGTGAGCTGCTGAGTGTGTGACGGCCGGTTCGGGAGGAGAGTGTCTGT 960
QY 961 GCCTGTGTGACATCGCTACGGGGGAGCCAGTGTGCCACCAAGTGTCCATTTCCCTTCC 1020
Db 961 GCCTGTGTGACATCGCTACGGGGGAGCCAGTGTGCCACCAAGTGTCCATTTCCCTTCC 1020
QY 1021 ACACCTGTGACCTGAGGATCGACGAGACTGCTTTCATGTGTCTTCAGAGCAGACACT 1080
Db 1021 ACACCTGTGACCTGAGGATCGACGAGACTGCTTTCATGTGTCTTCAGAGCAGACACT 1080
QY 1081 ATTACAGAGCAGATGAATGTGAGAGAAAGCGGGGTGCTGCCCCAGATCAAGAGCC 1140
Db 1081 ATTACAGAGCAGATGAATGTGAGAGAAAGCGGGGTGCTGCCCCAGATCAAGAGCC 1140
QY 1141 AGAAGTGCAGGACATCTCGCTTCATCTGCGCGCTGTGAGACCAACAGAGGTGA 1200
Db 1141 AGAAGTGCAGGACATCTCGCTTCATCTGCGCGCTGTGAGACCAACAGAGGTGA 1200
QY 1201 CTGACAGTGAATCCAGACCAAGAACTTCTGGATCGGGCTCACCTACAGACCGCAAGG 1260
Db 1201 CTGACAGTGAATCCAGACCAAGAACTTCTGGATCGGGCTCACCTACAGACCGCAAGG 1260
QY 1261 ACTCTTCCTGGGTCAGAGGAGCAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1320
Db 1261 ACTCTTCCTGGGTCAGAGGAGCAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1320
QY 1321 CTGACACCAAGGCTGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1380
Db 1321 CTGACACCAAGGCTGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1380
QY 1381 TGCAGGCTTACGCTTCACTGAGGAGCAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1440
Db 1381 TGCAGGCTTACGCTTCACTGAGGAGCAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1440
QY 1441 TCTGCCAGTTTCCAGGAGCAGATCTCCCGTGGGGCCAGGGTCTTCCAGGCTGACCA 1500
Db 1441 TCTGCCAGTTTCCAGGAGCAGATCTCCCGTGGGGCCAGGGTCTTCCAGGCTGACCA 1500
QY 1501 CATGCTCCCTCGCTGCTGCTGAGGAGCAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1560
Db 1501 CATGCTCCCTCGCTGCTGCTGAGGAGCAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1560
QY 1561 GGAACAGGGCCAGGTTAAGACCATGCTCATGCTCCAAAGAGGCTCAGACCTTGCAC 1620
Db 1561 GGAACAGGGCCAGGTTAAGACCATGCTCATGCTCCAAAGAGGCTCAGACCTTGCAC 1620
QY 1621 AATGCCAAGTTGGGTCAGAGAGGAGGAGGAGTGTGAGGAGGAGGAGTGTGAGTGTGAGTGTGAG 1680
Db 1621 AATGCCAAGTTGGGTCAGAGAGGAGGAGGAGTGTGAGGAGGAGGAGTGTGAGTGTGAGTGTGAG 1680
QY 1681 AGAAGAAGTGGGGCCCTTCCGCTTGTGATGGAAGATGGGCTTCAATTAGATGGC 1740
Db 1681 AGAAGAAGTGGGGCCCTTCCGCTTGTGATGGAAGATGGGCTTCAATTAGATGGC 1740
QY 1741 GAAGAGAGGAGCAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1800
Db 1741 GAAGAGAGGAGCAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1800

QY 1801 TGTGGGCGAGCGAGCTTCCCTGTGGCATGAACCCACCGGGTATTAAATATGAATCAG 1860
Db 1801 TGTGGGCGAGCGAGCTTCCCTGTGGCATGAACCCACCGGGTATTAAATATGAATCAG 1860
QY 1861 CTGAAAAAAGAAAAA 1876
Db 1861 CTGAAAAAAGAAAAA 1876

RESULT 3

US-09-944-896-49
; Sequence 49, Application US/09944896
; Patent No. US20020168715A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944, 896
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866, 028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/069, 334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069, 696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 894
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069, 873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068, 017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070, 440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074, 086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074, 092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075, 945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112, 850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113, 296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146, 222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330

;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 49
;; LENGTH: 1876
;; TYPE: DNA
;; ORGANISM: Homo Sapien
us-09-944-896-49

Query Match 100.08; Score 1876; DB 9; Length 1876;
Best Local Similarity 100.08; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCCTTTTCCACCGCCAGCCCTGACTCTCTGGAGATTGTAATAGCTCCATCCAGCCCTG 60
Db 1 CTCCTTTTCCACCGCCAGCCCTGACTCTCTGGAGATTGTAATAGCTCCATCCAGCCCTG 60
Qy 61 AGAACACAGCCGGTGGCTGAGCCAGGCTGTGCAGGAGCACCTGACGGGCCCAACAGAC 120
Db 61 AGAACACAGCCGGTGGCTGAGCCAGGCTGTGCAGGAGCACCTGACGGGCCCAACAGAC 120
Qy 121 CCATGCTGCATCCAGACACCTCCCTGCGCGGGGCACTCTCTGGCTGCTCTCCGCCCC 180
Db 121 CCATGCTGCATCCAGACACCTCCCTGCGCGGGGCACTCTCTGGCTGCTCTCCGCCCC 180
Qy 181 TCCTTGGACACCACTGGGCAGAGGTGTGCCCCACCCAGCTGCAGGAGCAGGCTCCGATGG 240
Db 181 TCCTTGGACACCACTGGGCAGAGGTGTGCCCCACCCAGCTGCAGGAGCAGGCTCCGATGG 240
Qy 241 CCGGAGCCCTCAACAGGAGAGAGTTCTTGTCTCTCTCCCTGCAACACCCCTGCGCA 300
Db 241 CCGGAGCCCTCAACAGGAGAGAGTTCTTGTCTCTCTCCCTGCAACACCCCTGCGCA 300
Qy 301 GCTGGGTCCAGCCCTGCGGCTGACATGCGGAGGCTGGAGTGGAGTGCACACCCCTGGGCC 360
Db 301 GCTGGGTCCAGCCCTGCGGCTGACATGCGGAGGCTGGAGTGGAGTGCACACCCCTGGGCC 360
Qy 361 AACTGGGTCAAGCCAGGCGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCC 420

Db 361 AACTGGGTCAAGCCAGGCGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCC 420
Qy 421 TGTGGCGCACCTGCAAGTGGCTGGAACATGCAAGTGTCTGCGCGGGGCTTGGCGCTCT 480
Db 421 TGTGGCGCACCTGCAAGTGGCTGGAACATGCAAGTGTCTGCGCGGGGCTTGGCGCTCT 480
Qy 481 TTGTTGAAGTGTGTCAGCCCTATGTTTGCAGAGGGGAGCGGTACAGCACCGCGCAGGAG 540
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Db 541 AGTGTGCTCGCAACGCCACCTGCACCCACCTACACGAGCTCCTGTGGCGCCACCTCAAGCC 600
Qy 601 AGCTGGGCTGTGGCGGCGCACCTGTCTGCTGTCAGAGGCGAGCATAGAGCCTTTTGTCT 660
Db 601 AGCTGGGCTGTGGCGGCGCACCTGTCTGCTGTCAGAGGCGAGCATAGAGCCTTTTGTCT 660
Qy 661 GTGCTACTCTCCCGGAGGCAACTGGAGGTCAACGGGAGAGCAATCATCCCTATAAGA 720
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Qy 721 AGGTGCTCTGTTGCTCTGTCAGAGCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACC 780
Db 721 AGGTGCTCTGTTGCTCTGTCAGAGCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACC 780
Qy 781 ATGACAGGGGCTCTGTAGGTCCCGAGGAATCTTGTGCGATGAGTGCAGAACCATG 840
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Qy 901 GCCAAGTGAAGTGCAGCCTGTCAGTGTGTGTCAGCGCGGTTCCGGGAGGAGGAGTCTCGT 960
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Db 1021 ACACCTGTGACCTGAGGATCGAGGAGTGTCTTATGTTGTCTTCAGAGGACAGACCT 1080
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Db 1801 TGTGGGAGGAGGAGCTTCCCTGCTGGCATGAACCCAGGGGTATTAAATATGAATCAG 1860
QY 1861 CTGAAAAAAGAAAAA 1876
Db 1861 CTGAAAAAAGAAAAA 1876

RESULT 5

US-09-866-028-49
; Sequence 49, Application us/09866028
; Patent No. US2002058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret

APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 49
LENGTH: 1876
TYPE: DNA
ORGANISM: Homo Sapien
US-09-866-028-49

Query Match 100.0%; Score 1876; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1861 CTGAAAAAATAAAAAA 1876

RESULT 6
US-09-944-449-49
; Sequence 49, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/09/944,449
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517

; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-09-944-449-49

Query Match 100.0%; Score 1876; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 49
;; LENGTH: 1876
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-09-944-457-49

Query Match 100.0%; Score 1876; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 49
;; LENGTH: 1876
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-09-945-587-49

Query Match 100.0%; Score 1876; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1861 CTGAAAAAANAANA 1876
DB 1861 CTGAAAAAANAANA 1876

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: Sequence 49, Application US/09945015
: Patent No. US20020132768A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kljavin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOT
: FILE REFERENCE: P2548Plc1
: CURRENT APPLICATION NUMBER: US/09/945,015
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/067,411
: PRIOR FILING DATE: December 3, 1997
: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,335
: PRIOR FILING DATE: December 11, 1997
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: PRIOR APPLICATION NUMBER: 60/069,425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069,696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,694
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: PRIOR APPLICATION NUMBER: 60/069,702
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: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252

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; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
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; PRIOR FILING DATE: December 22, 1998
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; PRIOR FILING DATE: July 28, 1999
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; PRIOR APPLICATION NUMBER: PCT/US98/25108
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; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
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; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020132981A, September 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020132981A, September 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
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; PRIOR FILING DATE: February 11, 2000
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; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
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; PRIOR APPLICATION NUMBER: PCT/US00/08439
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; PRIOR FILING DATE: May 22, 2000
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; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 49
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
us-09-944-396-49

Query Match 100.0%; Score 1876; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-097-49

Query Match 100.0%; Score 1876; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 841 GAGCTCTCAACATCAGACCTGCCACTGCGCACTGTCCCTTGGCTACACGGGCGAGATCT 900
QY 901 GCCAAGTGAAGTGCAGCTCAGTGTCTGCACGCGCGGTTCCGGGAGGAGTCTCTGCT 960
DB 901 GCCAAGTGAAGTGCAGCTCAGTGTCTGCACGCGCGGTTCCGGGAGGAGTCTCTGCT 960
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961 GGCTCTGTGACATCGGTACGGGGAGCCAGTGTGCCCAAGGTGCATTTTCCCTTCC 1020
961 GGCTCTGTGACATCGGTACGGGGAGCCAGTGTGCCCAAGGTGCATTTTCCCTTCC 1020
1021 ACACCTGTGACCTGAGGATCGACGGAGACTGCTTATGTTGTTCTTTCAGAGGAGACCT 1080
1021 ACACCTGTGACCTGAGGATCGACGGAGACTGCTTATGTTGTTCTTTCAGAGGAGACCT 1080
1081 ATTACAGAGCCAGGATGAATGTCAGAGAAAGGGGGTGTGGCCACATCAAGAGCC 1140
1081 ATTACAGAGCCAGGATGAATGTCAGAGAAAGGGGGTGTGGCCACATCAAGAGCC 1140
1141 AGAAGTGCAGGACATCTCGCTTCTATCTGGCGCCCTGGAGACCAACCAAGAGTGA 1200
1141 AGAAGTGCAGGACATCTCGCTTCTATCTGGCGCCCTGGAGACCAACCAAGAGTGA 1200
1201 CTGACAGTGAATCTCGAGACCAAGAACTTCTGGATCGGGTCTACCTACAGACGCCAAG 1260
1201 CTGACAGTGAATCTCGAGACCAAGAACTTCTGGATCGGGTCTACCTACAGACGCCAAG 1260
1261 ACTCTTCCGCTGGGCCACAGGGAGCACCAGGCTTCCAGTCTTTCCTTTGGGCGAGC 1320
1261 ACTCTTCCGCTGGGCCACAGGGAGCACCAGGCTTCCAGTCTTTCCTTTGGGCGAGC 1320
1321 CTGACAAACACCGGGTGTGGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
1321 CTGACAAACACCGGGTGTGGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
1381 TGCAGGCTTCACTGCTTCACTGGAAGACAGCAGGCTGCAAAACCCGAAACCGTTTACA 1440
1381 TGCAGGCTTCACTGCTTCACTGGAAGACAGCAGGCTGCAAAACCCGAAACCGTTTACA 1440
1441 TCTGTCAGTTTCCAGAGGACATCTCCGGTGGGGCCAGGCTTCCAGGCTGCTGAGCC 1500
1441 TCTGTCAGTTTCCAGAGGACATCTCCGGTGGGGCCAGGCTTCCAGGCTGCTGAGCC 1500
1501 CATGGCTCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
1501 CATGGCTCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
1561 GGAACAAGGGCCAGGTTAAGACCATGCTCATGTCCTCAAGAGGCTCTCAGACCTTGAC 1620
1561 GGAACAAGGGCCAGGTTAAGACCATGCTCATGTCCTCAAGAGGCTCTCAGACCTTGAC 1620
1621 AATGCCAGAAAGTTGGCAGAGAGCAGGAGCCAGTGTGGGCCAGGAGTGTGAGTGT 1680
1621 AATGCCAGAAAGTTGGCAGAGAGCAGGAGCCAGTGTGGGCCAGGAGTGTGAGTGT 1680
1681 AGAAGAAGTGGGGCCCTTCCGCTGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1740
1681 AGAAGAAGTGGGGCCCTTCCGCTGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1740
1741 GAAGAGAGGACACCCCGAGTGTGTCCTCAAAAGGCTGCTCTTCCACCTGGCCAGACCC 1800
1741 GAAGAGAGGACACCCCGAGTGTGTCCTCAAAAGGCTGCTCTTCCACCTGGCCAGACCC 1800
1801 TGTGGGGCAGCGAGCTTCCCTGTGCTGATGAACCCAGGGGTATTAAATTTATCAATCAG 1860
1801 TGTGGGGCAGCGAGCTTCCCTGTGCTGATGAACCCAGGGGTATTAAATTTATCAATCAG 1860
1861 CTGAAAAAATAAAAAA 1876
1861 CTGAAAAAATAAAAAA 1876

RESULT 12
US-09-944-432-49
; Sequence 49, Application US/09944432
; Patent No. US20020142419A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan

Db 601 AGCTGGGCTGTGGGGGACCTGTCTCTGACGGCCAGACAGGATAGAAGCTTTGTCT 660
QY 661 GTGGCTACTCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGA 720
Db 661 GTGGCTACTCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGA 720
QY 721 AGGTGGCTGTGTGCTCTGCACAGCAGTGTCTCAGGCTGTCTCAAGCTGGGACC 780
Db 721 AGGTGGCTGTGTGCTCTGCACAGCAGTGTCTCAGGCTGTCTCAAGCTGGGACC 780
QY 781 ATGACGGGGGCTCTGTGAGTGTCCAGAGATCCTTGTGCGATGAGCTGCCAGAACCATG 840
Db 781 ATGACGGGGGCTCTGTGAGTGTCCAGAGATCCTTGTGCGATGAGCTGCCAGAACCATG 840
QY 841 GACGCTCAACATAGCAGCTGCCACTGCCACTGTCCCTCCCTGCTACACGGGAGATACT 900
Db 841 GACGCTCAACATAGCAGCTGCCACTGCCACTGTCCCTCCCTGCTACACGGGAGATACT 900
QY 901 GCCAGTGTGAGTGTGCTGTGACAGTGTGTCACGGCGGTTCGGGAGGAGGTGCTCGT 960
Db 901 GCCAGTGTGAGTGTGCTGTGACAGTGTGTCACGGCGGTTCGGGAGGAGGTGCTCGT 960
QY 961 CGCTGTGTGACATCGGCTACGGGGAGCCAGTGTGCCACCAAGGTGCATTTCCCTTCC 1020
Db 961 CGCTGTGTGACATCGGCTACGGGGAGCCAGTGTGCCACCAAGGTGCATTTCCCTTCC 1020
QY 1021 ACACCTGTGAGCTGAGGATCGAGGAGTGTCTTATGTGTCTTCAGAGGAGACACT 1080
Db 1021 ACACCTGTGAGCTGAGGATCGAGGAGTGTCTTATGTGTCTTCAGAGGAGACACT 1080
QY 1081 ATTACAGAGCAGGATGAAATGTACAGAGAAAGGGGTGTGGCCACAGATCAAGAGCC 1140
Db 1081 ATTACAGAGCAGGATGAAATGTACAGAGAAAGGGGTGTGGCCACAGATCAAGAGCC 1140
QY 1141 AGAAAGTCAGGACATCTCGCTTCTATCTGCGGCGCTTACAGTGTTCGCTTTGGGAGGTA 1200
Db 1141 AGAAAGTCAGGACATCTCGCTTCTATCTGCGGCGCTTACAGTGTTCGCTTTGGGAGGTA 1200
QY 1201 CTGACAGTACTTCAGACACGAGACTTCTGGATCGGGTTCACCTACAGACCGCCAAAG 1260
Db 1201 CTGACAGTACTTCAGACACGAGACTTCTGGATCGGGTTCACCTACAGACCGCCAAAG 1260
QY 1261 ACTCTTCGGTGGGCGACAGGGGAGCAGGCGCTTACAGTGTTCGCTTTGGGAGG 1320
Db 1261 ACTCTTCGGTGGGCGACAGGGGAGCAGGCGCTTACAGTGTTCGCTTTGGGAGG 1320
QY 1321 CTGACACACGCGGTGTGTGGTGTGAGTGTGCCATGGGTTTGGCACTGCGTGGAGC 1380
Db 1321 CTGACACACGCGGTGTGTGGTGTGAGTGTGCCATGGGTTTGGCACTGCGTGGAGC 1380
QY 1381 TGCAGGCTTCAGCTGCCTCACTGAAGCAGCAGCGCTGCAAAACCGAAACCGTTACA 1440
Db 1381 TGCAGGCTTCAGCTGCCTCACTGAAGCAGCAGCGCTGCAAAACCGAAACCGTTACA 1440
QY 1441 TCTGCCAGTTTCCAGGAGCAGATCTCCCGTGGGGCCAGGCTCTCAGGCTGACCA 1500
Db 1441 TCTGCCAGTTTCCAGGAGCAGATCTCCCGTGGGGCCAGGCTCTCAGGCTGACCA 1500
QY 1501 CATGGCTCCCTGCTGCTGCTGGGAGCAGCGCTGTGCTTACCTGTCTGCTGCCACCTGTCT 1560
Db 1501 CATGGCTCCCTGCTGCTGCTGGGAGCAGCGCTGTGCTTACCTGTCTGCTGCCACCTGTCT 1560
QY 1561 GGAACAGGGCCAGTTAGACACATGCTCATGTCCAAAGAGGTCTCAGACCTTGCAC 1620
Db 1561 GGAACAGGGCCAGTTAGACACATGCTCATGTCCAAAGAGGTCTCAGACCTTGCAC 1620
QY 1621 AATGCCAGAAGTTGGGAGAGAGCAGGAGGCGGCGAGTGGGCGGAGGAGTGAAGTGT 1680
Db 1621 AATGCCAGAAGTTGGGAGAGAGCAGGAGGCGGCGAGTGGGCGGAGGAGTGAAGTGT 1680
QY 1681 AGAAGAGCTGGGGCCCTTGGCTGCTTTGTATGGAGAGATGGGCTTCAATTAGATGGC 1740
Db 1681 AGAAGAGCTGGGGCCCTTGGCTGCTTTGTATGGAGAGATGGGCTTCAATTAGATGGC 1740

Db 1681 AGAAGAGCTGGGGCCCTTGGCTGCTTTGTATGGAGAGATGGGCTTCAATTAGATGGC 1740
QY 1741 GAAGGAGAGACACCGCCAGTGGTCCAAAGAGGTGCTCTTCCACCTGGGCCCCAGACC 1800
Db 1741 GAAGGAGAGACACCGCCAGTGGTCCAAAGAGGTGCTCTTCCACCTGGGCCCCAGACC 1800
QY 1801 TGTGGGCGAGCGGAGCTTCCCTGTGGCATGAACCCAGCGGGGTATTAAATTATGAATCAG 1860
Db 1801 TGTGGGCGAGCGGAGCTTCCCTGTGGCATGAACCCAGCGGGGTATTAAATTATGAATCAG 1860
QY 1861 CTGAAAAAAGAAAAA 1876
Db 1861 CTGAAAAAAGAAAAA 1876

RESULT 13

US-09-943-762-49
; Sequence 49, Application US/09943762
; Patent No. US20020142958A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/943,762
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998

[illegible]

; ORGANISM: Homo sapien
US-09-944-654-49

Query Match				Score 1876; DB 10; Length 1876;			
Best Local Similarity				100.0%; Pred. No. 0;			
Matches 1876; Conservative				0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	CTCTTTTGTCCACAGCCAGCCTGACTCTCTGGAGATTGTGAATAGTTCATCCAGCCTG	60				
Db	1	CTCTTTTGTCCACAGCCAGCCTGACTCTCTGGAGATTGTGAATAGTTCATCCAGCCTG	60				
Qy	61	AGAAACAAGCCGGTGGCTGAGCCAGGCTGTGCAGCAGACCTGACGGGCCACACAGAC	120				
Db	61	AGAAACAAGCCGGTGGCTGAGCCAGGCTGTGCAGCAGACCTGACGGGCCACACAGAC	120				
Qy	121	CGATGTGATCCAGAGACCTCCCTGGCGGGGGCATCTCTGGCTGTGCTTCCCTGGGCC	180				
Db	121	CGATGTGATCCAGAGACCTCCCTGGCGGGGGCATCTCTGGCTGTGCTTCCCTGGGCC	180				
Qy	181	TGCTTGGACACCTGGCGAGAGGTGTGGCCACCCAGCTGCAGAGCAGGTCGATGG	240				
Db	181	TGCTTGGACACCTGGCGAGAGGTGTGGCCACCCAGCTGCAGAGCAGGTCGATGG	240				
Qy	241	CGGAGCCCTGAACAGAGAGAGTTTCTGTCTCTCTCCCTGCACAAACCGCTCGCGCA	300				
Db	241	CGGAGCCCTGAACAGAGAGAGTTTCTGTCTCTCTCCCTGCACAAACCGCTCGCGCA	300				
Qy	301	GCTGGTCCAGCCCTGCGGCTGACATGGCGAGGCTGGAGTGGAGTGCACAGCCTGGGCC	360				
Db	301	GCTGGTCCAGCCCTGCGGCTGACATGGCGAGGCTGGAGTGGAGTGCACAGCCTGGGCC	360				
Qy	361	AAGTGGTCAAGCCAGGCGAGCCTCTGTGGAAATCCCAACCCGAGCCTGGGCC	420				
Db	361	AAGTGGTCAAGCCAGGCGAGCCTCTGTGGAAATCCCAACCCGAGCCTGGGCC	420				
Qy	421	TGTGGCGCACCTGCAAGTGGGCTGGAAACATGACAGTGTCTCCCGGGCTTGGGCTCT	480				
Db	421	TGTGGCGCACCTGCAAGTGGGCTGGAAACATGACAGTGTCTCCCGGGCTTGGGCTCT	480				
Qy	481	TTGTTGAAGTGTGAGCCTATGTTTTCAGAGGGGCGAGCGGTACAGCCCGCGGAGGAG	540				
Db	481	TTGTTGAAGTGTGAGCCTATGTTTTCAGAGGGGCGAGCGGTACAGCCCGCGGAGGAG	540				
Qy	541	AGTGTCTCCCAAGCCACCTGCACCCACTACAGCAGCTGTGTGGCCACCTCAAGCC	600				
Db	541	AGTGTCTCCCAAGCCACCTGCACCCACTACAGCAGCTGTGTGGCCACCTCAAGCC	600				
Qy	601	AGTGGGCTGTGGCGCACCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCT	660				
Db	601	AGTGGGCTGTGGCGCACCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCT	660				
Qy	661	GTGCTACTCCCGGAGGCAACTGGGAGGTCAAGGGGAAGACAATCATCCCTATAAGA	720				
Db	661	GTGCTACTCCCGGAGGCAACTGGGAGGTCAAGGGGAAGACAATCATCCCTATAAGA	720				
Qy	721	AGGCTGCTGTGCTCTGTCACAGCCAGTGTCTCAGGCTGTCTCAAAGCCTGGGACC	780				
Db	721	AGGCTGCTGTGCTCTGTCACAGCCAGTGTCTCAGGCTGTCTCAAAGCCTGGGACC	780				
Qy	781	ATCAGGGGGCTGTGTGAGTTCGCCAGGAATCTTTGTGATGAGTGCACAGACCATG	840				
Db	781	ATCAGGGGGCTGTGTGAGTTCGCCAGGAATCTTTGTGATGAGTGCACAGACCATG	840				
Qy	841	GAGCTCTCAACATCAGACCTGCCACTGTGCCCTGTGCCCTGTGCCCTGTGCCCT	900				
Db	841	GAGCTCTCAACATCAGACCTGCCACTGTGCCCTGTGCCCTGTGCCCTGTGCCCT	900				
Qy	901	GCCAAGTGTGAGTGTGAGTGTGTCAGCGCCGCTTCCGGGAGGAGTGTGCTCT	960				
Db	901	GCCAAGTGTGAGTGTGAGTGTGTCAGCGCCGCTTCCGGGAGGAGTGTGCTCT	960				
Qy	961	GCCTGTGTGATCGGCTACGGGGAGCCCGAGTGTGCCACCAAGTGTGATTTCCCTTCC	1020				
Db	961	GCCTGTGTGATCGGCTACGGGGAGCCCGAGTGTGCCACCAAGTGTGATTTCCCTTCC	1020				

RESULT 15

US-09-943-851A-49
; Sequence 49, Application US/09943851A
; Patent No. US20020150976A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey

Qy	1021	ACACCTGTGACCTGAGGATCAGCGAGACTGCTTCATGGTGTCTTCAGAGGCGAGACCT	1080
Db	1021	ACACCTGTGACCTGAGGATCAGCGAGACTGCTTCATGGTGTCTTCAGAGGCGAGACCT	1080
Qy	1081	ATTACAGAGCCAGGATGAATGTCTAGAGAAAGCGGGTCTGGCCCGAGATCAAGAGCC	1140
Db	1081	ATTACAGAGCCAGGATGAATGTCTAGAGAAAGCGGGTCTGGCCCGAGATCAAGAGCC	1140
Qy	1141	AGAAAGTGCAGGACATCTCGCCTTCTATCTGGCGCCTGGAGACCAACAGAGGTGA	1200
Db	1141	AGAAAGTGCAGGACATCTCGCCTTCTATCTGGCGCCTGGAGACCAACAGAGGTGA	1200
Qy	1201	CTGACAGTGTCTGAGACAGGAACTTCTGGATCGGGTCTACCTACAGACCCGCAAGG	1260
Db	1201	CTGACAGTGTCTGAGACAGGAACTTCTGGATCGGGTCTACCTACAGACCCGCAAGG	1260
Qy	1261	ACTCTTCCGCTGGGCCACAGGGAGCAGCGCTTCCACAGTGTTCGCTTTGGGCGAGC	1320
Db	1261	ACTCTTCCGCTGGGCCACAGGGAGCAGCGCTTCCACAGTGTTCGCTTTGGGCGAGC	1320
Qy	1321	CTGACAAACCCAGGGCTGTGTGGCTGAGTGTGCCATGGGGTTTGGCAACTGCGTGGAGC	1380
Db	1321	CTGACAAACCCAGGGCTGTGTGGCTGAGTGTGCCATGGGGTTTGGCAACTGCGTGGAGC	1380
Qy	1381	TGCAAGGCTTCAGCTGCCCTTCAACTGGAAGCAGGCTGCAAAAACCCGAAACCGTTACA	1440
Db	1381	TGCAAGGCTTCAGCTGCCCTTCAACTGGAAGCAGGCTGCAAAAACCCGAAACCGTTACA	1440
Qy	1441	TCTCCAGTTTGGCCAGGAGCACATCTCCCGTGGGGCCAGGGTCTTGAGGCTGACCA	1500
Db	1441	TCTCCAGTTTGGCCAGGAGCACATCTCCCGTGGGGCCAGGGTCTTGAGGCTGACCA	1500
Qy	1501	CATGGCTCCCTCGCTGCCCTGGGAGCACCGGCTCTGTCTTACCTGTCTGCCACCTGTCT	1560
Db	1501	CATGGCTCCCTCGCTGCCCTGGGAGCACCGGCTCTGTCTTACCTGTCTGCCACCTGTCT	1560
Qy	1561	GGAACAGGGCCAGGTTAAGACCACATGCTCATGTCGAAGAGTCTCAGACCTTGAC	1620
Db	1561	GGAACAGGGCCAGGTTAAGACCACATGCTCATGTCGAAGAGTCTCAGACCTTGAC	1620
Qy	1621	AATCCCAAGCTTGGCCAGAGAGGAGGAGGCGGAGGCGGAGGAGGAGTGTGTT	1680
Db	1621	AATCCCAAGCTTGGCCAGAGAGGAGGAGGAGGCGGAGGAGGAGTGTGTT	1680
Qy	1681	AGAAAGCTGGGGCCTTTCGCTTGTGATTTGGGAAGATGGGCTTCAATTAGATGGC	1740
Db	1681	AGAAAGCTGGGGCCTTTCGCTTGTGATTTGGGAAGATGGGCTTCAATTAGATGGC	1740
Qy	1741	GAAGGAGGAGCACCGCCAGTGGTCCAAAAGGCTCTCTCTCCACCTGCCCCAGACCC	1800
Db	1741	GAAGGAGGAGCACCGCCAGTGGTCCAAAAGGCTCTCTCTCCACCTGCCCCAGACCC	1800
Qy	1801	TGTGGGGCAGCGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTTATGAATCAG	1860
Db	1801	TGTGGGGCAGCGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTTATGAATCAG	1860
Qy	1861	CTGAAAAAATAAAAA 1876	
Db	1861	CTGAAAAAATAAAAA 1876	

QY	402	CCGAGCCTGGCATCCGGCCCTGTGGCGCACCCCTGCAAGTGGCTGGAACATGCAGCTGCTG	461
Db	374	CGAGACCTGGCGTCCGGCCCTGTGGCGCACCCCTGCAAGTGGCTGGAACATGCAGCTGCTG	433
QY	462	CCCGGGGCTTGGCGTCCCTTTGTTGAAGTGGTCAGCCTATGCTTTGCAGAGGGGCAGCGG	521
Db	434	CCCGGGGCTTGGCGTCCCTTTGTTGAAGTGGTCAGCCTATGCTTTGCAGAGGGGCAGCGG	493
QY	522	TACAGCCACGGCAGGAGAGTGTGCTCGGAACGCCACCTGCACCCACTACACGAGCTC	581
Db	494	TACAGCCACGGCAGGAGAGTGTGCTCGGAACGCCACCTGCACCCACTACACGAGCTC	553
QY	582	GTGTGGCCACCTCAAGCCAGCTGGGTGTGGGCGGCACCTGTGCTCTGCAGGCCAGACA	641
Db	554	GTGTGGCCACCTCAAGCCAGCTGGGTGTGGGCGGCACCTGTGCTCTGCAGGCCAGACA	613
QY	642	GCATAGAAGCCTTGTGCTGTGCCCTACTCCCGCGAGGCAACTGGAGGTCAAACGGGAAG	701
Db	614	GCATAGAAGCCTTGTGCTGTGCCCTACTCCCGCGAGGCAACTGGAGGTCAAACGGGAAG	673
QY	702	ACAATCATCCCTATAAGAAGGGTGCCCTGTGCTCTGCACAGCCAGTGTCTCAGGC	761
Db	674	ACAATCATCCCTATAAGAAGGGTGCCCTGTGCTCTGCACAGCCAGTGTCTCAGGC	733
QY	762	TGCTTAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGTCCCCCAGGAATCCTTGTCCG	821
Db	734	TGCTTAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGTCCCCCAGGAATCCTTGTCCG	793
QY	822	ATGAGCTGCCAGAACCATGGACGCTCAACATCAGCACTGCCACTGCCACTGTCCCCCT	881
Db	794	ATGAGCTGCCAGAACCATGGACGCTCAACATCAGCACTGCCACTGCCACTGTCCCCCT	853
QY	882	GGCTACACGGGCAGATACTGCCAAGTAGGTGCGACGCTGCAGTGTGTGCACGGCGGTTTC	941
Db	854	GGCTACACGGGCAGATACTGCCAAGTAGGTGCGACGCTGCAGTGTGTGCACGGCGGTTTC	913
QY	942	CGGAGAGGAGTGTCTGTGCTGTGTGCATCTGGCTACGGGGGAGCCAGTGTGCCACC	1001
Db	914	CGGAGAGGAGTGTCTGTGCTGTGTGCATCTGGCTACGGGGGAGCCAGTGTGCCACC	973
QY	1002	AAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTTTCATGGTG	1061
Db	974	AAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTTTCATGGTG	1033
QY	1062	TCCTTCAGAGGCAGACACTATTACAGAGCCAGGATCAATGTTCAGAGAAAGCGGGGTG	1121
Db	1034	TCCTTCAGAGGCAGACACTATTACAGAGCCAGGATCAATGTTCAGAGAAAGCGGGGTG	1093
QY	1122	CTGGCCAGATCAAGAGCCAGAAAGTGCAGGACATCTCGCCTTCTATCTGGGCCCCCTG	1181
Db	1094	CTGGCCAGATCAAGAGCCAGAAAGTGCAGGACATCTCGCCTTCTATCTGGGCCCCCTG	1153
QY	1182	GAGACCCACAGAGGTGACTGCAGTGNCTTCGAGACCAGGAACCTCTGGATCGGGCTC	1241
Db	1154	GAGACCCACAGAGGTGACTGCAGTGNCTTCGAGACCAGGAACCTCTGGATCGGGCTC	1213
QY	1242	ACCTACAAAGCCGCAAGGACTCCCTTCGCTGGGCCACAGGGGAGCACCAGGCGCTTCACC	1301
Db	1214	ACCTACAAAGCCGCAAGGACTCCCTTCGCTGGGCCACAGGGGAGCACCAGGCGCTTCACC	1273
QY	1302	AGTTTGTGCTTTGGCAGCGCTGACAAACACGGG	1334
Db	1274	AGTTTGTGCTTTGGCAGCGCTGACAAACACGGG	1306

RESULT 17

RESOLUTION
US-10-042-141-12

03 10 042 111 112 : Sequence 12, Application US/10042141

; publication No. US20020183503A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

; TITLE OF INVENTION: 26 Human secreted proteins

QY	882	GGTTACACGGGCAGATACTGCCAACTGAGGTGCAGCTTCAGTGTGTGCACGGCCGGTTC	941
Db	899	GGCTACACGGGCAGATACTGCCAACTGAGGTGCAGCTTCAGTGTGTGCACGGCCGGTTC	958
QY	942	CGGGAGGAGAGTGTCCTGTCGCTCTGTACATCGGCTACGGGGAGGCCAGTGTGCCACC	1001
Db	959	CGGGAGGAGAGTGTCCTGTCGCTCTGTACATCGGCTACGGGGAGGCCAGTGTGCCACC	1018
QY	1002	AAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTTCATCGTG	1061
Db	1019	AAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTTCATCGTG	1078
QY	1062	TCCTCAGAGGCAGACACTATTACAGCCAGGATGAAATGTCAGAGGAAGCGGGGGTG	1121
Db	1079	TCCTCAGAGGCAGACACTATTACAGCCAGGATGAAATGTCAGAGGAAGCGGGGGTG	1138
QY	1122	CTGGCCCCAGATCAAGAGCCAGAAAGTCAGAGACATCCGCGCTTCATCTGGGCCCGCTG	1181
Db	1139	CTGGCCCCAGATCAAGAGCCAGAAAGTCAGAGACATCCGCGCTTCATCTGGGCCCGCTG	1198
QY	1182	GAGACACACAGAGGTGACTGACAGTGACTTCGAGACACAGGAACCTCTCGATCGGGCTC	1241
Db	1199	GAGACACACAGAGGTGATTGACAGTGACTTCGAGACACAGGAACCTCTCGATCGGGCTC	1258
QY	1242	ACCTACAAGACCGCCAAAGGACTCCCTCCGCTGGCCACAGGGGAGCACAGGCGCTTCACC	1301
Db	1259	ACCTACAAGACCGCCAAAGGACTCCCTCCGCTGGCCACAGGGGAGCACAGGCGCTTCACC	1318
QY	1302	AGTTTGGCTTTGGGCAGCCCTGCAACACCACGGG	1334
Db	1319	AGTTTGGCTTTGGGCAGCCCTGCAACACCACGGG	1351

RESULT 18

US-09-726-643-12
; Sequence 12, Application US/09726643
; Patent No. US20020028449A1

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; ORGANIZATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 26 Human secreted proteins
; FILE REFERENCE: PZ040P1
; CURRENT APPLICATION NUMBER: US/09/726,643
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/15187
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/137,725
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 12
; LENGTH: 1923
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-726-643-12

```

Query Match 54.9%; Score 1029; DB 10; Length 1923;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

102	CCTGACGGGCCCAACAGACCCATGTCGATCCAGAGACCTCCCTTGGCCGGGGGCATCTC	161
QY		
119	CCTGACGGGCCCAACAGACCCATGTCGATCCAGAGACCTCCCTTGGCCGGGGGCATCTC	178
Db		
162	CTGGCTGTGCTCTGCTGGCCCTCCTTGGCACCACTCTGGGCAGAGGTGGCCACCCCCAGCTG	221
QY		
179	CTGGCTGTGCTCTGCTGGCCCTCCTTGGCACCGCCTGGGCAGAGGTGGCCACCCCCAGCTG	238
Db		
222	CAGGAGCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAGSAGAGTTTCTGCTCCTCTCC	281
QY		
239	CAGGAGCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAGSAGAGTTTCTGCTCCTCTCC	298
Db		
282	CTGCACACCGCGCTGCGCAGCTGGGTCCAGCCCCCTGGCGCTGCATGCGGAGGCTGGAC	341
QY		


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Query Match          25.9%; Score 485; DB 10; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 604 TGGGCTGTGGGGCCACCTGTGCTCTCAGGCGCCAGACAGCATAGAGCCTTTGTCTGTGG 663
DB 1 TGGGCTGTGGGGCCACCTGTGCTCTCAGGCGCCAGACAGCATAGAGCCTTTGTCTGTGG 60
QY 664 CCTACTCCCGCGGAGCAACTGGGAGGTCAACGGAGCAACATCATCCCTATAAGAAAG 723
DB 61 CCTACTCCCGCGGAGCAACTGGGAGGTCAACGGAGCAACATCATCCCTATAAGAAAG 120
QY 724 GTCCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGTCTTCAAAGCCTGGGACCATG 783
DB 121 GTCCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGTCTTCAAAGCCTGGGACCATG 180
QY 784 CAGGGGGGCTGTGAGGTCCCAAGGAATCCTTGTGCGATGAGCTGCGAGAACCATGGAC 843
DB 181 CAGGGGGGCTGTGAGGTCCCAAGGAATCCTTGTGCGATGAGCTGCGAGAACCATGGAC 240
QY 844 GTCTCAACATCAGACACCTGCCACTGCCACTGTCCCTGGCTACACGGCGAGATAGTCC 903
DB 241 GTCTCAACATCAGACACCTGCCACTGTCCCTGGCTACACGGCGAGATAGTCC 300
QY 904 AAGTAGGTCAGCCTCAGTGTGTGCACGCCCGGTTCGGGAGGAGGAGTGTCTGCTGG 963
DB 301 AAGTAGGTCAGCCTCAGTGTGTGCACGCCCGGTTCGGGAGGAGGAGTGTCTGCTGG 360
QY 964 TCTGTGACATCGGTACGGGGAGCCAGTGTGCCACCAAGGTGATTTTCCCTTCCACA 1023
DB 361 TCTGTGACATCGGTACGGGGAGCCAGTGTGCCACCAAGGTGATTTTCCCTTCCACA 420
QY 1024 CCGTGTACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGCAGACACCTATT 1083
DB 421 CCGTGTACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGCAGACACCTATT 480
QY 1084 ACAGA 1088
DB 481 ACAGA 485

RESULT 21
US-09-944-413-53
; Sequence 53, Application US/09944413
; Patent No. US20020156004A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,413
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; SEQ ID NO 53
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 53
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; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-413-53

Query Match          2.4%; Score 45; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1254 GCGAAGGACTCCTTCGGTGGCCACAGGGGAGCAGCAGGCCTTC 1298
      |||||||||||||||||||||||||||||||||||||||||||
Db 1 GCGAAGGACTCCTTCGGTGGCCACAGGGGAGCAGCAGGCCTTC 45

RESULT 22
US-09-944-403-53
; Sequence 53, Application US/09944403
; Patent No. US20020165143A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavini, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tamas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,403
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945

; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 53
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-403-53

Query Match          2.4%; Score 45; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1254 GCGAAGGACTCCTTCGGTGGCCACAGGGGAGCAGCAGGCCTTC 1298
      |||||||||||||||||||||||||||||||||||||||||||
Db 1 GCGAAGGACTCCTTCGGTGGCCACAGGGGAGCAGCAGGCCTTC 45

RESULT 23
US-09-944-896-53
; Sequence 53, Application US/099444896
; Patent No. US20020168715A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
```

APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT FILING DATE: 2001-08-31
PRIORITY APPLICATION NUMBER: US/09/944,896
PRIORITY FILING DATE: 2001-05-25
PRIORITY APPLICATION NUMBER: 60/069,334
PRIORITY FILING DATE: December 11, 1997
PRIORITY APPLICATION NUMBER: 60/069,335
PRIORITY FILING DATE: December 11, 1997
PRIORITY APPLICATION NUMBER: 60/069,278
PRIORITY FILING DATE: December 11, 1997
PRIORITY APPLICATION NUMBER: 60/069,425
PRIORITY FILING DATE: December 12, 1997
PRIORITY APPLICATION NUMBER: 60/069,696
PRIORITY FILING DATE: December 16, 1997
PRIORITY APPLICATION NUMBER: 60/069,694
PRIORITY FILING DATE: December 16, 1997
PRIORITY APPLICATION NUMBER: 60/069,702
PRIORITY FILING DATE: December 16, 1997
PRIORITY APPLICATION NUMBER: 60/069,870
PRIORITY FILING DATE: December 17, 1997
PRIORITY APPLICATION NUMBER: 60/069,873
PRIORITY FILING DATE: December 17, 1997
PRIORITY APPLICATION NUMBER: 60/068,017
PRIORITY FILING DATE: December 18, 1997
PRIORITY APPLICATION NUMBER: 60/070,440
PRIORITY FILING DATE: January 5, 1998
PRIORITY APPLICATION NUMBER: 60/074,086
PRIORITY FILING DATE: February 9, 1998
PRIORITY APPLICATION NUMBER: 60/074,092
PRIORITY FILING DATE: February 9, 1998
PRIORITY APPLICATION NUMBER: 60/075,945
PRIORITY FILING DATE: February 25, 1998
PRIORITY APPLICATION NUMBER: 60/112,850
PRIORITY FILING DATE: December 16, 1998
PRIORITY APPLICATION NUMBER: 60/113,296
PRIORITY FILING DATE: December 22, 1998
PRIORITY APPLICATION NUMBER: 60/146,222
PRIORITY FILING DATE: July 28, 1999
PRIORITY APPLICATION NUMBER: PCT/US98/19330
PRIORITY FILING DATE: September 16, 1998
PRIORITY APPLICATION NUMBER: PCT/US98/25108
PRIORITY FILING DATE: December 1, 1998
PRIORITY APPLICATION NUMBER: 09/216,021
PRIORITY FILING DATE: December 16, 1998
PRIORITY APPLICATION NUMBER: 09/218,517
PRIORITY FILING DATE: December 22, 1998
PRIORITY APPLICATION NUMBER: 09/254,311
PRIORITY FILING DATE: March 3, 1999
PRIORITY APPLICATION NUMBER: PCT/US99/12252
PRIORITY FILING DATE: June 22, 1999
PRIORITY APPLICATION NUMBER: PCT/US99/21090
PRIORITY FILING DATE: September 15, 1999
PRIORITY APPLICATION NUMBER: PCT/US99/28409
PRIORITY FILING DATE: No. US20020168715A1ember 30, 1999
PRIORITY APPLICATION NUMBER: PCT/US99/28313
PRIORITY FILING DATE: No. US20020168715A1ember 30, 1999
PRIORITY APPLICATION NUMBER: PCT/US99/28301
PRIORITY FILING DATE: December 1, 1999
PRIORITY APPLICATION NUMBER: PCT/US99/30095

PRIORITY FILING DATE: December 16, 1999
PRIORITY APPLICATION NUMBER: PCT/US00/03565
PRIORITY FILING DATE: February 11, 2000
PRIORITY APPLICATION NUMBER: PCT/US00/04414
PRIORITY FILING DATE: February 22, 2000
PRIORITY APPLICATION NUMBER: PCT/US00/05841
PRIORITY FILING DATE: March 2, 2000
PRIORITY APPLICATION NUMBER: PCT/US00/08439
PRIORITY FILING DATE: March 30, 2000
PRIORITY APPLICATION NUMBER: PCT/US00/14042
PRIORITY FILING DATE: May 22, 2000
PRIORITY APPLICATION NUMBER: PCT/US00/20710
PRIORITY FILING DATE: July 28, 2000
PRIORITY APPLICATION NUMBER: PCT/US00/32678
PRIORITY FILING DATE: December 1, 2000
PRIORITY APPLICATION NUMBER: PCT/US01/06520
PRIORITY FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 53
LENGTH: 45
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-896-53

Query Match 2.4%; Score 45; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1254 GCCAAGGACTCTTCGCTGGCCACAGGGGAGCAGGCCTTC 1298
|||||
Db 1 GCCAAGGACTCTTCGCTGGCCACAGGGGAGCAGGCCTTC 45

RESULT 24
US-09-944-944-53
Sequence 53, Application US/09944944
Patent No. US20020173463A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT FILING DATE: 2001-09-26
PRIORITY APPLICATION NUMBER: 09/866,028
PRIORITY FILING DATE: 2001-05-25
PRIORITY APPLICATION NUMBER: 60/067,411
PRIORITY FILING DATE: December 3, 1997
PRIORITY APPLICATION NUMBER: 60/069,334
PRIORITY FILING DATE: December 11, 1997
PRIORITY APPLICATION NUMBER: 60/069,335
PRIORITY FILING DATE: December 11, 1997
PRIORITY APPLICATION NUMBER: 60/069,278
PRIORITY FILING DATE: December 11, 1997
PRIORITY APPLICATION NUMBER: 60/069,425
PRIORITY FILING DATE: December 12, 1997

;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 53
;; LENGTH: 45
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-896-49

Query Match 2.4%; Score 45; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1254 GCCAAGGACTCCTTCGCTGGGCGACAGGGGAGGAGCACCAGGCCTTC 1298
Db 1 GCCAAGGACTCCTTCGCTGGGCGACAGGGGAGGAGCACCAGGCCTTC 45
RESULT 25
US-09-866-028-53
; Sequence 53, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 53
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-866-028-53
Query Match 2.4%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1254 GCCAAGGACTCCTTCGCTGGGCGACAGGGGAGGAGCACCAGGCCTTC 1298
Db 1 GCCAAGGACTCCTTCGCTGGGCGACAGGGGAGGAGCACCAGGCCTTC 45
RESULT 26
US-09-944-449-53
; Sequence 53, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret

APPLICANT: Tumas,Daniel
APPLICANT: Wood,William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,449
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000

PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 53
LENGTH: 45
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-449-53

Query Match 2.4% Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1254 GCCAAGGACTCTTCGCTGGCCACAGGGGAGCACCAGGCCTTC 1298
Db 1 GCCAAGGACTCTTCGCTGGCCACAGGGGAGCACCAGGCCTTC 45

RESULT 27
US-09-944-457-53
Sequence 53, Application US/09944457
Patent No. US20020110859A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein,David
APPLICANT: Eaton,Dan
APPLICANT: Ferrara,Napoleone
APPLICANT: Filvaroff,Ellen
APPLICANT: Gerritsen,Mary
APPLICANT: Goddard,Audrey
APPLICANT: Godowski,Paul
APPLICANT: Grimaldi,Christopher
APPLICANT: Gurney,Austin
APPLICANT: Hillan,Kenneth
APPLICANT: Kljavin,Ivar
APPLICANT: Napier,Mary
APPLICANT: Roy,Margaret
APPLICANT: Tumas,Daniel
APPLICANT: Wood,William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,457
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870

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; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 53
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-457-53

Query Match      2.4%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1254 GCGAAGACTCTTCGCTGGGGACACAGGGGAGACACAGGCCCTTC 1298
|||||
Db 1 GCGAAGACTCTTCGCTGGGGACACAGGGGAGACACAGGCCCTTC 45

RESULT 28
US-09-945-587-53
; Sequence 53, Application US/09945587
; Patent No. US20020127643A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerriksen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
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;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: NO. US20020127643A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: NO. US20020127643A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 53
;; LENGTH: 45
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-945-587-53

Query Match 2.4%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1254 GCCAAGACTCCTTCCTGGCCACAGGGGAGGACACCGGCTTC 1298
|||||
Db 1 GCCAAGACTCCTTCCTGGCCACAGGGGAGGACACCGGCTTC 45

RESULT 29

US-09-945-015-53
;; Sequence 53, Application US/09945015
;; Patent No. US20020132768A1
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin
;; APPLICANT: Botstein, David
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gerritsen, Mary
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Kljavin, Ivar
;; APPLICANT: Napier, Mary
;; APPLICANT: Roy, Margaret
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Wood, William
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; ACIDS ENCODING THE SAME
;; FILE REFERENCE: P2548P1C1

;; CURRENT APPLICATION NUMBER: US/09/945,015
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: 09/866,028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/067,411
;; PRIOR FILING DATE: December 3, 1997
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,335
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: NO. US20020132768A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: NO. US20020132768A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710

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; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 53
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-945-015-53

Query Match          2.4%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1254 GCCAAGGACTCTTCGCTGGCCACAGGGGAGGACACAGGCCTTC 1298
      |||||||
Db 1 GCCAAGGACTCTTCGCTGGCCACAGGGGAGGACACAGGCCTTC 45

RESULT 30
US-09-944-396-53
; Sequence 53, Application US/09944396
; Patent No. US20020132981A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,396
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
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; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 53
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-396-53

Query Match          2.4%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1254 GCCAAGGACTCTTCGCTGGCCACAGGGGAGGACACAGGCCTTC 1298
      |||||||
Db 1 GCCAAGGACTCTTCGCTGGCCACAGGGGAGGACACAGGCCTTC 45

RESULT 31
US-09-944-097-53
; Sequence 53, Application US/09944097
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; Patent No. US20020133675A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,097
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999

; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020133675A1 September 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020133675A1 September 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 53
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-097-53

Query Match 2.4%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1254 GCCAAGGACTCTTCGCTGGGCCACAGGGAGCAGGCCTTC 1298
|||||
Db 1 GCCAAGGACTCTTCGCTGGGCCACAGGGAGCAGGCCTTC 45

RESULT 32
US-09-944-432-53
; Sequence 53, Application US/09944432
; Patent No. US20020142419A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,432
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334

;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069335
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020142419A1e1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020142419A1e1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 53

;; LENGTH: 45
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-432-53

Query Match 2.4%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1254 GCCAAGGACTCTTCGCTGGCCACACAGGGGAGCACCAGGCCTTC 1298
|||||
Db 1 GCCAAGGACTCTTCGCTGGCCACACAGGGGAGCACCAGGCCTTC 45

RESULT 33
US-09-943-762-53
; Sequence 53, Application US/09943762
; Patent No. US20020142958A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945

;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/28313
;; PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 53
;; LENGTH: 45
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-943-762-53

Query Match 2.4%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1254 GCCAAGGACTCTTCGGCTGGCCACAGGGAGCACCAGGCCTTC 1298
|||||
Db 1 GCCAAGGACTCTTCGGCTGGCCACAGGGAGCACCAGGCCTTC 45

RESULT 34
US-09-944-654-53
;; Sequence 53, Application US/09944654
;; Patent No. US20020142959A1
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin
;; APPLICANT: Botstein, David
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gerritsen, Mary
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Kljavin, Ivar
;; APPLICANT: Napier, Mary
;; APPLICANT: Roy, Margaret
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Wood, William
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P2548P1C1
;; CURRENT APPLICATION NUMBER: US/09/944,654
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: 09/866,028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/067,411
;; PRIOR FILING DATE: December 3, 1997
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,335
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020142959A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020142959A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301

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; PRIOR FILING DATE: December1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 53
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-654-53

Query Match          2.4%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1254 GCCAAGACTCTTCCTCCGCTGGCCACAGGGGACACAGGCGCTTC 1298
Db 1 GCCAAGACTCTTCCTCCGCTGGCCACAGGGGACACAGGCGCTTC 45

RESULT 35
US-09-943-851A-53
; Sequence 53, Application US/09943851A
; Patent No. US20020150976A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Flvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/943,851A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US/09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; OTHER INFORMATION: Synthetic oligonucleotide probe
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
```

US-09-943-851A-53

Query Match 2.4%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1254 GCCAAGACTCCTTCGCTGGCCACAGGGGAGCACCAGGCCTTC 1298
|||||
Db 1 GCCAAGACTCCTTCGCTGGCCACAGGGGAGCACCAGGCCTTC 45

RESULT 36

US-09-790-264-5/c

Sequence 5, Application US/09790264

Patent No. US2002028508A1

GENERAL INFORMATION:

APPLICANT: Holtzman, Douglas A.

APPLICANT: Goodearl, Andrew D.J.

APPLICANT: McCarthy, Sean A.

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING

TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER

TITLE OF INVENTION: US

FILE REFERENCE: 07334-322001

CURRENT APPLICATION NUMBER: US/09/790,264

CURRENT FILING DATE: 2001-02-21

PRIOR APPLICATION NUMBER: US 09/065,661

PRIOR FILING DATE: 1998-04-23

PRIOR APPLICATION NUMBER: US 09/298,531

PRIOR FILING DATE: 1999-04-23

PRIOR APPLICATION NUMBER: US 09/065,363

PRIOR FILING DATE: 1998-04-23

PRIOR APPLICATION NUMBER: US 09/337,930

PRIOR FILING DATE: 1999-06-22

PRIOR APPLICATION NUMBER: US 09/102,705

PRIOR FILING DATE: 1998-06-22

PRIOR APPLICATION NUMBER: US 09/363,630

PRIOR FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: US 09/124,538

PRIOR FILING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 30

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: oligonucleotide for PCR

US-09-790-264-5

Query Match

Best Local Similarity 1.6%; Score 30; DB 10; Length 30;

Sequence 103, Application US/09944413

Patent No. US20020156004A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Botstein, David

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher

APPLICANT: Gurney, Austin

US-09-944-413-103/c

Sequence 103, Application US/09944413

Patent No. US20020156004A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Botstein, David

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher

APPLICANT: Gurney, Austin

APPLICANT: Hillan, Kenneth

APPLICANT: Klijavin, Ivar

APPLICANT: Napier, Mary

APPLICANT: Roy, Margaret

APPLICANT: Tumas, Daniel

APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P2548P1C1

CURRENT APPLICATION NUMBER: US/09/944,413

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 09/866,028

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/067,411

PRIOR FILING DATE: December 3, 1997

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,335

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,425

PRIOR FILING DATE: December 12, 1997

PRIOR APPLICATION NUMBER: 60/069,696

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,694

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,702

PRIOR FILING DATE: December 17, 1997

PRIOR APPLICATION NUMBER: 60/069,870

PRIOR FILING DATE: December 17, 1997

PRIOR APPLICATION NUMBER: 60/069,873

PRIOR FILING DATE: December 18, 1997

PRIOR APPLICATION NUMBER: 60/070,440

PRIOR FILING DATE: January 5, 1998

PRIOR APPLICATION NUMBER: 60/074,086

PRIOR FILING DATE: February 9, 1998

PRIOR APPLICATION NUMBER: 60/074,092

PRIOR FILING DATE: February 9, 1998

PRIOR APPLICATION NUMBER: 60/075,945

PRIOR FILING DATE: February 25, 1998

PRIOR APPLICATION NUMBER: 60/112,850

PRIOR FILING DATE: December 16, 1998

PRIOR APPLICATION NUMBER: 60/113,296

PRIOR FILING DATE: December 22, 1998

PRIOR APPLICATION NUMBER: 60/146,222

PRIOR FILING DATE: July 28, 1999

PRIOR APPLICATION NUMBER: PCT/US98/19330

PRIOR FILING DATE: September 16, 1998

PRIOR APPLICATION NUMBER: PCT/US98/25108

PRIOR FILING DATE: December 1, 1998

PRIOR APPLICATION NUMBER: 09/216,021

PRIOR FILING DATE: December 16, 1998

PRIOR APPLICATION NUMBER: 09/218,517

PRIOR FILING DATE: December 22, 1998

PRIOR APPLICATION NUMBER: 09/254,311

PRIOR FILING DATE: March 3, 1999

PRIOR APPLICATION NUMBER: PCT/US99/12252

PRIOR FILING DATE: June 22, 1999

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: September 15, 1999

PRIOR APPLICATION NUMBER: PCT/US99/28409

PRIOR FILING DATE: No. US20020156004A1ember 30, 1999

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: No. US20020156004A1ember 30, 1999

PRIOR APPLICATION NUMBER: PCT/US99/28301

PRIOR FILING DATE: December 1, 1999

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: December 16, 1999

PRIOR APPLICATION NUMBER: PCT/US00/03565

PRIOR FILING DATE: February 11, 2000

;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 103
;; LENGTH: 27
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-413-103

Query Match 1.4%; Score 27; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1714 TGGGAAGATGGCTCAATTAGATGGC 1740
|||||
Db 27 TGGGAAGATGGCTCAATTAGATGGC 1

RESULT 38

US-09-944-403-103/c
;; Sequence 103, Application US/09944403
;; Patent No. US20020165143A1
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin
;; APPLICANT: Batson, David
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gerritsen, Mary
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Kljavin, Ivar
;; APPLICANT: Napier, Mary
;; APPLICANT: Roy, Margaret
;; APPLICANT: Tomas, Daniel
;; APPLICANT: Wood, William
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P2548P1C1
;; CURRENT APPLICATION NUMBER: US/09/944,403
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: 09/866,028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/067,411
;; PRIOR FILING DATE: December 3, 1997
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,335
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694

;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 103
;; LENGTH: 27
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-403-103

Query Match 1.4%; Score 27; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1714 TGGGAAGATGGGCTTCAATTAGATGGC 1740
|||||
Db 27 TGGGAAGATGGGCTTCAATTAGATGGC 1

RESULT 39

US-09-944-896-103/c
; Sequence 103, Application US/09944896
; Patent No. US20020168715A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/944,896
; CURRENT FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997

; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997

; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998

; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998

; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998

; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998

; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998

; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998

; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999

; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998

; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998

; PRIOR APPLICATION NUMBER: 09/216,021

; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020168715A1
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020168715A1
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 103
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-896-103

Query Match 1.4%; Score 27; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1714 TGGGAAGATGGGCTTCAATTAGATGGC 1740

Db 27 TGGGAAGATGGGCTTCAATTAGATGGC 1

RESULT 40

US-09-944-896-103/c

; Sequence 103, Application US/09944894

; Patent No. US20020173463A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

```
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548PIC1
; CURRENT APPLICATION NUMBER: US/09/944,944
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
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; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 103
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-944-103

Query Match 1.4%; Score 27; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1714 TGGGAGAGATGGGCTTCAATTAGATGGC 1740
DB 27 TGGGAGAGATGGGCTTCAATTAGATGGC 1

RESULT 41
US-09-866-028-103/C
; Sequence 103, Application US/098666028
; Patent No. US20020038309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavini, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PIC1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 103
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-866-028-103

Query Match 1.4%; Score 27; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1714 TGGGAGAGATGGGCTTCAATTAGATGGC 1740
DB 27 TGGGAGAGATGGGCTTCAATTAGATGGC 1

RESULT 42
US-09-944-449-103/c
; Sequence 103, Application US/099444449
```

Patent No. US20020102647A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavini, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PIC1
; CURRENT APPLICATION NUMBER: US/09/944,449
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/224,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999

; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: NO. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: NO. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 103
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-449-103

Query Match 1.4%; Score 27; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1714 TGGGAAGATGGGCTTCAATTAGATGGC 1740
Db 27 TGGGAAGATGGGCTTCAATTAGATGGC 1

RESULT 43
US-09-944-457-103/c
; Sequence 103, Application US/09944457
; Patent No. US20020110859A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavini, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PIC1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411

;; PRIOR FILING DATE: December 3, 1997
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,335
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001

;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 103
;; LENGTH: 27
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-457-103
Query Match 1.4%; Score 27; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.016; 0; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0;
QY 1714 TGGGAAGATGGGCTTCATTAGATGC 1740
|||||
DB 27 TGGGAAGATGGGCTTCATTAGATGC 1
RESULT 44
US-09-945-587-103/C
;; Sequence 103, Application US/09945587
;; Patent No. US20020127643A1
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin
;; APPLICANT: Botstein, David
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gerritsen, Mary
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Kljavin, Ivar
;; APPLICANT: Napier, Mary
;; APPLICANT: Roy, Margaret
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Wood, William
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P2548P1C1
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: 09/866,028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/067,411
;; PRIOR FILING DATE: December 3, 1997
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,335
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092

;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
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;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,335
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
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;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
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;; PRIOR APPLICATION NUMBER: 09/216,021
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;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 103
;; LENGTH: 27
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic oligonucleotide probe

US-09-945-587-103

Query Match 1.4%; Score 27; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1714 TGGGAAGATGGGCTCAATTAGATGCC 1740
Db 27 TGGGAAGATGGGCTCAATTAGATGCC 1

RESULT 45

US-09-945-015-103/c
; Sequence 103, Application US/09945015
; Patent No. US20020132768A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan

;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gerritsen, Mary
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Kljavin, Ivar
;; APPLICANT: Napier, Mary
;; APPLICANT: Roy, Margaret
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Wood, William
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P2548P1C1
;; CURRENT APPLICATION NUMBER: US/09/945,015
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: 09/866,028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/067,411
;; PRIOR FILING DATE: December 3, 1997
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,335
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313

;; PRIOR FILING DATE: NO. US20020132768A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 103
;; LENGTH: 27
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic oligonucleotide probe

US-09-945-015-103

Query Match 1.4%: Score 27; DB 10; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1714 TGGGAAGATGGCTTCAATTAGATGGC 1740

Db 27 TGGGAAGATGGCTTCAATTAGATGGC 1

RESULT 46

US-09-944-396-103/c

;; Sequence 103, Application US/09944396

;; Patent No. US20020132981A1

;; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin

;; APPLICANT: Botstein, David

;; APPLICANT: Eaton, Dan

;; APPLICANT: Ferrara, Napoleone

;; APPLICANT: Filvaroff, Ellen

;; APPLICANT: Gerritsen, Mary

;; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul

;; APPLICANT: Grimaldi, Christopher

;; APPLICANT: Gurney, Austin

;; APPLICANT: Hillan, Kenneth

;; APPLICANT: Kljavin, Ivar

;; APPLICANT: Napier, Mary

;; APPLICANT: Roy, Margaret

;; APPLICANT: Tumas, Daniel

;; APPLICANT: Wood, William

;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

;; TITLE OF INVENTION: ACIDS ENCODING THE SAME

;; FILE REFERENCE: P2548P1C1

;; CURRENT APPLICATION NUMBER: US/09/944,396

;; CURRENT FILING DATE: 2001-09-26

;; PRIOR APPLICATION NUMBER: 09/866,028

;; PRIOR FILING DATE: 2001-05-25

;; PRIOR APPLICATION NUMBER: 60/067,411

;; PRIOR FILING DATE: December 3, 1997

;; PRIOR APPLICATION NUMBER: 60/069,334

;; PRIOR FILING DATE: December 11, 1997

;; PRIOR APPLICATION NUMBER: 60/069335

;; PRIOR FILING DATE: December 11, 1997

;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 103
;; LENGTH: 27
;; TYPE: DNA
;; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-396-103

Query Match 1.4%; Score 27; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1714 TGGGAAGATGGGCTTCAATTAGATGGC 1740

Db 27 TGGGAAGATGGGCTTCAATTAGATGGC 1

RESULT 47

US-09-944-097-103/c

; Sequence 103, Application US/09944097

; Patent No. US20020133675A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/944, 097

; CURRENT FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: 09/866, 028

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/069, 334

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069, 335

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069, 278

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069, 425

; PRIOR FILING DATE: December 12, 1997

; PRIOR APPLICATION NUMBER: 60/069, 696

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069, 694

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069, 702

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069, 870

; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/069, 873

; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/068, 017

; PRIOR FILING DATE: December 18, 1997

; PRIOR APPLICATION NUMBER: 60/070, 440

; PRIOR FILING DATE: January 5, 1998

; PRIOR APPLICATION NUMBER: 60/074, 086

; PRIOR FILING DATE: February 9, 1998

; PRIOR APPLICATION NUMBER: 60/074, 092

; PRIOR FILING DATE: February 9, 1998

; PRIOR APPLICATION NUMBER: 60/075, 945

; PRIOR FILING DATE: February 25, 1998

; PRIOR APPLICATION NUMBER: 60/112, 850

; PRIOR FILING DATE: December 16, 1998

; PRIOR APPLICATION NUMBER: 60/113, 296

; PRIOR FILING DATE: December 22, 1998

; PRIOR APPLICATION NUMBER: 60/146, 222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216, 021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218, 517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254, 311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: NO. US20020133675A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: NO. US20020133675A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 103
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-097-103

Query Match 1.4%; Score 27; DB 10; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1714 TGGGAAGATGGGCTTCAATTAGATGGC 1740

Db 27 TGGGAAGATGGGCTTCAATTAGATGGC 1

RESULT 48

US-09-944-432-103/c

; Sequence 103, Application US/09944432

; Patent No. US20020142419A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; PRIOR FILING DATE: December 16, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,702
 ; PRIOR FILING DATE: December 16, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,870
 ; PRIOR FILING DATE: December 17, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,873
 ; PRIOR FILING DATE: December 17, 1997
 ; PRIOR APPLICATION NUMBER: 60/068,017
 ; PRIOR FILING DATE: December 18, 1997
 ; PRIOR APPLICATION NUMBER: 60/070,440
 ; PRIOR FILING DATE: January 5, 1998
 ; PRIOR APPLICATION NUMBER: 60/074,086
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/074,092
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/075,945
 ; PRIOR FILING DATE: February 25, 1998
 ; PRIOR APPLICATION NUMBER: 60/112,850
 ; PRIOR FILING DATE: December 16, 1998
 ; PRIOR APPLICATION NUMBER: 60/113,296
 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 60/146,222
 ; PRIOR FILING DATE: July 28, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US98/19330
 ; PRIOR FILING DATE: September 16, 1998
 ; PRIOR APPLICATION NUMBER: PCT/US98/25108
 ; PRIOR FILING DATE: December 1, 1998
 ; PRIOR APPLICATION NUMBER: 09/216,021
 ; PRIOR FILING DATE: December 16, 1998
 ; PRIOR APPLICATION NUMBER: 09/218,517
 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 09/254,311
 ; PRIOR FILING DATE: March 3, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252
 ; PRIOR FILING DATE: June 22, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: September 15, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28409
 ; PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28301
 ; PRIOR FILING DATE: December 1, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: December 16, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US00/03565
 ; PRIOR FILING DATE: February 11, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: February 22, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841
 ; PRIOR FILING DATE: March 2, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/08439
 ; PRIOR FILING DATE: March 30, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/14042
 ; PRIOR FILING DATE: May 22, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/20710
 ; PRIOR FILING DATE: July 28, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678
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 ; PRIOR FILING DATE: February 28, 2001
 ; SEQ ID NO 103
 ; LENGTH: 27
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic oligonucleotide probe
 US-09-943-762-103

Query Match 1.4%; Score 27; DB 10; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ; Patent No. US20020142959A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin
 ; APPLICANT: Botstein, David
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gottard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Kljavin, Ivar
 ; APPLICANT: Napier, Mary
 ; APPLICANT: Roy, Margaret
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P2548P1C1
 ; CURRENT FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 09/866,028
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/067,411
 ; PRIOR FILING DATE: December 3, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,334
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 ; PRIOR FILING DATE: December 12, 1997
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 ; PRIOR APPLICATION NUMBER: 60/068,017
 ; PRIOR FILING DATE: December 18, 1997
 ; PRIOR APPLICATION NUMBER: 60/070,440
 ; PRIOR FILING DATE: January 5, 1998
 ; PRIOR APPLICATION NUMBER: 60/074,086
 ; PRIOR FILING DATE: February 9, 1998
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 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/075,945
 ; PRIOR FILING DATE: February 25, 1998
 ; PRIOR APPLICATION NUMBER: 60/112,850
 ; PRIOR FILING DATE: December 16, 1998
 ; PRIOR APPLICATION NUMBER: 60/113,296
 ; PRIOR FILING DATE: December 22, 1998
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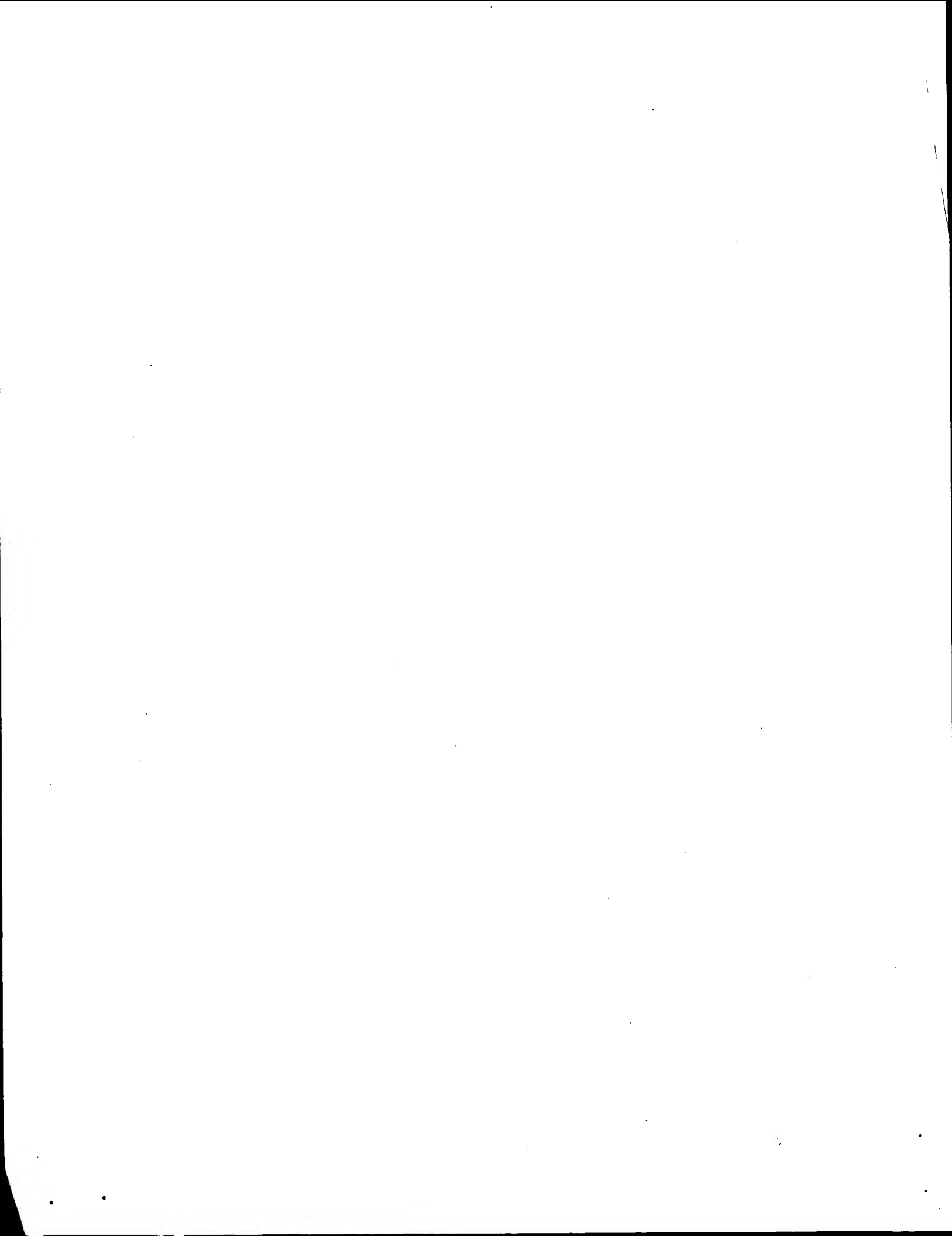
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JOURNAL Patent: WO 0149728-A 25 12-JUL-2001;
Protegene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP)
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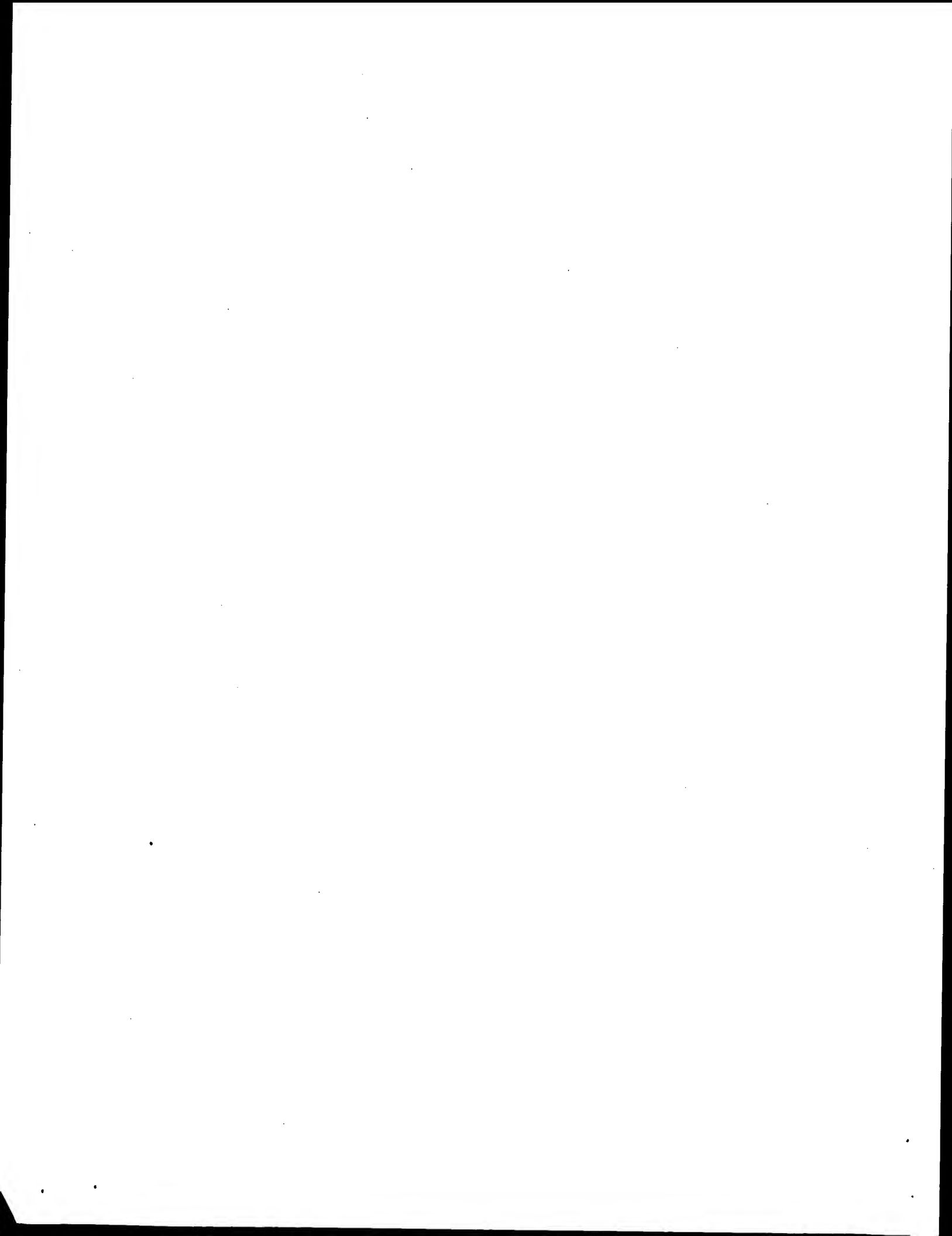
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Best Local Similarity 97.9%; Pred. No. 0;
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Query Match 96.8%; Score 2447.5; DB 22; Length 446;
Best Local Similarity 97.1%; Pred. No. 2.4e-177;
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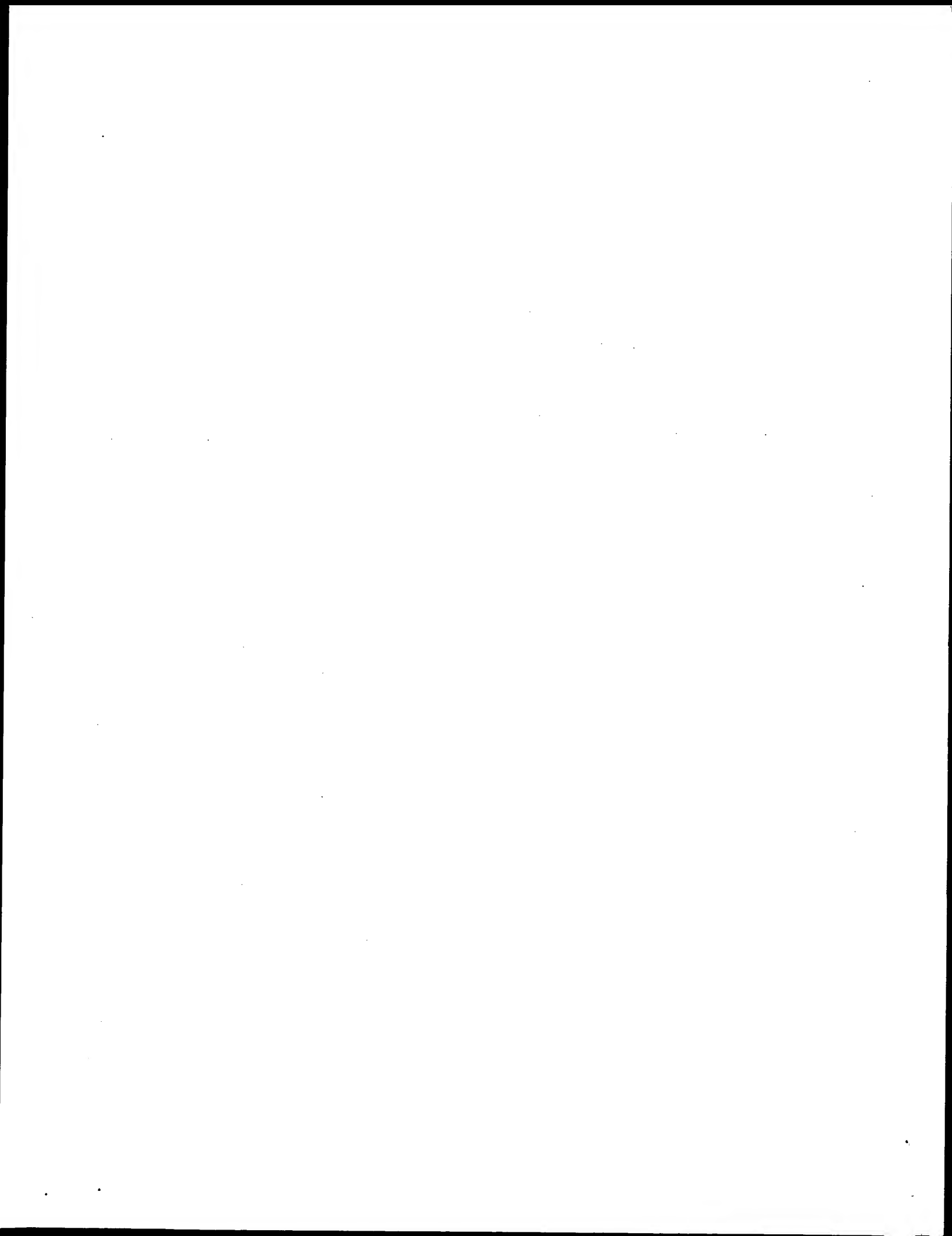
RESULT 1
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 XX DE cDNA clone encoding human PRO347, amplified in tumour cells.
 XX KW PRO347; UNQ306; cancer; tumour; diagnosis; therapy; human; ss.
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 XX FH Key
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 XX WO9935170-A2.
 XX PD 15-JUL-1999.
 XX PF 05-JAN-1999; 99WO-US00106.
 XX PR 20-NOV-1998; 98US-0109304.
 XX PR 05-JAN-1998; 98US-0070440.
 XX PR 29-APR-1998; 98US-0083500.
 XX PR 22-MAY-1998; 98US-0086414.

PR 10-JUN-1998; 98US-0088742.
 PR 10-NOV-1998; 98US-0107783.
 XX (GETH) GENENTECH INC.
 XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
 XX Roy MA, Wood WI;
 XX WPI; 1999-430385/36.
 DR P-PSDB; AAY06483.
 XX
 PT Antibody against proteins expressed in neoplastic cells, useful for
 PT tumor diagnosis and treatment
 XX
 PS Example 1; Fig 13; 162pp; English.
 XX
 CC This is the nucleotide sequence of cDNA clone DNA44176 (ATCC 209532)
 CC coding for human PRO347 (UNQ306) (see AAY06482). The clone was
 CC isolated from a foetal kidney library. Amplification of DNA44176
 CC occurs in various tumours, suggesting an association with tumour
 CC formation or growth. Antagonists (e.g. antibodies) directed against
 CC PRO347 may have use in cancer therapy. The invention identifies 14
 CC genes (see AAX87254-67) that are amplified in the genome of tumour
 CC cells. Such amplification is expected to be associated with
 CC overexpression of the gene product and to contribute to
 CC tumorigenesis. The encoded proteins (see AAY06477-90) may be useful
 CC targets for the diagnosis and/or treatment (including prevention)
 CC of certain cancers, and may act as predictors of the prognosis of
 CC tumour treatment.
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 QY 1659 TGAGGGCCAGGGAGTGTAGTGTAGAAAGCTGGGSCCTTCGCCCTGCTTTTGTATGGGA 1718
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 QY 1719 AGATGGGCTTCAATTAGATGGCGAAGGAGGACACCGCCAGTGTCCAAAAAGGCTGCT 1778
 Db 152 AGATGGGCTTCAATTAGATGGCGAAGGAGGACACCGCCAGTGTCCAAAAAGGCTGCT 93
 QY 1779 CTCCTCCACCTGGCCACACCTGTGGGCGACCGGAGCTTCCCTGTGGCATGAACCCAC 1838
 Db 92 CTCCTCCACCTGGCCACACCTGTGGGCGACCGGAGCTTCCCTGTGGCATGAACCCAC 33
 QY 1839 GGGGTATTAAATTTATGAATCAGCTGAAAAAAA 1870
 Db 32 GGGGTATTAAATTTATGAATCAGCTGAAAAAAA 1

RESULT 2
 AI307814/c
 LOCUS
 DEFINITION
 tb28d11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2055669 3'
 similar to TR:Q61830 Q61830 MANNOSE RECEPTOR, C TYPE 1 PRECURSOR ;,
 mRNA sequence.

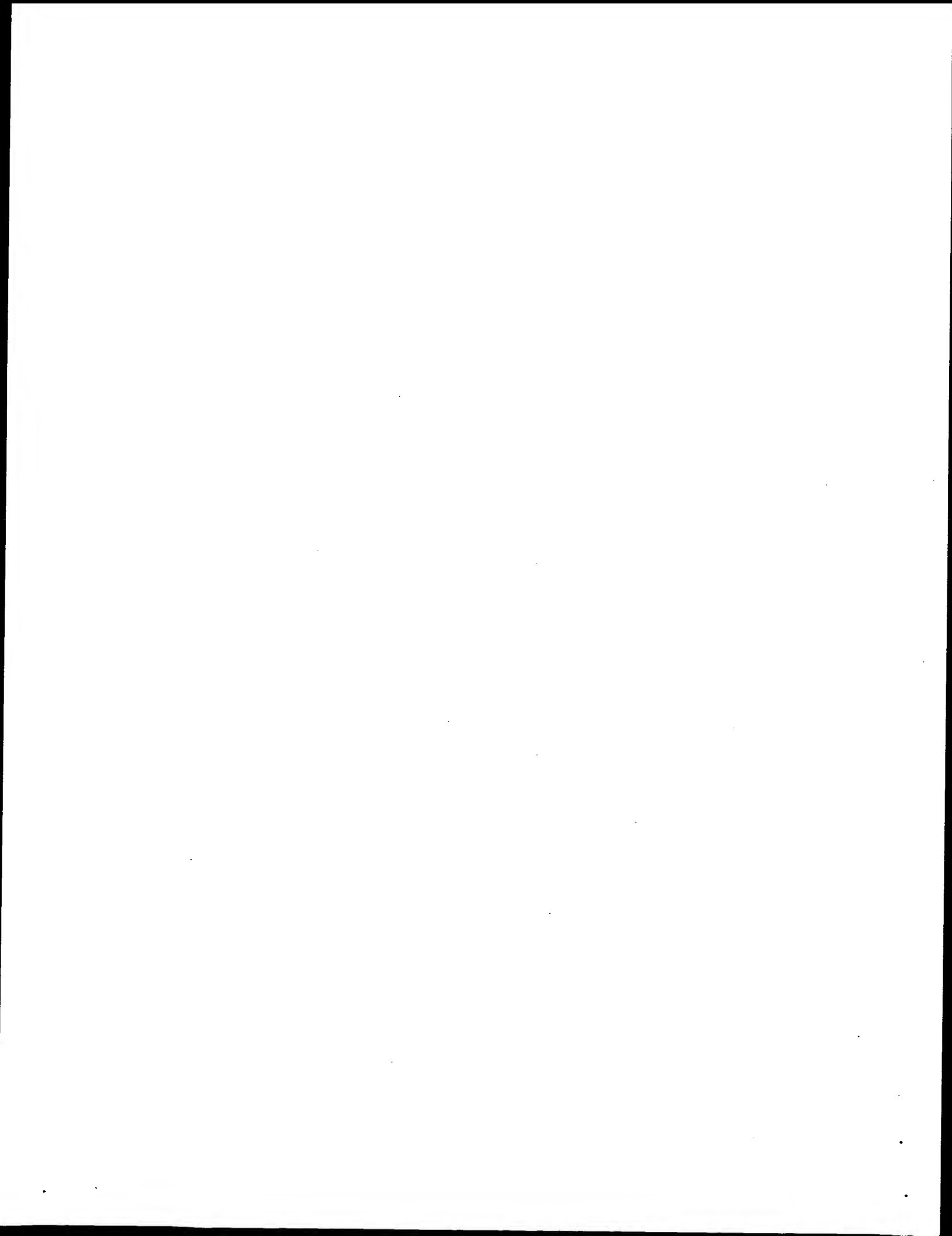
ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AI307814 617 bp mRNA linear EST 08-APR-1999
 tb28d11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2055669 3'
 similar to TR:Q61830 Q61830 MANNOSE RECEPTOR, C TYPE 1 PRECURSOR ;,
 mRNA sequence.
 AI307814 1 GI:4002418
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 617)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
 Insert Length: 725 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 451.

FEATURES
 source

1..617
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 /tissue_type="2 pooled tumors (clear cell type)"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site:1: Not 1; Site:2: Eco RI;
 Plasmid DNA from the normalized library NCI_CGAP_Kid5 was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (cloneIDs 1323912-1325831, 1471368-1472903 and
 1492104-1493255). Subtraction by Bento Soares and M.
 Fatima Bonaldo."
 BASE COUNT 118 a 182 c 179 g 138 t
 ORIGIN

Query Match 27.3%; Score 512; DB 9; Length 617;
 Best Local Similarity 100.0%; Pred. No. 1.8e-161;
 Matches 512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1359 GGGTTGGCACTGGCTGAGCTGAGGCTTCAGCTGCTCACTGAACGACGACCGC 1418
 Db 512 GGGTTGGCACTGGCTGAGCTGAGGCTTCAGCTGCTCACTGAACGACGACCGC 453



241 CTGGCTCAGCCAGGCAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCGTCCGGCCTG 300

38

RESULT 39.
HSU22027/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

HSU22027 7215 bp DNA linear PRI 01-JAN-1997
Human cytochrome P450 (CYP2A6V2) gene, complete cds.

U22027 GI:1008461
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 7215)
Fernandez-Salguero,P., Hoffman,S.M., Cholerton,S., Mohrenweiser,H.,
Raunio,H., Rautio,A., Pelkonen,O., Huang,J.D., Evans,W.E.,
Idle,J.R. et al.
A genetic polymorphism in coumarin 7-hydroxylation: sequence of the
human CYP2A genes and identification of variant CYP2A6 alleles
Am. J. Hum. Genet. 57 (3), 651-660 (1995)
95397851
7668294
2 (bases 1 to 7215)
Fernandez-Salguero,P.
Direct Submission
Submitted (01-MAR-1995) Pedro Fernandez-Salguero, National
Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20894, USA
Location/Qualifiers
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791..6489
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RSTHGANIPTPLFTSVNVIISVFGDRFDKDEFLSLRMMLGIFQFTSTGQ
LYEMFSSVMKHLPGQQAFQOLLOGLEDTAKVHEHQRIIDPNSPRDFDSFLIRMQ
EEKNPTEFYLLNMAMTNLNIAGTETVTYLHYFLLMKHPFEAKVHEEIDRV
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PMLGSVLRDLFTSNPRDFNPQHFELKEKGQFKRDFAVPFSIRKRNCFGEGRLAMELF
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/number=4
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5577..5718
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FEATURES
source

5'UTR
gene
CDS
exon
exon
exon
exon
exon
exon
exon
exon
exon
exon
3'UTR

BASE COUNT
BRIGIN

1646 a 2196 c 1746 g 1627 t

